

GenCore version 5.1.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:01 ; Search time 57.3529 Seconds
(without alignments)
196.114 Million cell updates/sec

Title: US-09-016-061-6
Perfect score: 612
Sequence: 1 EVQLVESGGGLVKGPSRLRL.....RHNYGSFAYWGQGLTVTVSA 117

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 9613422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	494.5	80.8	254	B31790	Ig heavy chain V r
2	486.5	79.5	121	H27888	Ig heavy chain V r
3	486	79.4	138	S09258	Ig heavy chain V r
4	483.5	79.0	112	A27889	Ig heavy chain V r
5	480.5	78.5	548	S38864	Ig epsilon chain C
6	479.5	78.3	113	S26468	Ig heavy chain V r
7	477.5	78.0	121	D27888	Ig heavy chain V r
8	476.5	77.9	123	G27888	Ig heavy chain V r
9	476	77.8	122	E27888	Ig heavy chain V r
10	472.5	77.2	119	F27888	Ig heavy chain V r
11	471	77.0	120	S55336	Ig heavy chain V r
12	467	76.3	111	PH1007	Ig heavy chain V r
13	466	76.1	117	HVMS34	Ig heavy chain V r
14	466	76.1	118	S20641	Ig heavy chain pre
15	466	76.1	119	S31108	Ig heavy chain V r
16	464.5	75.9	119	D27889	Ig heavy chain - h
17	463.5	75.7	123	S63597	Ig heavy chain V r
18	462	75.5	117	S78486	Ig heavy chain V r
19	462	75.5	119	C36005	Ig heavy chain V r
20	462	75.5	119	S31107	Ig heavy chain V r
21	462	75.5	120	S55337	Ig heavy chain - h
22	462	75.5	140	S31588	Ig heavy chain V r
23	461.5	75.4	128	PH0095	Ig heavy chain V r
24	461	75.3	117	PL0249	Ig kappa chain V r
25	461	75.3	120	S55339	Ig heavy chain V r
26	461	75.3	140	S31686	Ig heavy chain V r
27	461	75.3	152	B26471	Ig heavy chain pre
28	460	75.2	124	C27888	Ig heavy chain V r
29	459.5	75.1	118	PH0096	Ig heavy chain V r

30	459.5	75.1	118	2	PH0097	Ig heavy chain V r
31	459.5	75.1	121	2	I27887	Ig heavy chain V r
32	458	74.8	124	2	I27888	Ig heavy chain V r
33	457.5	74.8	128	2	PH0094	Ig heavy chain V r
34	456	74.5	142	2	C34903	Ig heavy chain pre
35	454.5	74.3	139	2	S38808	Ig heavy chain - m
36	454	74.2	117	2	PL0252	Ig heavy chain V r
37	453	74.0	119	2	D36005	Ig heavy chain V r
38	453	74.0	120	2	S55338	Ig heavy chain V r
39	453	74.0	123	2	S31114	Ig heavy chain - h
40	453	74.0	127	2	S38489	Ig heavy chain - h
41	453	74.0	138	2	S31666	Ig heavy chain V r
42	452.5	73.9	120	2	S48798	Ig heavy chain V r
43	451.5	73.8	121	2	S55540	Ig heavy chain V r
44	451	73.7	111	2	S40090	Ig heavy chain - m
45	450	73.5	121	2	S19666	Ig heavy chain V r

ALIGNMENTS

RESULT 1
B31790
Ig heavy chain V region (17/9) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 23-May-1997
C:Accession: B31790
R:Schulze-Gahmen, U.; Rini, J.M.; Arevalo, J.; Stura, E.A.; Kenten, J.H.; Wilson, I.A
J. Biol. Chem. 263, 17100-17105, 1988
A:Title: Preliminary crystallographic data, primary sequence, and binding data for an
A:Reference number: A92686; MUID:89034213; PMID:3182835
A:Accession: B31790
A:Molecule type: mRNA
A:Residues: 1-254 <SCH>
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 80.8%; Score 494.5; DB 2; Length 254;
Best Local Similarity 80.0%; Pred. No. 8.6e-39;
Matches 96; Conservative 10; Mismatches 11; Indels 3; Gaps 1;

Qy	1	EVQLVESGGGLVKGPSRLRLSCAASGFAFSSYDMGVRQIPEKRLWEAKVSGGGSTYY	60
Db	1	EVQLVESGGDLVKGPGSLKSCAASGFSYSGMSWVRQTPDKRLWEVATISNGGCTYY	60
Qy	61	LDTVQGRFTISRDNKNTLYLQMSSLESDTAMYCA---RHNYGSFAYWGQGLTVTVSA	117
Db	61	PDSVKGRFTISRDNKNTLYLQMSSLSKSDSAMYCARRERYDENGFAFWGQGLTVTVSA	120

RESULT 2
H27888
Ig heavy chain V region (H37-40) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996
C:Accession: H27888
R:Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
EMBO J. 5, 1577-1587, 1986
A:Title: Structural and functional implications of a restricted antibody response to
A:Reference number: A91043; MUID:86300658; PMID:2427335
A:Accession: H27888
A:Molecule type: DNA
A:Residues: 1-121 <CAT>
A:Experimental source: strain Balb/c
A:Note: This sequence was determined from the germline gene
C:Comment: This chain was isolated from a hybridoma protein that binds influenza viru
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 79.5%; Score 486.5; DB 2; Length 121;
Best Local Similarity 81.0%; Pred. No. 2.2e-38;

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Matches 98: Conservative 4: Mismatches 14: Indels 5: Gaps 2:
QY 1 EVLVESGGGLVKPGRSLRLSCAASGFAFSYDMSWVRQIQPEKLEWAKVSSGGSTYY 60
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 EVLVESGGGLVPGGSLNLSCAASGFTFSYAMSWVRQSPKLEWVAEISSGGSTYY 60

QY 61 LDTVQGRFTISRDNKNTLYLQMSLSNSEDAMYICARHN--YGS---FAYWGOGTLTV 115
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 PDTVTGFTISRDNKNTLYLEMSLSRSEDAMYICAREEGYIGSSDAMDYWGOGTLTV 120

QY 116 S 116
      |
Db 121 S 121

RESULT 3
S09258
Ig heavy chain V region precursor - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 23-Jul-1999
C:Accession: S09258
R:Hamada, H.; Maezawa, K.; Tsuruo, T.
Nucleic Acids Res. 18, 1900, 1990
A:Title: Nucleotide sequences of the variable regions of a mouse monoclonal anti-
A:Reference number: S09258; MUID:90245594; PMID:2110659
A:Accession: S09258
A:Molecule type: DNA
A:Residues: 1-138 <HAM>
A:Cross-references: EMBL:X51719; NID:g53207; PIDN:CAA36012.1; PID:g297545
C:Genetics:
A:Introns: 16/1
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 79.4%; Score 486; DB 2: Length 138;
Best Local Similarity 81.5%; Pred. No. 2.8e-38;
Matches 97: Conservative 8: Mismatches 12: Indels 2: Gaps 2:
QY 1 EVLVESGGGLVKPGRSLRLSCAASGFAFSYDMSWVRQIQPEKLEWAKVSSGGSTYY 60
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 20 EVILVESGGGLVKPGGSLKSLCAASGFTFSYTWMSVRQTEKLEWVATISSGGNTYY 79

QY 61 LDTVQGRFTISRDNKNTLYLQMSLSNSEDAMYICAR-HNYGS-FAYWGOGTLTVTSA 117
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 80 PDSYKGRFTISRDNKNNLYLQMSLSRSEDALYICARYRYEAFWAFSGOGTLTVTSA 138

RESULT 4
A27889
Ig heavy chain V region (HIC5-401) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996
C:Accession: A27889
R:Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
EMBO J. 5, 1577-1587, 1986
A:Title: Structural and functional implications of a restricted antibody respon
A:Reference number: A91043; MUID:86300658; PMID:2427335
A:Accession: A27889
A:Molecule type: DNA
A:Residues: 1-112 <CAT>
A:Experimental source: strain Balb/c
C:Note: This sequence was determined from the germline gene
C:Comment: This chain was isolated from a hybridoma protein that binds influen
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:12-95/Domain: immunoglobulin homology <IMM>

Query Match 79.0%; Score 483 5; DB 2: Length 112;
Best Local Similarity 83.2%; Pred. No. 3.8e-38;
Matches 94: Conservative 5: Mismatches 13: Indels 1: Gaps 1;
QY 4 LVESSGGGLVKPGRSLRLSCAASGFAFSYDMSWVRQIQPEKLEWAKVSSGGSTYYLDT 63

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C;Species: Mus musculus (house mouse)
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996
C;Accession: D27888
R;Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
EMBO J. 5, 1577-1587, 1986
A;Title: Structural and functional implications of a restricted antibody response to a
A;Reference number: A91043; MUID:86300658; PMID:2427335
A;Accession: D27888
A;Molecule type: DNA
A;Residues: 1-121 <CAT>
A;Experimental source: strain Balb/c
A;Note: This sequence was determined from the germline gene
C;Comment: This chain was isolated from a hybridoma protein that binds influenza virus H
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 78.0%; Score 477.5; DB 2; Length 121;
Best Local Similarity 77.7%; Pred. No. 1.5e-37;
Matches 94; Conservative 8; Mismatches 14; Indels 5; Gaps 1;
QY 1 EVQLVESGGGLVPGKSLRLSCAASGFAFSSYDMVSWVRQIPEKRLWAKVSSGGSTYY 60
DB 1 EVNLVESGGDLVPGGSLKLSCAASGFAFSSYDMVSWVRQSPKRLWVATISSGGSYTDY 60
QY 61 LDTVQGRFTISRDNKNTLYLQMSLSNSEDAMYCARHNYGS-----FAYWGQGLTVV 115
DB 61 PDSVKGRFTISRDNKNTLYLQMSLSNSEDAMYCARQDYNYDDFTYWGQGLTVV 120
QY 116 S 116
DB 121 S 121

RESULT 8
G27888
Ig heavy chain V region (H28-A2) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996
C;Accession: G27888
R;Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
EMBO J. 5, 1577-1587, 1986
A;Title: Structural and functional implications of a restricted antibody response to a
A;Reference number: A91043; MUID:86300658; PMID:2427335
A;Accession: G27888
A;Molecule type: DNA
A;Residues: 1-123 <CAT>
A;Experimental source: strain Balb/c
A;Note: This sequence was determined from the germline gene
C;Comment: This chain was isolated from a hybridoma protein that binds influenza virus H
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 77.9%; Score 476.5; DB 2; Length 123;
Best Local Similarity 78.9%; Pred. No. 1.9e-37;
Matches 97; Conservative 4; Mismatches 15; Indels 7; Gaps 2;
QY 1 EVQLVESGGGLVPGKSLRLSCAASGFAFSSYDMVSWVRQIPEKRLWAKVSSGGSTYY 60
DB 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSSYAMVSWVRQSPKRLWVATISSGGSTYY 60
QY 61 LDTVQGRFTISRDNKNTLYLQMSLSNSEDAMYCAR----HNYGS---FAYWGQGLTV 113
DB 61 PDIIVTGRFTISRDNKNTLYLQMSLSNSEDAMYCARQDYNYDDFTYWGQGLTV 120
QY 114 TVS 116
DB 121 TVS 123

RESULT 9
E27888
Ig heavy chain V region pe20 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 23-Jul-1999

Ig heavy chain V region (H35-C6) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996
C;Accession: E27888
R;Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
EMBO J. 5, 1577-1587, 1986
A;Title: Structural and functional implications of a restricted antibody response to
A;Reference number: A91043; MUID:86300658; PMID:2427335
A;Accession: E27888
A;Molecule type: DNA
A;Residues: 1-122 <CAT>
A;Experimental source: strain Balb/c
A;Note: This sequence was determined from the germline gene
C;Comment: This chain was isolated from a hybridoma protein that binds influenza viru
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 77.8%; Score 476; DB 2; Length 122;
Best Local Similarity 77.0%; Pred. No. 2.1e-37;
Matches 94; Conservative 8; Mismatches 14; Indels 6; Gaps 2;
QY 1 EVQLVESGGGLVPGKSLRLSCAASGFAFSSYDMVSWVRQIPEKRLWAKVSSGGSTYY 60
DB 1 DVKLVESGGGLVPGGSLKLSCAASGFTFSSYTMVSWVRQTPKRLWVATISSGGSTYY 60
QY 61 LDTVQGRFTISRDNKNTLYLQMSLSNSEDAMYCAR----HNYGSFA--YWGQGLTV 114
DB 61 PDSVKGRFTISRDNKNTLYLQMSLSKSEDAMYCTRGEGYRYYDDYAMDYWGQGLTV 120
QY 115 VS 116
DB 121 VS 122

RESULT 10
F27888
Ig heavy chain V region (H158-89H4) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996
C;Accession: F27888
R;Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
EMBO J. 5, 1577-1587, 1986
A;Title: Structural and functional implications of a restricted antibody response to
A;Reference number: A91043; MUID:86300658; PMID:2427335
A;Accession: F27888
A;Molecule type: DNA
A;Residues: 1-119 <CAT>
A;Experimental source: strain Balb/c
A;Note: This sequence was determined from the germline gene
C;Comment: This chain was isolated from a hybridoma protein that binds influenza viru
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 77.2%; Score 472.5; DB 2; Length 119;
Best Local Similarity 79.0%; Pred. No. 4.3e-37;
Matches 94; Conservative 7; Mismatches 15; Indels 3; Gaps 2;
QY 1 EVQLVESGGGLVPGKSLRLSCAASGFAFSSYDMVSWVRQIPEKRLWAKVSSGGSTYY 60
DB 1 DVKLVESGGGLVPGGSLKLSCAASGFTFSSYTMVSWVRQTPKRLWVATISSGGSTYY 60
QY 61 LDTVQGRFTISRDNKNTLYLQMSLSNSEDAMYCAR--HNYGSFA--YWGQGLTV 116
DB 61 PDSVKGRFTISRDNKNTLYLQMSLSKSEDAMYCYPRGETYYDYAMDYWGQGLTV 119

RESULT 11
S55536
Ig heavy chain V region pe20 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 23-Jul-1999

A:Residues: 1-117 <LEV>
A:Experimental source: strain BALB/cJ
A>Note: this sequence belongs to the VH183 subfamily
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence; #status predicted <SIG>
F:20-117/Product: Ig heavy chain V region (345) #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>
F:41-115/Disulfide bonds: #status predicted

Query Match 76.1%; Score 466; DB 1; Length 117;
Best Local Similarity 91.8%; Pred. No. 1.7e-36;
Matches 90; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVPGKSRISLCAASGFAFSYDSMSWVRQIPEKRLWAKVSSGGSTYY 60
||||| ||||| ||||| ||||| ||||| ||||| ||||| : |||||
Db 20 EVQLVESGGGLVPGGSLKLSCAASGFAFSYDSMSWVRQIPEKRLWAVISSGGSTYY 79
||||| ||||| ||||| ||||| ||||| ||||| ||||| : |||||

Qy 61 LDTVGQRFTISRDNKNTLYLQMSSLNSEDAMTYICAR 98
||| : ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 80 PDTVKGRTISRDNKNTLYLQMSSLKSEDTAMYICAR 117
||| : ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 14
S20641
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C:Accession: S20641
R:Losman, M.; Fasy, T.M.; Novick, K.E.; Monestier, M.
submitted to the EMBL Data Library, February 1992
A:Description: Relationships among antinuclear antibodies from autoimmune MRL mice re ce
A:Reference number: S20639
A:Accession: S20641
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-118 <LOS>
A:Cross-references: EMBL:X65003; NID:g52602; PIDN:CAA46136.1; PID:g52603
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 76.1%; Score 466; DB 2; Length 118;
Best Local Similarity 76.3%; Pred. No. 1.7e-36;
Matches 90; Conservative 10; Mismatches 16; Indels 2; Gaps 1;

Qy 1 EVQLVESGGGLVPGKSRISLCAASGFAFSYDSMSWVRQIPEKRLWAKVSSGGSTYY 60
||||| ||||| ||||| ||||| ||||| ||||| ||||| : |||||
Db 1 EVLVESGGGLVPGGSLKLSCAASGFTFSNYIMFWRQTPAKRLEWVANISSGGNTYY 60
||||| ||||| ||||| ||||| ||||| ||||| ||||| : |||||

Qy 61 LDTVGQRFTISRDNKNTLYLQMSSLNSEDAMTYICARHNYGSFA--YWGOGTLTVTS 116
||| : ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 PDSVKGRFTISRDNVNMLYLQMSSLKSEDTAMYICARRAYSNALDFWGGTSTVTS 118
||| : ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 15
S31108
Ig heavy chain - human
C:Species: Homo sapiens (man)
C:Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C:Accession: S31108
R:Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuur
Eur J Immunol. 22, 247-251, 1992
A>Title: Restricted utilization of germ-line VH(3) genes and short diverse third comp
A:Reference number: S31104; MUID:92111633; PMID:I730252
A:Accession: S31108
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-119 <RAA>
A:Cross-references: EMBL:X62956
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

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Query Match      76.1%; Score 466; DB 2; Length 119;
Best Local Similarity 75.6%; Pred. No. 1.7e-36;
Matches 90; Conservative 12; Mismatches 15; Indels 2; Gaps 1;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGFAFSSYVDMSWVRQIPEKRLIEWAKVSSGGSTYY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFAFSSYVDMSWVRQIPEKRLIEWAKVSSGGSTYY 60

Qy 61 LDTVQGRFTISRDNKNTLYLQMSSLNSEDAMYCA--RHNYGSFAYWGQGTFLVTVSA 117
Db 61 ADSVKGRFTISRDNKNTLYLQMSSLNSEDAMYCA--RHNYGSFAYWGQGTFLVTVSS 119
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Search completed: November 18, 2002, 17:46:58
Job time : 58.3529 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:00 ; Search time 28.6765 Seconds
(without alignments)
169.223 Million cell updates/sec

Title: us-09-016-061-6

Perfect score: 612

Sequence: 1 EVQLVESGGGLVKPGKSLRL.....RHNYGSFAYWGQGLTVTVSA 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	466	76.1	117	1 HV55_MOUSE	P18526 mus musculus
2	439	71.7	117	1 HV34_MOUSE	P18525 mus musculus
3	438.5	71.7	136	1 HV16_MOUSE	P01783 mus musculus
4	433.5	70.8	122	1 HV3G_HUMAN	P01768 homo sapien
5	422.5	69.0	97	1 HV56_MOUSE	P18527 mus musculus
6	419	68.5	98	1 HV57_MOUSE	P18528 mus musculus
7	417.5	68.2	116	1 HV3T_HUMAN	P01781 homo sapien
8	412	67.3	117	1 HV53_MOUSE	P18524 mus musculus
9	408.5	66.7	119	1 HV37_MOUSE	P01807 mus musculus
10	408.5	66.7	119	1 HV40_MOUSE	P01810 mus musculus
11	408	66.7	117	1 HV58_MOUSE	P18529 mus musculus
12	407	66.5	121	1 HV3J_HUMAN	P01771 homo sapien
13	406.5	66.4	114	1 HV3B_HUMAN	P01763 homo sapien
14	403	65.8	117	1 HV3C_HUMAN	P01764 homo sapien
15	403	65.8	119	1 HV3I_HUMAN	P01770 homo sapien
16	401.5	65.6	126	1 HV3K_HUMAN	P01772 homo sapien
17	397.5	65.0	122	1 HV3L_HUMAN	P01769 homo sapien
18	393	64.2	117	1 HV59_MOUSE	P18530 mus musculus
19	389.5	63.6	122	1 HV3A_HUMAN	P01762 homo sapien
20	387	63.2	115	1 HV32_MOUSE	P01801 mus musculus
21	387	63.2	117	1 HV02_CANFA	P01785 canis famill
22	385	62.9	119	1 HV3L_HUMAN	P01773 homo sapien
23	384	62.7	120	1 HV3E_HUMAN	P01766 homo sapien
24	383.5	62.7	120	1 HV3U_HUMAN	P01782 homo sapien
25	382	62.4	113	1 HV30_MOUSE	P01799 mus musculus
26	381	62.3	115	1 HV3F_HUMAN	P01767 homo sapien
27	380.5	62.2	119	1 HV3M_HUMAN	P01774 homo sapien
28	379.5	62.0	119	1 HV38_MOUSE	P01808 mus musculus
29	379	61.9	115	1 HV33_MOUSE	P01802 mus musculus
30	378.5	61.8	114	1 HV01_CANFA	P01784 canis famill
31	378.5	61.8	116	1 HV05_CARAU	P19181 carassius a
32	377	61.6	113	1 HV27_MOUSE	P01796 mus musculus
33	375	61.3	118	1 HV39_MOUSE	P01809 mus musculus

ALIGNMENTS

RESULT 1

ID	HV55_MOUSE	STANDARD;	PRT;	117 AA.
AC	P18526;			
DT	01-NOV-1990 (Rel. 16, Created)			
DT	01-NOV-1990 (Rel. 16, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	Ig heavy chain V region 345 precursor.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BALE/CJ;			
RX	MEDLINE=89279149; PubMed=249654;			
RA	Levy N.S., Mallipiero U.V., Lebecque S.G., Gearhart P.J.;			
RT	"Early onset of somatic mutation in immunoglobulin VH genes during			
RT	the primary immune response.";			
RL	J. Exp. Med. 169:2007-2019(1989).			
CC	-I- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.			
DR	PIR; JT0502; HVMS34.			
DR	HSSP; P01810; 2FBJ.			
DR	InterPro; IPR003006; Ig_MHC.			
DR	InterPro; IPR003596; Ig_V.			
DR	Pfam; PF00047; Ig; 1.			
DR	SMART; SM00406; IGV; 1.			
KW	Immunoglobulin V region; Signal.			
FT	SIGNAL 1 19			
FT	CHAIN 20 117			
FT	DOMAIN 20 49			
FT	DOMAIN 50 54			
FT	DOMAIN 55 68			
FT	DOMAIN 69 85			
FT	DOMAIN 86 117			
FT	DISULFID 41 115			
FT	NON_TER 117 117			
SQ	SEQUENCE 117 AA; 12902 MW; 49380E4627ACA99A CRC64;			

Query Match 76.1%; Score 466; DB 1; Length 117;
Best Local Similarity 91.8%; Pred. No. 1.le-41;
Matches 90; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVKPGKSLRLSCAASGFAFSYDMSVSRQIPKRLKLEWAKVSSGGSTYY 60

Db 20 EVQLVESGGGLVKPGKSLKLSAASGFAFSYDMSVSRQIPKRLKLEWAKVSSGGSTYY 79

Qy 61 LDTVOGRFTISRDNKAKNPLYLQMSLSNSEDAMYYCAR 98

Db 80 PDTVKGRFTISRDNKAKNPLYLQMSLSKSEDAMYYCAR 117

RESULT 2

HV54_MOUSE

ID HV54_MOUSE STANDARD; PRT; 117 AA.

AC P18525;

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Nature 265:299-304(1977).
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DR EMBL: J00522; AAD15290.1; -.
DR PIR: A02066; GIMS21.
DR HSSP: P01772; 2FB4.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT NON_TER 1 1
FT SIGNAL <1 16
FT CHAIN 17 136 IG HEAVY CHAIN V REGION MOPC 21.
FT DOMAIN 115 119 D SEGMENT.
FT DOMAIN 120 136 JH4 SEGMENT.
FT DISULFID 38 112
FT CONFLICT 75 78 HYAD -> DYAH (IN REF. 2).
FT CONFLICT 89 90 DN -> ND (IN REF. 2).
FT CONFLICT 115 115 W -> H (IN REF. 2).
FT CONFLICT 120 120 Y -> W (IN REF. 2).
FT NON_TER 136 136
SQ SEQUENCE 136 AA; 2276A98DBDBF7016 CRC64;
Query Match 71.7%; Score 438.5; DB 1; Length 136;
Best Local Similarity 72.5%; Pred. No. 9.5e-39;
Matches 87; Conservative 12; Mismatches 18; Indels 3; Gaps 2;
QY 1 EVLVESGGGLVPGKRLRLSCAASGAFPSYMSWVRQIPKRLLEWAKVSSGGSTYY 60
:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 17 DVQLVESGGGLVPGGSRKLSCAASGFTFSFGHHVWVQAPEKGLEWAVYISSGSSLHY 76
QY 61 LDTVQGRFTISRDNAKNTLYQLMSSLNSETAMYYCAR--HNYGSEA--YVGQGTLTVSA 117
:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 77 ADTVKGRFTISRDNPKNLTFLQMTLSRSDTAMYYCARGNYPYAMDYWGQGTSTVSS 136
-----
RESULT 4
HV3G_HUMAN STANDARD; PRT; 122 AA.
ID HV3G_HUMAN
AC P01768;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-III region CAM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
RP SEQUENCE.
RX MEDLINE=81013859; PubMed=6774332;
RA Lehman D.W., Putnam F.W.;
RT "Amino acid sequence of the variable region of a human mu chain:
RT location of a possible JH segment.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980).
CC -I- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM THE PLASMA OF A
CC PATIENT WITH MACROGLOBULINEMIA.
DR PIR: A02051; M3HUAM.
DR HSSP: P01772; 2FB4.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region.
FT MOD_RES 1 1
FT PYRROLIDONE CARBOXYLIC ACID.

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FT NON_TER 122 122
SQ SEQUENCE 122 AA; 13668 MW; A42D0F17D252F1C2 CRC64;

Query Match
Best Local Similarity 70.8%; Score 433.5; DB 1; Length 122;
Matches 81; Conservative 19; Mismatches 17; Indels 5; Gaps 1;

QY 1 EVQLVESGGGLVQPGSRSLRLSCAASGFAFSSYDMSWVRQIPEKRLIEWAKVSSGGSTYY 60
DB 1 QVELVESGGGVVZPGSRSLRLSCAASGFTFSNYAMHWVRQTPKRLIEWAVISYBGBBKYY 60
QY 61 LDTVQGRFTISRDNKNTLYLQMSLSNSEDATMYTCARH-----NYGSFAYWGQGLTVTV 115
DB 61 ABSVKGRTISRDNKNTLYLQMSLSNSEDATMYTCARH-----NYGSFAYWGQGLTVTV 120
QY 116 SA 117
DB 121 SS 122

RESULT 5
HV56_MOUSE
ID HV56_MOUSE STANDARD; PRT; 97 AA.
AC P18527;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 914.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP STRAIN=BALB/CJ;
RC MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response."
J. Exp. Med. 169:2007-2019(1989).
-CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH17183 SUBFAMILY.
DR PIR: J0504; HVMS91.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_V.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT NON_TER 97
SQ SEQUENCE 97 AA; 10661 MW; C23CB33FF55DA893 CRC64;

Query Match
Best Local Similarity 69.08; Score 422.5; DB 1; Length 97;
Matches 83; Conservative 6; Mismatches 8; Indels 1; Gaps 1;

QY 1 EVQLVESGGGLVQPGSRSLRLSCAASGFAFSSYDMSWVRQIPEKRLIEWAKVSSGGSTYY 60
DB 1 EVKLVESGGGLVQPGSGSLKLSCAASGFTFSYAMSWVRQTPKRLIEWASISS-GGSTYY 59
QY 61 LDTVQGRFTISRDNKNTLYLQMSLSNSEDATMYTCAR 98
DB 60 PDSVKGRFTISRDNARNILYLQMSLSRSEDATMYTCAR 97

RESULT 6
HV57_MOUSE
ID HV57_MOUSE STANDARD; PRT; 98 AA.
AC P18528;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 6.96.
OS Mus musculus (Mouse).
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RC MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response."
J. Exp. Med. 169:2007-2019(1989).
-CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH17183 SUBFAMILY.
DR PIR: J0501; HVMS96.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT NON_TER 98
SQ SEQUENCE 98 AA; 11007 MW; B8644F7F92FBF95B CRC64;

Query Match
Best Local Similarity 68.5%; Score 419; DB 1; Length 98;
Matches 81; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGSRSLRLSCAASGFAFSSYDMSWVRQIPEKRLIEWAKVSSGGSTYY 60
DB 1 EVQLVESGGGLVQPGSGSLKLSCAASGFTFSYMYVVRQTPKRLIEWATISDGGSTYY 60
QY 61 LDTVQGRFTISRDNKNTLYLQMSLSNSEDATMYTCAR 98
DB 61 PDSVKGRFTISRDNKNTLYLQMSLSKSEDATMYTCAR 98

RESULT 7
HV3T_HUMAN
ID HV3T_HUMAN STANDARD; PRT; 116 AA.
AC P01781;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ig heavy chain V-III region GAL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=75059123; PubMed=4803843;
RA Watanabe S., Barnikol H.U., Horn J., Bertram J., Hilschmann N.;
RT "The primary structure of a monoclonal IgM-immunoglobulin
(macroglobulin Gal.), II: the amino acid sequence of the H-chain (mu-
type), subgroup H III. Architecture of the complete IgM-molecule."
Hoppe-Seyler's Z. Physiol. Chem. 354:1505-1509(1973).
-CC -!- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM A WALDENSTROM'S
REVISION TO 28-33.
RA Hilschmann N.;
RL Submitted (JUN-1975) to the PIR data bank.
-CC -!- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM A WALDENSTROM'S
MACROGLOBULIN.
DR PIR: A02064; M3HUGL.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT NON_TER 116
SQ SEQUENCE 116 AA; 12730 MW; 2C67CA9AAAAA1282 CRC64;

Query Match
Best Local Similarity 68.2%; Score 417.5; DB 1; Length 116;
Matches 81; Conservative 4; Mismatches 13; Indels 0; Gaps 0;
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Matches 82; Conservative 10; Mismatches 23; Indels 1; Gaps 1;

QY 1 EVQLVESGGGLVQPGSRSLRLSCAASGFAFSSYDMSWVRQIPEKRLWVAKVSSGGSTYY 60
Db 1 EVQLVESGGDLVQPGSRSLRLSCAASGFBFBGLGWTWVRQAPGKGLGVANIKZBGSZBY 60

QY 61 LDTVGQRTISRDNKNTLYLQMSLSNSEDFTAMYYCAR-HNYGSFAYWGQGLTVTVS 116
Db 61 VDSVKGRTISRDNKNTLYLQMSLSNSEDFTALYYCAR-GWGGDYGQGLTVTVS 115

RESULT 8
HV53_MOUSE
ID HV53_MOUSE STANDARD; PRT; 117 AA.
AC P18524;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region RF precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebeque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RT the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH183 SUBFAMILY.
DR PIR; J0503; HVMSRF.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR Immunoglobulin V region;
DR NON_TER 117 AA; 12866 MW; 2CE3295F390F725B CRC64;
KW Immunoglobulin V region; Hybridoma; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION RF.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 66 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12866 MW; 2CE3295F390F725B CRC64;

Query Match 67.3%; Score 412; DB 1; Length 117;
Best Local Similarity 82.7%; Pred. No. 4.6e-36;
Matches 81; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGSRSLRLSCAASGFAFSSYDMSWVRQIPEKRLWVAKVSSGGSTYY 60
Db 20 DVKLVESGGGLVQLGSLKLSCAASGFTFSYMSVSWVRQTPKRLLELVAAINSGGSYY 79

QY 61 LDTVGQRTISRDNKNTLYLQMSLSNSEDFTAMYYCAR 98
Db 80 PDTVGRTISRDNKNTLYLQMSLSKSEDFTALYYCAR 117

RESULT 9
HV37_MOUSE
ID HV37_MOUSE STANDARD; PRT; 119 AA.
AC P01807;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region X44.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 1;
RP SEQUENCE.
RA Rao D.N., Rudikoff S., Krutzsch H., Potter M.;
RT "Structural evidence for independent joining region gene in
RT immunoglobulin heavy chains from anti-galactan myeloma proteins and
RT its potential role in generating diversity in
RT complementarity-determining regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894(1979).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGA MYELOMA PROTEIN
CC THAT BINDS GALACTAN.
DR PIR; A02077; AVMSX4.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR Immunoglobulin V region.
DR NON_TER 119 119
SQ SEQUENCE 119 AA; 13246 MW; BC34FC8F31CD41B3 CRC64;

Query Match 66.7%; Score 408.5; DB 1; Length 119;
Best Local Similarity 66.9%; Pred. No. 1.1e-35;
Matches 79; Conservative 15; Mismatches 23; Indels 1; Gaps 1;

QY 1 EVQLVESGGGLVQPGSRSLRLSCAASGFAFSSYDMSWVRQIPEKRLWVAKVSSGGSTYY 60
Db 1 EVKLLESGGGLVQPGSLKLSCAASGFDPSRYWMSVWRQAPGKGLWGEINPDSSTINY 60

QY 61 LDTVGQRTISRDNKNTLYLQMSLSNSEDFTAMYYCAR-HNYGSFAYWGQGLTVTVS 117
Db 61 TPCLKDKFTISRDNKNTLYLQMSKVRSEDFTALYYCARLHYGYAAYWGQGLTVTVS 118

RESULT 10
HV40_MOUSE
ID HV40_MOUSE STANDARD; PRT; 119 AA.
AC P01810;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region J539.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 1;
RP PRELIMINARY SEQUENCE.
RX MEDLINE=79223895; PubMed=111245;
RA Rao D.N., Rudikoff S., Krutzsch H., Potter M.;
RT "Structural evidence for independent joining region gene in
RT immunoglobulin heavy chains from anti-galactan myeloma proteins and
RT its potential role in generating diversity in
RT complementarity-determining regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894(1979).
RN 1;
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
RX MEDLINE=88217852; PubMed=3449853;
RA Suh S.W., Bhat T.N., Navia M.A., Cohen G.H., Rao D.N., Rudikoff S.,
RA Davies D.R.;
RT "The galactan-binding immunoglobulin Fab J539: an X-ray diffraction
RT study at 2.6-A resolution.";
RL Proteins 1:74-80(1986).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS GALACTAN.
DR PIR; A02080; AVMSJ5.
DR PDB; 2FBJ; 15-OCT-90.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.

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KW Immunoglobulin V region: 3D-structure.
FT NON_TER Y 119 119
FT STRAND 3 7
FT TURN 10 12
FT STRAND 14 15
FT TURN 14 15
FT STRAND 18 25
FT HELIX 29 31
FT STRAND 34 39
FT STRAND 41 42
FT TURN 41 42
FT STRAND 45 51
FT TURN 53 54
FT STRAND 58 60
FT TURN 62 67
FT STRAND 68 72
FT STRAND 78 83
FT HELIX 88 90
FT STRAND 92 100
FT TURN 101 103
FT STRAND 104 108
FT STRAND 112 116
SQ SEQUENCE 119 AA; 13240 MW; 577B4F1DB675C1F1 CRC64;

Query Match 66.7%; Score 408.5; DB 1; Length 119;
Best Local Similarity 66.9%; Pred. No. 1.1e-35;
Matches 79; Conservative 15; Mismatches 23; Indels 1; Gaps 1;

QY 1 EVQLVESGGGLVKPGKSLRLSCAASGFAFSSYDMWVRQIPEKRLWVAKVSSGGSTYY 60
DB 1 EVKLSEGGGLVQPGSLKSLSCAASGDFSKYWMWVRQAPKGLWIGTHPDSGTINY 60

QY 61 LDTVQGRFTISRDNKNTLYLQMSLSNSEDYAMYICAR-HNYGSFAYWGQGLTVTVA 117
DB 61 TPSLKDRFTISRDNKNTLYLQMSKVRSEPTALYICARLHYGYNAYWGQGLTVTVA 118

RESULT 11
HV58_MOUSE
ID HV58_MOUSE STANDARD; PRT; 117 AA.
AC P18529;
RX MEDLINE=89279149; PubMed=2499654;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 5-76 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; JTO506; HYMS57.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 5-76.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12991 MW; 93A04782B78B8FA0 CRC64;

Immunoglobulin V region: 3D-structure.
FT NON_TER Y 119 119
FT STRAND 3 7
FT TURN 10 12
FT STRAND 14 15
FT TURN 14 15
FT STRAND 18 25
FT HELIX 29 31
FT STRAND 34 39
FT STRAND 41 42
FT TURN 41 42
FT STRAND 45 51
FT TURN 53 54
FT STRAND 58 60
FT TURN 62 67
FT STRAND 68 72
FT STRAND 78 83
FT HELIX 88 90
FT STRAND 92 100
FT TURN 101 103
FT STRAND 104 108
FT STRAND 112 116
SQ SEQUENCE 119 AA; 13240 MW; 577B4F1DB675C1F1 CRC64;

Query Match 66.7%; Score 408.5; DB 1; Length 119;
Best Local Similarity 66.9%; Pred. No. 1.1e-35;
Matches 79; Conservative 15; Mismatches 23; Indels 1; Gaps 1;

QY 1 EVQLVESGGGLVKPGKSLRLSCAASGFAFSSYDMWVRQIPEKRLWVAKVSSGGSTYY 60
DB 1 EVKLSEGGGLVQPGSLKSLSCAASGDFSKYWMWVRQAPKGLWIGTHPDSGTINY 60

QY 61 LDTVQGRFTISRDNKNTLYLQMSLSNSEDYAMYICAR-HNYGSFAYWGQGLTVTVA 117
DB 61 TPSLKDRFTISRDNKNTLYLQMSKVRSEPTALYICARLHYGYNAYWGQGLTVTVA 118

RESULT 11
HV58_MOUSE
ID HV58_MOUSE STANDARD; PRT; 117 AA.
AC P18529;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; JTO506; HYMS57.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 5-76.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12991 MW; 93A04782B78B8FA0 CRC64;

Immunoglobulin V region: 3D-structure.
FT NON_TER Y 119 119
FT STRAND 3 7
FT TURN 10 12
FT STRAND 14 15
FT TURN 14 15
FT STRAND 18 25
FT HELIX 29 31
FT STRAND 34 39
FT STRAND 41 42
FT TURN 41 42
FT STRAND 45 51
FT TURN 53 54
FT STRAND 58 60
FT TURN 62 67
FT STRAND 68 72
FT STRAND 78 83
FT HELIX 88 90
FT STRAND 92 100
FT TURN 101 103
FT STRAND 104 108
FT STRAND 112 116
SQ SEQUENCE 119 AA; 13240 MW; 577B4F1DB675C1F1 CRC64;

Query Match 66.7%; Score 408.5; DB 1; Length 117;
Best Local Similarity 80.6%; Pred. No. 1.2e-35;
Matches 79; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVKPGKSLRLSCAASGFAFSSYDMWVRQIPEKRLWVAKVSSGGSTYY 60
DB 20 EVHLVESGGGLVKPGSLKSLSCVSGFTFNKYAMWVRQTPKRLWVATISSGLTYTY 79

QY 61 LDTVQGRFTISRDNKNTLYLQMSLSNSEDYAMYICAR 98
DB 80 PDSVKGRFTISRDNAGNTLYLQMSLSRSEDYAMYICAR 117

RESULT 12
HV3J_HUMAN
ID HV3J_HUMAN STANDARD; PRT; 121 AA.
AC P01771;
RX MEDLINE=79124695; PubMed=420800;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-III region HIL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX Chiu Y.-Y.H., Lopez de Castro J.A., Poljak R.J.;
RT "Amino acid sequence of the VH region of human myeloma
cryoimmunoglobulin IgG HIL.";
RL Biochemistry 18:553-560(1979).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
PROTEIN.
DR PIR; A02054; GLHUHL.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
KW Immunoglobulin V region.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT NON_TER 121 121
SQ SEQUENCE 121 AA; 13566 MW; 480FC53610EF5DAB CRC64;

Query Match 66.5%; Score 407; DB 1; Length 121;
Best Local Similarity 64.5%; Pred. No. 1.6e-35;
Matches 78; Conservative 17; Mismatches 22; Indels 4; Gaps 1;

QY 1 EVQLVESGGGLVKPGKSLRLSCAASGFAFSSYDMWVRQIPEKRLWVAKVSSGGSTYY 60
DB 1 QVKLVAGGGVQVQPSRLSCIASGFTFSNGMHVWRQAPKGLWVAVIYNGSRYY 60

QY 61 LDTVQGRFTISRDNKNTLYLQMSLSNSEDYAMYICARH---NYGSFAYWGQGLTVTVS 116
DB 61 GDSVKGRFTISRDNKNTLYLQMSLSRSEDYAVYICARDPDLITAFSDYWGQGLTVTVS 120

QY 117 A 117
DB 121 S 121

RESULT 13
HV3B_HUMAN
ID HV3B_HUMAN STANDARD; PRT; 114 AA.
AC P01763;
RX MEDLINE=79124695; PubMed=420800;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-III region WEA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```


DR	SMART; SM00406; IGV: 1.
KW	Immunoglobulin V region; Signal.
FT	SIGNAL 1 19
FT	CHAIN 20 117 IG HEAVY CHAIN V-III REGION VH26.
FT	NON_TER 117 117
SEQ	SEQUENCE 117 AA; 12582 MW; EB26733FLA3CB0F1 CRC64;
Query Match 65.8%; Score 403; DB 1; Length 117;	
Best Local Similarity 77.6%; Pred. No. 3.9e-35;	
Matches 76; Conservative 11; Mismatches 11; Indels 0; Gaps	
Qy	1 EVOLVESGGGLVKGRSLRLSCAASGFAFSFYDMSVWRQIPEKRLWEAKVSSGGGSTYY 60
Dd	20 EQVLSEGGGLVPGGSURLSCAASGFFTSFYAMSWSVRQAPGKLEWVAISGSGGSTYY 79
Qy	61 LDTVGRTTISRDNKNTLYLQMNSLNSEDATMYCYCAR 98
Dd	80 GDSVKGRTTISRDNKNTLYLQMNSLRADETAYVCAC 117
RESULT 15	
HV3I_HUMAN	
ID	HV3I_HUMAN STANDARD; PRT; 119 AA.
AC	P01770;
DT	21-JUL-1986 (Rel. 01, Created)
DT	21-JUL-1986 (Rel. 01, Last sequence update)
DT	15-JUL-1999 (Rel. 38, Last annotation update)
DE	Ig heavy chain V-III region NIE.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE.
RX	MEDLINE=77070269; PubMed=826475;
RA	Ponstingl H., Hilschmann N.;
RT	"The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure.";
RT	Hepe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
RL	[2]
RN	
RP	DISULFIDE BOND.
RX	MEDLINE=77070267; PubMed=1002129;
RA	Dreker L., Schwarz J., Reichel W., Hilschmann N.;
RT	"Rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nie). I: Purification and characterization of the protein, the L- and H-chains, the cyanogen bromide cleavage products, and the disulfide bridges.";
RT	Hepe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
RL	- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA PROTEIN.
CC	PIR: A02053; GIHUNI.
DR	HSP; P01772; 2FB4.
DR	InterPro; IPR003006; Ig_MHC.
DR	InterPro; IPR003596; Ig_v.
DR	Pfam; PF00047; Ig; 1.
DR	SMART; SM00406; IGV: 1.
KW	Immunoglobulin V region.
FT	MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT	DISULFID 22 96
FT	NON_TER 119 119
SEQ	SEQUENCE 119 AA; 13242 MW; C96935A6E5E165B CRC64;
Query Match 65.8%; Score 403; DB 1; Length 119;	
Best Local Similarity 66.4%; Pred. No. 4e-35;	
Matches 79; Conservative 16; Mismatches 22; Indels 2; Gaps	
Qy	1 EVOLVESGGGLVKGRSLRLSCAASGFAFSFYDMSVWRQIPEKRLWEAKVSSGGGSTYY 60
Dd	1 QQLVQSOGGGLVPGGSURLSCAASGFFTSRYTHWVRQAPGKLEWVAISYGBBBKH 96
Qy	61 LDTVGRTTISRDNKNTLYLQMNSLNSEDATMYCARNHYCS--FAWGQGTTLVTVA 117

Db 61 ADSNGREFTISRNDKNTLYLNNSLRPEDTAVYYCARIRODTAMFFAHWGQGLTVYSS 119

Search completed: November 18, 2002, 17:33:17
Job time : 29.6765 secs

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	499	81.5	119	11	Q920E7	Q920e7 mus	musculu
2	475.5	77.7	487	11	Q99K44	Q99ka4 mus	musculu
3	455	74.3	479	11	Q91WP5	Q91wp5 mus	musculu
4	448	73.2	597	4	Q96BB9	Q96bb9 homo	sapien
5	441.5	72.1	473	11	Q91Z05	Q91z05 mus	musculu
6	441	72.1	486	11	Q91Z07	Q91z07 mus	musculu
7	440	71.9	116	4	Q9UL93	Q9ul93 homo	sapien
8	437.5	71.5	471	4	Q8TC77	Q8tc77 homo	sapien
9	433	70.8	480	11	Q91XE1	Q91xe1 mus	musculu
10	432.5	70.7	613	4	Q8WUK1	Q8wuk1 homo	sapien
11	430.5	70.3	573	4	Q8WU38	Q8wu38 homo	sapien
12	429.5	70.2	437	11	Q9R1A4	Q9r1a4 mus	musculu
13	429	70.1	121	4	Q9UL71	Q9ul71 homo	sapien
14	428	69.9	113	4	Q9UL90	Q9ul90 homo	sapien
15	426.5	69.7	112	4	Q9HCC1	Q9hcc1 homo	sapien
16	424.5	69.4	118	4	Q9UL91	Q9ul91 homo	sapien

RESULT 2

Q99KA4 PRELIMINARY; PRT; 487 AA.
 AC Q99KA4;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Hypothetical 52.6 kDa protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC004786; AAH04786.1;
 DR HSSP; P01810; 2FBJ
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR003597; Ig_cl.
 DR InterPro; IPR003600; Ig_like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 4
 DR SMART; SM00409; IG; 3.
 DR SMART; SM00407; IGC1; 3.
 DR SMART; SM00406; IGV; 1.
 DR SMART; SM00410; IG_like; 1.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KW Hypothetical protein
 SQ SEQUENCE 487 AA; 52554 MW; 7DC8E96DB333077B CRC64;

Query Match 77.7%; Score 475.5; DB 11; Length 487;
 Best Local Similarity 75.0%; Pred. No. 3.4e-40;
 Matches 93; Conservative 5; Mismatches 19; Indels 7; Gaps 1;
 QY 1 EVQLVESGGGLVPGKSLRLSCLSAASGFAFSSYDMSWVRQIPEKRLWAKVSSGGSTYY 60
 Db 20 EVQLVESGGGLVPGKSLRLSCLSAASGFAFSSYDMSWVRQIPEKRLWAKVSSGGSTYY 79
 QY 61 LDTVQGRFTISRDNKNTLYLQMSLSNEDTAMYYCARH-----NYGSFAYWGQGLV 113
 Db 80 PDNVKGRFTISRDNKNTLYLQMSLSNEDTAMYYCARH-----NYGSFAYWGQGLV 139

RESULT 3

Q91WP5 PRELIMINARY; PRT; 479 AA.
 AC Q91WP5;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Hypothetical 51.6 kDa protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC013656; AAH13656.1;
 DR InterPro; IPR003598; Ig_c2.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; ig; 4.
 DR SMART; SM00408; IGC2; 1.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KW Hypothetical protein; Immunoglobulin domain.

SQ SEQUENCE 479 AA; 51603 MW; ECB2D0877748584F CRC64;

Query Match 74.3%; Score 455; DB 11; Length 479;
 Best Local Similarity 75.2%; Pred. No. 4.1e-38;
 Matches 88; Conservative 10; Mismatches 17; Indels 2; Gaps 1;

QY 1 EVQLVESGGGLVPGKSLRLSCLSAASGFAFSSYDMSWVRQIPEKRLWAKVSSGGSTYY 60
 Db 20 EVQLVESGGGLVPGKSLRLSCLSAASGFAFSSYDMSWVRQIPEKRLWAKVSSGGSTYY 79
 QY 61 LDTVQGRFTISRDNKNTLYLQMSLSNEDTAMYYCARHNYGSFAYWGQGLVTVVSA 117
 Db 80 SDTMKGRFTISRDNKNTLYLQMSLSNEDTAMYYCARHNYGSFAYWGQGLVTVVSS 134

RESULT 4

Q96BB9 PRELIMINARY; PRT; 597 AA.
 AC Q96BB9;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Hypothetical 65.0 kDa protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=B-CELL;
 RA Strausberg R.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC015760; AAH15760.1;
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; ig; 5_MHC; UNKNOWN_3.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
 KW Hypothetical protein.
 SQ SEQUENCE 597 AA; 65039 MW; 4FCA3AD8E263D9 CRC64;

Query Match 73.2%; Score 448; DB 4; Length 597;
 Best Local Similarity 68.8%; Pred. No. 2.8e-37;
 Matches 86; Conservative 16; Mismatches 15; Indels 8; Gaps 1;

QY 1 EVQLVESGGGLVPGKSLRLSCLSAASGFAFSSYDMSWVRQIPEKRLWAKVSSGGSTYY 60
 Db 20 EVQLVESGGGLVPGKSLRLSCLSAASGFAFSSYDMSWVRQIPEKRLWAKVSSGGSTYY 79
 QY 61 LDTVQGRFTISRDNKNTLYLQMSLSNEDTAMYYCARH-----NYGSFAYWGQGLV 112
 Db 80 ADSVKGRFTISRDNKNTLYLQMSLSNEDTAMYYCARH-----NYGSFAYWGQGLV 139

RESULT 5

Q91Z05 PRELIMINARY; PRT; 473 AA.
 AC Q91Z05;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Hypothetical 51.9 kDa protein.
 GN A0044919.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

```
DR EMBL; BC010327; AAH10327.1; -.
DR MGD; MGI;2144967; AU044919.
DR InterPro; IPR000345; CytC_heme_bind.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 3.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;

Query Match 72.1%; Score 441.5; DB 11; Length 473;
Best Local Similarity 72.9%; Pred. No. 9.6e-37;
Matches 86; Conservative 10; Mismatches 21; Indels 1; Gaps 1;

QY 1 EVLVESGGGLVKPGRSLRLSCAASGAFAPSSYDMSWVRQIPEKRLWAKVSSGGGSTYY 60
Db 20 EVLVESGGGLVKPGGSLRLSCAASGFTFSYDMHWVRQAPKGLWAVVINGSGSTYY 79
QY 61 LDTVOGRTTISRDNKNTLYLQMSLSNSEDAMYCARHNY-GSFAYWGQGLTVTVA 117
Db 80 ADTVKGRFTTISRDNKNTLYLQMSLSNSEDAMYCARLWLRIDYWGQGLTVTSS 137

RESULT 6
Q91Z07 PRELIMINARY; PRT; 486 AA.
AC Q91Z07;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical 52.7 kDa protein.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC010324; AAH10324.1; -.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein; Immunoglobulin domain.
SQ SEQUENCE 486 AA; 52682 MW; 4FEF835125DA870B CRC64;

Query Match 72.1%; Score 441; DB 11; Length 486;
Best Local Similarity 71.0%; Pred. No. 1.1e-36;
Matches 88; Conservative 12; Mismatches 16; Indels 8; Gaps 3;

QY 1 EVLVESGGGLVKPGRSLRLSCAASGAFAPSSYDMSWVRQIPEKRLWAKVSSGGGSTYY 60
Db 20 EVLVESGGGLVKPGGSLRLSCVVSFSTSYDMSWVRQTPERRLEWVAITSGNTYY 78
QY 61 LDTVOGRTTISRDNKNTLYLQMSLSNSEDAMYCARHN-----YGSFAY---WGQGLTV 113
Db 79 PDNVKGRFTTISRDNKNTLYLQMSLSKSEDTAMCYCVRPEIPIYYSGSYFDSWGQGLTI 138
QY 114 TVSA 117
Db 139 TVSS 142

RESULT 7
Q9UL93 PRELIMINARY; PRT; 116 AA.
AC Q9UL93;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
```

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DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035021; AAD56257.1; -.
DR HSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1 116
FT SEQUENCE 116 AA; 12434 MW; 0DA0348154DD6061 CRC64;

Query Match 71.9%; Score 440; DB 4; Length 116;
Best Local Similarity 73.3%; Pred. No. 2.4e-37;
Matches 85; Conservative 10; Mismatches 21; Indels 0; Gaps 0;

QY 2 VOLVESGGGLVKPGRSLRLSCAASGAFAPSSYDMSWVRQIPEKRLWAKVSSGGGSTYYL 61
Db 1 VOLVESGGGVVQPGGRSLRLSCAASGFTFSYAMHWVRQAPKGLWAVVSYDGSNKYYA 60
QY 62 DTVOGRTTISRDNKNTLYLQMSLSNSEDAMYCARHNYGSFAYWGQGLTVTVA 117
Db 61 DSVKGRFTTISRDNKNTLYLQMSLSRAEDTAMCYCAGGGGLGLGYWGQGLTVTSS 116

RESULT 8
Q8TC77 PRELIMINARY; PRT; 471 AA.
ID Q8TC77;
AC Q8TC77;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 51.8 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SPLEEN;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC024289; AAH24289.1; -.
KW Hypothetical protein.
SQ SEQUENCE 471 AA; 51791 MW; 388F7F4CF588660E CRC64;

Query Match 71.5%; Score 437.5; DB 4; Length 471;
Best Local Similarity 70.5%; Pred. No. 2.5e-36;
Matches 86; Conservative 12; Mismatches 19; Indels 5; Gaps 1;

QY 1 EVLVESGGGLVKPGRSLRLSCAASGAFAPSSYDMSWVRQIPEKRLWAKVSSGGGSTYY 60
Db 20 EVLVESGGGLVKPGGSLRLSCAASGFTFSYSMNWVRQAPKGLWVSSSSSSYY 79
QY 61 LDTVOGRTTISRDNKNTLYLQMSLSNSEDAMYCARH-----NYGSFAYWGQGLTVT 115
Db 80 ADSVKGRFTTISRDNKNTLYLQMSLSRAEDTAVYYCARDLRQLTSYWFYFELWGRGLTV 139
QY 116 SA 117
Db 140 SS 141
```

	Matches	83; Conservative	15; Mismatches	19; Indels	3; Gaps	
Qy	1	EVQVSGGGLVPGRLSLRSLCAASGFAFSYDMSKVRQIPEKRLWEVAKVSSGGSTYY	60			RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal antibody (Mab 7, its light and heavy chains) and construction of a
						RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
						RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;

RT single chain antibody (scFV).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF152372; AAD40243.1; -

DR HSP; P01842; 7FAB.

DR MGD; MGI:96446; Igh-4.

DR InterPro; IPR003600; Ig_Like.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_v.

DR Pfam; PF00047; Ig; 4.

DR SMART; SM00406; IGV; 1.

DR SMART; SM00410; Ig_Like; 2.

DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.

FT NON_TER 1

FT NON_TER 437

SQ SEQUENCE 437 AA; 48142 MW; 5C3A7B3BEE7D697C CRC64;

Query Match 70.2%; Score 429.5; DB 11; Length 437;

Best Local Similarity 75.9%; Pred. No. 1.5e-35;

Matches 88; Conservative 6; Mismatches 19; Indels 3; Gaps 2;

QY 2 VOLVESGGGLVKGPRSLRSLSCAASGFSSYDMSWVRQIPEKRLWAKVSSGGGSTYYL 61

Db 1 VOLVESGGGLVKGPRSLRSLSCAASGFSSYDMSWVRQIPEKRLWAKVSSGGGSTYYL 61

QY 62 DTVOGRTISRDNKNTLYLQMSLSNSEDYAMVYCARHNYGSFAYWGQGLTVTVSA 117

Db 60 DSVKGRFTISRDNKNTLYLQMSLSNSEDYAMVYCARHNYGSFAYWGQGLTVTVSA 113

RESULT 13

QY 62 DTVOGRTISRDNKNTLYLQMSLSNSEDYAMVYCARHNYGSFAYWGQGLTVTVSA 117

Db 60 DSVKGRFTISRDNKNTLYLQMSLSNSEDYAMVYCARHNYGSFAYWGQGLTVTVSA 113

QY 62 DTVOGRTISRDNKNTLYLQMSLSNSEDYAMVYCARHNYGSFAYWGQGLTVTVSA 117

Db 60 DSVKGRFTISRDNKNTLYLQMSLSNSEDYAMVYCARHNYGSFAYWGQGLTVTVSA 113

QY 62 DTVOGRTISRDNKNTLYLQMSLSNSEDYAMVYCARHNYGSFAYWGQGLTVTVSA 117

Db 60 DSVKGRFTISRDNKNTLYLQMSLSNSEDYAMVYCARHNYGSFAYWGQGLTVTVSA 113

QY 62 DTVOGRTISRDNKNTLYLQMSLSNSEDYAMVYCARHNYGSFAYWGQGLTVTVSA 117

Db 60 DSVKGRFTISRDNKNTLYLQMSLSNSEDYAMVYCARHNYGSFAYWGQGLTVTVSA 113

QY 62 DTVOGRTISRDNKNTLYLQMSLSNSEDYAMVYCARHNYGSFAYWGQGLTVTVSA 117

Db 60 DSVKGRFTISRDNKNTLYLQMSLSNSEDYAMVYCARHNYGSFAYWGQGLTVTVSA 113

QY 62 DTVOGRTISRDNKNTLYLQMSLSNSEDYAMVYCARHNYGSFAYWGQGLTVTVSA 117

Db 60 DSVKGRFTISRDNKNTLYLQMSLSNSEDYAMVYCARHNYGSFAYWGQGLTVTVSA 113

QY 62 DTVOGRTISRDNKNTLYLQMSLSNSEDYAMVYCARHNYGSFAYWGQGLTVTVSA 117

Db 60 DSVKGRFTISRDNKNTLYLQMSLSNSEDYAMVYCARHNYGSFAYWGQGLTVTVSA 113

QY 62 DTVOGRTISRDNKNTLYLQMSLSNSEDYAMVYCARHNYGSFAYWGQGLTVTVSA 117

Db 60 DSVKGRFTISRDNKNTLYLQMSLSNSEDYAMVYCARHNYGSFAYWGQGLTVTVSA 113

QY 62 DTVOGRTISRDNKNTLYLQMSLSNSEDYAMVYCARHNYGSFAYWGQGLTVTVSA 117

Db 60 DSVKGRFTISRDNKNTLYLQMSLSNSEDYAMVYCARHNYGSFAYWGQGLTVTVSA 113

QY 62 DTVOGRTISRDNKNTLYLQMSLSNSEDYAMVYCARHNYGSFAYWGQGLTVTVSA 117

Db 60 DSVKGRFTISRDNKNTLYLQMSLSNSEDYAMVYCARHNYGSFAYWGQGLTVTVSA 113

QY 62 DTVOGRTISRDNKNTLYLQMSLSNSEDYAMVYCARHNYGSFAYWGQGLTVTVSA 117

Db 60 DSVKGRFTISRDNKNTLYLQMSLSNSEDYAMVYCARHNYGSFAYWGQGLTVTVSA 113

QY 62 DTVOGRTISRDNKNTLYLQMSLSNSEDYAMVYCARHNYGSFAYWGQGLTVTVSA 117

Db 60 DSVKGRFTISRDNKNTLYLQMSLSNSEDYAMVYCARHNYGSFAYWGQGLTVTVSA 113

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Db 60 DSVKGRFTISRDNKNTLYLQMSLSNSEDYAMVYCARHNYGSFAYWGQGLTVTVSA 113

QY 62 DTVOGRTISRDNKNTLYLQMSLSNSEDYAMVYCARHNYGSFAYWGQGLTVTVSA 117

Db 60 DSVKGRFTISRDNKNTLYLQMSLSNSEDYAMVYCARHNYGSFAYWGQGLTVTVSA 113

QY 62 DTVOGRTISRDNKNTLYLQMSLSNSEDYAMVYCARHNYGSFAYWGQGLTVTVSA 117

Db 60 DSVKGRFTISRDNKNTLYLQMSLSNSEDYAMVYCARHNYGSFAYWGQGLTVTVSA 113

QY 62 DTVOGRTISRDNKNTLYLQMSLSNSEDYAMVYCARHNYGSFAYWGQGLTVTVSA 117

Db 60 DSVKGRFTISRDNKNTLYLQMSLSNSEDYAMVYCARHNYGSFAYWGQGLTVTVSA 113

QY 62 DTVOGRTISRDNKNTLYLQMSLSNSEDYAMVYCARHNYGSFAYWGQGLTVTVSA 117

Db 60 DSVKGRFTISRDNKNTLYLQMSLSNSEDYAMVYCARHNYGSFAYWGQGLTVTVSA 113

QY 62 DTVOGRTISRDNKNTLYLQMSLSNSEDYAMVYCARHNYGSFAYWGQGLTVTVSA 117

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QY 62 DTVOGRTISRDNKNTLYLQMSLSNSEDYAMVYCARHNYGSFAYWGQGLTVTVSA 117

Db 60 DSVKGRFTISRDNKNTLYLQMSLSNSEDYAMVYCARHNYGSFAYWGQGLTVTVSA 113

QY 62 DTVOGRTISRDNKNTLYLQMSLSNSEDYAMVYCARHNYGSFAYWGQGLTVTVSA 117

Db 60 DSVKGRFTISRDNKNTLYLQMSLSNSEDYAMVYCARHNYGSFAYWGQGLTVTVSA 113

QY 62 DTVOGRTISRDNKNTLYLQMSLSNSEDYAMVYCARHNYGSFAYWGQGLTVTVSA 117

Db 60 DSVKGRFTISRDNKNTLYLQMSLSNSEDYAMVYCARHNYGSFAYWGQGLTVTVSA 113

QY 62 DTVOGRTISRDNKNTLYLQMSLSNSEDYAMVYCARHNYGSFAYWGQGLTVTVSA 117

Db 60 DSVKGRFTISRDNKNTLYLQMSLSNSEDYAMVYCARHNYGSFAYWGQGLTVTVSA 113

QY 62 DTVOGRTISRDNKNTLYLQMSLSNSEDYAMVYCARHNYGSFAYWGQGLTVTVSA 117

Db 60 DSVKGRFTISRDNKNTLYLQMSLSNSEDYAMVYCARHNYGSFAYWGQGLTVTVSA 113

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SQ SEQUENCE 112 AA; 12243 MW; 24F1A45EC3B84788 CRC64;  
  
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Search completed: November 18, 2002, 17:40:31  
Job time : 123.212 secs
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GenCore version 5.1.3

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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:21:57 ; Search time 161.735 Seconds
(without alignments)
96.394 Million cell updates/sec

Title: US-09-016-061-6

Perfect score: 612

Sequence: 1 EQVLVESGGGLVKPGSLRL.....RHNYGSFAFWGGTLTVTSA 117

Scoring table: BLOSOM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_101002.*

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- 2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
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- 22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
- 23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	612	100.0	117	19	AAW76003
2	612	100.0	117	22	AAW63589
3	612	100.0	117	22	AAW61361
4	596	97.4	117	20	AAW06381
5	582	95.1	130	20	AAW06379
6	552	90.2	117	19	AAW76001
7	552	90.2	117	22	AAW63587
8	552	90.2	117	22	AAW61359
9	531	86.8	123	19	AAW66099
10	510	83.3	136	11	AAW06251

11	508.5	83.1	139	15	AAW52773	Murine KC-4 immuno
12	508.5	83.1	139	15	AAW52791	Murine KC-4 immuno
13	501	81.9	117	19	AAW48865	Murine monoclonal
14	501	81.9	117	20	AAW86139	Protein sequence o
15	501	81.9	136	15	AAW56962	MAB A33 heavy chai
16	498	81.4	643	19	AAW73048	A33 chimeric recep
17	497	81.2	237	20	AAW95440	A33/212 single-cha
18	497	81.2	237	21	AAW54836	Linked fusion prot
19	497	81.2	241	21	AAW95441	A33/218 single-cha
20	497	81.2	241	21	AAW54837	Linked fusion prot
21	497	81.2	245	20	AAW97891	A33/218 single cha
22	497	81.2	265	23	AAW75159	A33/218 sfv with o
23	495	80.9	117	16	AAW79155	Human IgE receptor
24	495	80.9	117	18	AAW27357	Heavy chain variab
25	495	80.9	117	18	AAW27354	Heavy chain variab
26	494	80.7	117	16	AAW79157	Human IgE receptor
27	494	80.7	249	22	AAW20434	Anti-FIX/FIXa anti
28	493	80.6	117	18	AAW27526	Heavy chain variab
29	493	80.6	239	20	AAW73874	Human antiFc epsil
30	493	80.6	242	20	AAW73876	Human antiFc epsil
31	487.5	79.7	139	18	AAW21656	Chimeric MAB 15 PC
32	486	79.4	138	13	AAW20064	MRK16-H chain. Ch
33	486	79.4	247	16	AAW11917	Murine MAB SK48-E2
34	485.5	79.3	118	19	AAW57576	Chimeric H chain S
35	485.5	79.3	118	20	AAW89627	Mouse humanised an
36	485.5	79.3	118	21	AAW77502	Peptide seq ID No:
37	485.5	79.3	118	22	AAW63382	Anino acid sequenc
38	485.5	79.3	118	22	AAW64764	Mouse anti-PTHrP m
39	485.5	79.3	118	22	AAW76880	Human PTHrP mouse
40	485.5	79.3	118	22	AAW76899	Human PTHrP mouse
41	485.5	79.3	118	22	AAW76918	Human PTHrP mouse
42	485.5	79.3	118	23	AAW95197	Mouse joint diseas
43	485.5	79.3	124	22	AAW97193	Murine anti-PI-3,4
44	485.5	79.3	137	19	AAW57592	Chimeric antibody
45	485.5	79.3	137	20	AAW89625	Mouse humanised an

ALIGNMENTS

RESULT 1

AAW76003
ID AAW76003 standard; Protein: 117 AA.

XX AAW76003;

XX AC

XX DT 02-NOV-1998 (first entry)

XX DE LM609 antibody heavy chain variable region protein fragment.

XX KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
XX KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
XX KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
XX KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
XX KW macular degeneration; osteoporosis.

XX OS Mus sp.

XX PN WO9833919-A2.

XX PD 06-AUG-1998.

XX PF 30-JAN-1998; 98WO-US01826.

XX PR 30-JAN-1997; 97US-0791391.

XX PA (IXSY-) IXSYS INC.

XX PI Glaser SM, Huse WD;

XX XX A heavy chain vari

XX DR WPI; 1998-437472/37.

XX DR N-PSDB; AAW49822.

XX XX

The present sequence represents the heavy chain variable region of the monoclonal antibody LM609. LM609 is a murine antibody which specifically recognises the integrin alphavbeta3, and inhibits its functional activity. The specification describes a LM609 grafted antibody which has the complementarity determining regions (CDRs) substituted into a non-murine framework. Nucleic acids encoding LM609 grafted heavy and light chain polypeptides and fragments are useful in diagnostic and therapeutic purposes, such as in the production of LM609 grafted antibodies and fragments having binding specificity and inhibitory activity against the integrin alphavbeta3. The antibody can be used for the diagnosis or treatment of alphavbeta3-mediated diseases (e.g. inflammatory disorders, chronic articular rheumatism, psoriasis, disorders associated with inappropriate or inopportune invasion of vessels such as diabetic retinopathy, neovascular glaucoma and capillary proliferation in atherosclerotic plaques, or cancers), and to inhibit binding activity of alphavbeta3 that are necessary for progression of an alphavbeta3-mediated disease.

XX XX Sequence 117 AA;

Query Match 100.0%; Score 612; DB 22; Length 117;
Best Local Similarity 100.0%; Pred. No. 7.9e-51;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVPGKSLRLSCAASGFAFSSYDMSWVRQIPEKLEWVAKVSSGGSTYY 60
Db 1 EVQLVESGGGLVPGKSLRLSCAASGFAFSSYDMSWVRQIPEKLEWVAKVSSGGSTYY 60

QY 61 LDTVOGRFTISRDAKNTLYLQMNSLSNEDTAMYYCARHNYGSFAYWGCGTLVTWSA 117
Db 61 LDTVOGRFTISRDAKNTLYLQMNSLSNEDTAMYYCARHNYGSFAYWGCGTLVTWSA 117

RESULT 3

AAB61361

ID AAB61361 standard; protein; 117 AA.

XX AAB61361;

XX 03-APR-2001 (first entry)

XX Antibody LM609 heavy chain variable region protein.

XX LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
KW inflammatory; cancer; retina; restenosis; osteoporosis.
XX Unidentified.
OS WO200078815-A1.
PN 28-DEC-2000.
PD 23-JUN-2000; 200WO-US17454.
PF 24-JUN-1999; 99US-0339922.
XX (MOLE-) APPLIED MOLECULAR EVOLUTION.
PA Huse WD, Wu H;
XX WPI; 2001-050110/06.
DR Enhanced LM609 grafted antibodies exhibiting selective binding affinity
XX to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
PT osteoporosis -
XX Disclosure; Fig 2; 132pp; English.
PS The present invention relates to enhanced LM609 grafted antibodies
CC exhibiting selective binding affinity to alphavbeta_3 integrin or
CC their functional fragments. The antibodies or their functional
CC fragments can be used in the diagnosis and treatment of

CC alpha/beta.3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism).
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.

XX Sequence 117 AA;

Query Match 100.0%; Score 612; DB 22; Length 117;

Best Local Similarity 100.0%; Pred. No. 7.9e-51;

Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVLVESGGGLVKPGKSLRLSCAASGFAFSSYDMSWVRQIPEKRLKLVKAVSSGGSTYY 60

DB 1 EVLVESGGGLVKPGKSLRLSCAASGFAFSSYDMSWVRQIPEKRLKLVKAVSSGGSTYY 60

QY 61 LDTVQGRFTISRDNKNTLYLQMSLSNSEDAMYCARHNYGSFAYWGQGLTLTVSA 117

DB 61 LDTVQGRFTISRDNKNTLYLQMSLSNSEDAMYCARHNYGSFAYWGQGLTLTVSA 117

RESULT 4

AAV06381

ID AAY06381 standard; Protein; 117 AA.

XX AC AAY06381;

XX DT 06-SEP-1999 (first entry)

XX DE Murine monoclonal antibody LM609 VH region.

XX KW Humanised antibody; antibody humanisation; antibody engineering;
 KW LM609; monoclonal antibody; complementarity determining region;
 KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
 KW cancer; therapy; diagnosis.

XX OS Mus musculus.

XX PN WO9929888-A1.

XX PD 17-JUN-1999.

XX PF 04-DEC-1998; 98WO-US25828.

XX PR 05-DEC-1997; 97US-0986016.

XX PA (SCRI) SCRIPPS RES INST.

XX PI Barbas CF, Rader C;

XX DR WPI; 1999-394979/33.

XX PT Production of humanized mouse monoclonal antibodies

XX PS Disclosure; Page 52-53; 55pp; English.

XX CC This sequence represents the heavy chain variable region of murine
 CC monoclonal antibody LM609. LM609 is directed to integrin
 CC alpha-v beta-3. It selectively promotes apoptosis of vascular
 CC cells that have been stimulated to undergo angiogenesis, making it
 CC a tool for cancer diagnosis and therapy. The invention provides
 CC humanised antibodies, especially humanised LM609. In such humanized
 CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
 CC grafted onto a human light chain, and a heavy chain CDR from a mouse
 CC antibody is grafted onto a human antibody heavy chain to produce
 CC libraries from which a humanised murine antibody having the desired
 CC specificity is selected. By preserving the original CDR sequences
 CC such as the HCDR3 and LCDR3 sequences of LM609 (see AAY06371-72), the
 CC humanisation strategy ensures epitope conservation.

XX Sequence 117 AA;

Query Match 97.4%; Score 596; DB 20; Length 117;

Best Local Similarity 97.4%; Pred. No. 2.6e-49;

Matches 114; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EVLVESGGGLVKPGKSLRLSCAASGFAFSSYDMSWVRQIPEKRLKLVKAVSSGGSTYY 60

DB 1 EVLVESGGGLVKPGKSLRLSCAASGFAFSSYDMSWVRQIPEKRLKLVKAVSSGGSTYY 60

QY 61 LDTVQGRFTISRDNKNTLYLQMSLSNSEDAMYCARHNYGSFAYWGQGLTLTVSA 117

DB 61 LDTVQGRFTISRDNKNTLYLQMSLSNSEDAMYCARHNYGSFAYWGQGLTLTVSA 117

RESULT 5

AAV06379

ID AAY06379 standard; Protein; 130 AA.

XX AC AAY06379;

XX DT 06-SEP-1999 (first entry)

XX DE Murine monoclonal antibody LM609 V kappa.

XX KW Humanised antibody; antibody humanisation; antibody engineering;
 KW LM609; monoclonal antibody; complementarity determining region;
 KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
 KW cancer; therapy; diagnosis.

XX OS Mus musculus.

XX FH Key Location/Qualifiers

FT Peptide 1..2

FT /note= "vector-encoded residues"

FT Region 28..32

FT /note= "CDR1"

FT Region 47..63

FT /note= "CDR2"

FT Region 96..103

FT /note= "CDR3"

XX PN WO9929888-A1.

XX PD 17-JUN-1999.

XX PF 04-DEC-1998; 98WO-US25828.

XX PR 05-DEC-1997; 97US-0986016.

XX PA (SCRI) SCRIPPS RES INST.

XX PI Barbas CF, Rader C;

XX DR WPI; 1999-394979/33.

XX PT Production of humanized mouse monoclonal antibodies

XX PS Disclosure; Page 49-50; 55pp; English.

XX CC This sequence represents the light chain V kappa region of murine
 CC monoclonal antibody LM609. LM609 is directed to integrin
 CC alpha-v beta-3. It selectively promotes apoptosis of vascular
 CC cells that have been stimulated to undergo angiogenesis, making it
 CC a tool for cancer diagnosis and therapy. The invention provides
 CC humanised antibodies, especially humanised LM609. In such humanized
 CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
 CC grafted onto a human light chain, and a heavy chain CDR from a mouse
 CC antibody is grafted onto a human antibody heavy chain to produce
 CC libraries from which a humanised murine antibody having the desired
 CC specificity is selected. By preserving the original CDR sequences
 CC such as the HCDR3 and LCDR3 sequences of LM609 (see AAY06371-72), the
 CC humanisation strategy ensures epitope conservation.

XX

SQ Sequence 130 AA;
 Query Match 95.1%; Score 582; DB 20; Length 130;
 Best Local Similarity 97.4%; Pred. No. 6.4e-48;
 Matches 111; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 LVESGGGLVKPGRSLRLSCAASGFAFSSYDMSWVRQIPEKRLWAKVSSGGSTYYLDT 63
 Db 1 LEESGGGLVKPGRSLRLSCAASGFAFSSYDMSWVRQIPEKRLWAKVSSGGSTYYLDT 60

QY 64 VQGRFTISRDNKNTLYLQMSLSNSEDAMYYCARHNYGSFAYWGQGLTVTVSA 117
 Db 61 VQGRFTISRDNKNTLYLQMSLSNSEDAMYYCARHNYGSFAYWGQGLTVTVSA 114

RESULT 6
 AAW76001
 ID AAW76001 standard; Protein; 117 AA.
 AC AAW76001;
 DT 02-NOV-1998 (first entry)
 XX Vitaxin antibody heavy chain variable region protein fragment.
 DE Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.
 XX Mus sp.
 OS WO9833919-A2.
 PN 06-AUG-1998.
 PD 30-JAN-1998; 98WO-US01826.
 PF 30-JAN-1997; 97US-0791391.
 PR (IXSY-) IXSY INC.
 PA Glaser SM, Huse WD;
 PI WPI: 1998-437472/37.
 DR N-PSDB; AAV49820.
 XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX Claim 1; Fig 1a; 129pp; English.
 PS This sequence represents a fragment of the vitaxin antibody variable
 CC heavy chain region. Vitaxin and the antibody LM609 bind selectively to
 CC integrin alphavbeta3 and can be used to inhibit binding of alphavbeta3
 CC to a ligand and thus block integrin-mediated signal transduction. This is
 CC useful in the treatment, prevention and diagnosis of alphavbeta3-mediated
 CC disease, specifically angiogenesis and restenosis (but also e.g.
 CC (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,
 CC cancer, psoriasis, rheumatoid arthritis, macular degeneration,
 CC osteoporosis etc.). The antibodies contain non-murine framework regions
 CC so are suitable for use in humans. Enhanced types of LM609 have affinity
 CC more than 90 times greater than that of parent the parent antibody.
 XX SQ Sequence 117 AA;

Query Match 90.2%; Score 552; DB 19; Length 117;
 Best Local Similarity 88.0%; Pred. No. 4.1e-45;
 Matches 103; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVKPGRSLRLSCAASGFAFSSYDMSWVRQIPEKRLWAKVSSGGSTYY 60
 Db 1 QVQLVESGGGVVQPGKSLRLSCAASGFTFSYDMSWVRQAPGKGLWAKVSSGGSTYY 60

QY 61 LDTVOGRFTISRDNKNTLYLQMSLSNSEDAMYYCARHNYGSFAYWGQGLTVTVSA 117
 Db 61 LDTVOGRFTISRDNKNTLYLQMSLSNSEDAMYYCARHNYGSFAYWGQGLTVTVSS 117

RESULT 7
 AAG63587
 ID AAG63587 standard; Protein; 117 AA.
 XX AAG63587;
 AC AAG63587;
 DT 15-OCT-2001 (first entry)
 XX A heavy chain variable region of LM609 grafted antibody.
 DE Grafted antibody; LM609; integrin; alphavbeta3; inflammatory disorder;
 KW chronic articular rheumatism; psoriasis; diabetic retinopathy;
 KW neovascular glaucoma; capillary proliferation; atherosclerotic plaque;
 KW cancer.
 XX Synthetic.
 OS Mus sp.
 XX US2001011125-A1.
 PN 02-AUG-2001.
 PD 30-JAN-1997; 97US-0790540.
 PF 30-JAN-1997; 97US-0790540.
 PR (HUSE/) HUSE W D.
 PA Huse WD;
 PI WPI: 2001-496171/54.
 DR N-PSDB; AAH74623.
 XX New LM609 grafted antibody exhibiting selective binding affinity to
 PT alphavbeta3, comprising at least one LM609 grafted heavy and light
 PT chain polypeptide, useful for diagnosing and treating e.g. inflammatory
 PT disorders or cancer
 XX Claim 1; Fig 1A; 25pp; English.
 PS The present sequence represents the heavy chain variable region of the
 CC grafted monoclonal antibody LM609. LM609 is a murine antibody which
 CC specifically recognises the integrin alphavbeta3, and inhibits its
 CC functional activity. The LM609 grafted antibody has the
 CC complementarity determining regions (CDRs) substituted into a non-murine
 CC framework. Nucleic acids encoding LM609 grafted heavy and light chain
 CC polypeptides and fragments are useful in diagnostic and therapeutic
 CC purposes, such as in the production of LM609 grafted antibodies and
 CC fragments having binding specificity and inhibitory activity against
 CC the integrin alphavbeta3. The antibody can be used for the diagnosis
 CC or treatment of alphavbeta3-mediated diseases (e.g. inflammatory
 CC disorders, chronic articular rheumatism, psoriasis, disorders
 CC associated with inappropriate or inopportune invasion of vessels such
 CC as diabetic retinopathy, neovascular glaucoma and capillary
 CC proliferation in atherosclerotic plaques, or cancers), and to inhibit
 CC binding activity of alphavbeta3 that are necessary for progression of
 CC an alphavbeta3-mediated disease.
 XX SQ Sequence 117 AA;

Query Match 90.2%; Score 552; DB 22; Length 117;
 Best Local Similarity 88.0%; Pred. No. 4.1e-45;
 Matches 103; Conservative 8; Mismatches 6; Indels 0; Gaps 0;


```

XX AC AAR06251;
XX DT 10-DEC-1990 (first entry)
XX DE Variable region of murine AHT 54 heavy chain.
XX KW Interleukin-2 receptor; IL-2; tumour necrosis factor; TNF; ss;
XX OS Mus sp.
XX PN EP380068-A.
XX PD 01-AUG-1990.
XX XX 24-JAN-1990; 90EP-0101351.
XX PF 04-DEC-1989; 89US-0441702.
XX PR 24-JAN-1989; 89US-0301216.
XX XX (MOLE-) MOLECULAR THERAPEUT.
XX PA Zerler B;
XX PI WPI; 1990-232892/31.
XX DR N-PSDB; AAQ05555.
XX XX Expression vectors for producing chimeric monoclonal antibodies -
XX PT which express human constant region and non-human variable region
XX XX Disclosure; ; p; English.
XX XX MABs comprising mouse CH and CL constant regions with human
XX CC variable regions may be used to create mouse/human hybrid MABs,
XX CC which have a longer serum half-life. Method can be used to produce
XX CC Abs against interleukin-2 receptor and tumour necrosis factor.
XX XX
SQ Sequence 136 AA;
Query Match 83.3%; Score 510; DB 11; Length 136;
Best Local Similarity 86.4%; Pred. No. 4.8e-41;
Matches 102; Conservative 5; Mismatches 9; Indels 2; Gaps 2;

Qy 1 EVQLVESGGGLVPGKSLRLSCAASGFAFSYDMSWVRQIPEKRLWAKVSSGGSTYY 60
Db 20 EVQLVESGGGLVPGKSLRLSCAASGFAFSYDMSWVRQIPEKRLWAKVSSGGSTYY 79
|||||
Qy 61 LDTVQGRFTISRDNKNTLYLQMSLSNSEDATMYICARHNYG-SFAYWGQGLTVTSA 117
Db 80 PDTVQGRFTISRDNKNTLYLQMSLSKSEDTAVYICAR-RYGLPFAYWGQGLTVTSA 136
|||||

RESULT 11
AAR52773
ID AAR52773 standard; Protein; 139 AA.
XX AC AAR52773;
XX DT 24-JAN-1995 (first entry)
XX DE Murine KC-4 immunoglobulin heavy chain variable region (deduced).
XX KW Immunoglobulin variable domain; primer; polymerase chain reaction;
XX KW chimeric antibody; human milk fat globule; human breast carcinoma;
XX KW murine anti-human carcinoma monoclonal antibody KC-4.
XX OS Mus musculus.
XX FH Key.
XX FT Protein
XX FT Location/Qualifiers
XX FT 20..139
XX FT /label= KC-4_mature_VL-chain
XX FT 20..49
XX FT /label= FR1

```

```

Region 50..54
FT /label= CDR1
FT Region 55..68
FT /label= FR2
FT Region 69..85
FT /label= CDR2
FT Region 86..117
FT /label= FR3
FT Region 118..128
FT /label= CDR3
FT Region 129..139
FT /label= FR4
XX WO9411508-A.
XX PN 26-MAY-1994.
XX PD 15-NOV-1993; 93WO-US11316.
XX PF 13-NOV-1992; 92US-0977706.
XX PR 13-NOV-1992; 92US-0977707.
XX PR 28-SEP-1993; 93US-0128015.
XX XX (CANC-) CANCER RES FUND CONTRA COSTA.
XX PA WPI; 1994-183509/22.
XX DR N-PSDB; AAQ62764.
XX XX Chimeric human-murine polypeptide(s) specific for human mammary
XX PT fat globule antigen - for imaging, diagnosing and treating
XX XX neoplasia, with less undesirable immunogenic response
XX PS Example 27; Page 41; 54pp; English.
XX XX An initial isolation of cDNAs coding for murine anti-human breast
XX CC carcinoma MAB KC-4 was performed using PCR with commercially
XX CC available primers (see AAQ62751-Q62758, available from NOVAGEN).
XX CC Subsequent cloning using PCR primers JO20, JO21, JO22 and JO24
XX CC (see AAQ62759-Q62762) resulted in the isolation of the mouse Ig
XX CC variable domains. The amplified cDNAs were sequenced (AAQ62763 and
XX CC AAQ62764) and amino acid sequences were deduced from them. Chimeric
XX CC mouse-human antibodies were constructed using human constant
XX CC regions so as to produce less immunogenic polypeptides which
XX CC retained the anti-human carcinoma binding specificity of KC-4.
XX XX
SQ Sequence 139 AA;
Query Match 83.1%; Score 508.5; DB 15; Length 139;
Best Local Similarity 82.5%; Pred. No. 6.8e-41;
Matches 99; Conservative 7; Mismatches 11; Indels 3; Gaps 1;

Qy 1 EVQLVESGGGLVPGKSLRLSCAASGFAFSYDMSWVRQIPEKRLWAKVSSGGSTYY 60
Db 20 EVQLVESGGGLVPGKSLRLSCAASGFAFSYDMSWVRQIPEKRLWAKVSSGGSTYY 79
|||||
Qy 61 LDTVQGRFTISRDNKNTLYLQMSLSNSEDATMYICARHNYG---FAYWGQGLTVTSA 117
Db 80 QDTVQGRFTISRDNKNTLYLQMSLSRSEDATMYICAREDTGIPAFAYWGQGLTVTSA 139
|||||

RESULT 12
AAR52791
ID AAR52791 standard; Protein; 139 AA.
XX AC AAR52791;
XX DT 24-JAN-1995 (first entry)
XX DE Murine KC-4 immunoglobulin heavy chain variable region (deduced).
XX KW Immunoglobulin variable domain; primer; polymerase chain reaction;
XX KW chimeric antibody; human milk fat globule; human breast carcinoma;
XX KW murine anti-human carcinoma monoclonal antibody KC-4.

```


DT 03-MAR-1999 (first entry)
DE Protein sequence of murine A33 Vh.
XX Non-immunogenic; epitope; T-cell; immunogenicity; immune system; SK;
KW immunoglobulin; therapeutic; streptokinase; A33.
XX Mus sp.
OS
XX
XX W09852976-A1.
XX
XX 26-NOV-1998.
XX
XX 21-MAY-1998; 98WO-GB01473.
XX
XX 14-APR-1998; 98GB-0007751.
PR 21-MAY-1997; 97GB-0010480.
PR 31-JUL-1997; 97GB-0016197.
PR 28-NOV-1997; 97GB-0025270.
PR 02-DEC-1997; 97US-0067235.
XX
XX (BIOV-) BIOVATION LTD.
XX
XX Carr FJ;
XX WPI; 1999-045301/04.
XX
XX Reducing immunogenicity of proteins - by modifying the amino acid
PT sequence of the protein to eliminate potential epitopes for T-cells
PT of a given species
XX
XX Example 6; Fig 26; 77pp; English.
XX
XX The invention relates to a method for the production of non-immunogenic
CC proteins. The method comprises determining at least part of the amino
CC acid sequence of the protein; (b) identifying in the amino acid sequence
CC one or more potential epitopes for T-cells (T-cell epitopes) of the given
CC species; and (c) modifying the amino acid sequence to eliminate at least
CC one of the T-cell epitopes identified in step (b) thereby to eliminate or
CC reduce the immunogenicity of the protein when exposed to the immune
CC system of the given species. A method of analysing a pre-existing protein
CC to predict the basis for immunogenic responses is also provided. The
CC methods can be used particularly for reducing the immunogenicity of
CC immunoglobulins or therapeutic proteins, e.g. Streptokinase (SK). The
CC products can be used for diagnosis and therapy. The present sequence
CC represents the protein sequence of murine A33 Vh.
XX
XX Sequence 117 AA;
SQ
Query Match 81.9%; Score 501; DB 20; Length 117;
Best Local Similarity 82.1%; Pred. No. 2.9e-40;
Matches 96; Conservative 9; Mismatches 12; Indels 0; Gaps 0;
QY 1 EVLVESGGGLVKGPSRLSLRSCAASGFAFSSYDMSWVRQIPKRLWAKVSSGGSTYY 60
||:||||||| ||:||||||| ||:||||||| ||:||||||| ||:||||||| ||:|||||||
Db 1 EVLVESGGGLVKGPSRLSLRSCAASGFAFSSYDMSWVRQIPKRLWAKVSSGGSTYY 60
||:||||||| ||:||||||| ||:||||||| ||:||||||| ||:||||||| ||:|||||||
QY 61 LDTVOGRTTISRDNKNTLYLQMSLSNSEDYAMYCARNHYGSPAYWGQGLTVTVA 117
||:||||||| ||:||||||| ||:||||||| ||:||||||| ||:||||||| ||:|||||||
Db 61 LDSVKGRFTISRDSARNTLYLQMSLSRSEDYALYYCAPTTVPFAYWGQGLTVTVA 117
||:||||||| ||:||||||| ||:||||||| ||:||||||| ||:||||||| ||:|||||||
RESULT 15
AAR56962
ID AAR56962 standard; Protein; 136 AA.
XX
XX AAR56962;
XX AC
XX
XX 13-FEB-1995 (first entry)
XX
XX MAb A33 heavy chain.
DE
XX Polymerase chain reaction; primer; amplify; PCR; variable region; light;

KW heavy; chains; VL; VH; humanised; antibody; vectors; expression; human;
KW secretion; A33; Fab' (gamma4deltaCys); pG16; ompA signal; C-kappa;
KW pSkompA; pMRR055; CH1 domains; hinge; deltaCys; pMRR022; pRO109;
KW antigen; diagnosis; treatment; colorectal cancer; metastases.
XX
OS Chimeric - Mus musculus.
OS Chimeric - Homo sapiens.
XX
XX Key Location/Qualifiers
FH Peptide 1..19
FT /note= "Signal peptide"
FT Misc-difference 5
FT /label= Leu, Phe
FT Misc-difference 8
FT /label= Val, Ile
FT /label= 20..136
FT Protein /note= "MAb A33 heavy chain"
FT /label= 50..54
FT Region /label= CDR1
FT Region /label= 69..85
FT Region /label= CDR2
FT Region /label= 118..125
FT /label= CDR3
XX
XX W09413805-A.
XX
XX 23-JUN-1994.
XX
XX 10-DEC-1993; 93WO-GB02529.
XX
XX 10-DEC-1992; 92GB-0025853.
PR 22-JUL-1993; 93GB-0015249.
XX
XX (CLLT) CELLTech LTD.
XX
XX Adair JR, King DJ, Owens RJ;
XX WPI; 1994-217881/26.
XX N-PSDB; AAO68650.
XX
XX Humanised antibodies raised against A33 antigen - are used for
PT diagnosis or treatment of colorectal tumours and metastases
PT
XX Example 1; Fig 3(ii); 90pp; English.
XX
XX The sequences given in AAR56961-62 represent the light and heavy chain
CC variable regions (VH and VL) of the humanised anti-A33 antibody of the
CC invention. The DNA fragments encoding these proteins were produced by
CC PCR using the primer sequences given in AAO68624-48. The amplified
CC fragments were used in the construction of vectors for the expression
CC and secretion of the chimeric humanised A33. The amplified products
CC were cleaved with BstBI and SphI for the light chain and HindIII and
CC ApaI for the heavy chain. These fragments were cloned into the human
CC kappa light chain acceptor vector, pMRR15.1, and the human heavy chain,
CC IgG1, acceptor vector, pMRR011 respectively, to give chimeric expression
CC vector pRO108 for the light chain and pRO107 for the heavy chain.
CC Proteins which bind the A33 antigen can be used in the diagnosis or
CC treatment of colorectal cancers and metastases.
XX
XX Sequence 136 AA;
SQ
Query Match 81.9%; Score 501; DB 15; Length 136;
Best Local Similarity 82.1%; Pred. No. 3.4e-40;
Matches 96; Conservative 9; Mismatches 12; Indels 0; Gaps 0;
QY 1 EVLVESGGGLVKGPSRLSLRSCAASGFAFSSYDMSWVRQIPKRLWAKVSSGGSTYY 60
||:||||||| ||:||||||| ||:||||||| ||:||||||| ||:||||||| ||:|||||||
Db 20 EVLVESGGGLVKGPSRLSLRSCAASGFAFSSYDMSWVRQIPKRLWAKVSSGGSTYY 79
||:||||||| ||:||||||| ||:||||||| ||:||||||| ||:||||||| ||:|||||||
QY 61 LDTVOGRTTISRDNKNTLYLQMSLSNSEDYAMYCARNHYGSPAYWGQGLTVTVA 117
||:||||||| ||:||||||| ||:||||||| ||:||||||| ||:||||||| ||:|||||||
Db 80 LDSVKGRFTISRDSARNTLYLQMSLSRSEDYALYYCAPTTVPFAYWGQGLTVTVA 136
||:||||||| ||:||||||| ||:||||||| ||:||||||| ||:||||||| ||:|||||||

Search completed: November 18, 2002, 17:31:31
Job time : 163.735 secs

GenCore version 5.1.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:54:45 : Search time 22,941.2 Seconds
(without alignments)
76.811 Million cell updates/sec

Title: US-09-016-061-6

Perfect score: 612

Sequence: 1 EQVLVESGGGLVKPGRSLRL.....RHNYGSFAYWGQGLTVTWSA 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 97044 seqs, 15060890 residues

Total number of hits satisfying chosen parameters: 97044

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1:	/cgn2.6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
2:	/cgn2.6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3:	/cgn2.6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4:	/cgn2.6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5:	/cgn2.6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6:	/cgn2.6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
7:	/cgn2.6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
8:	/cgn2.6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9:	/cgn2.6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
10:	/cgn2.6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
11:	/cgn2.6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
12:	/cgn2.6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
13:	/cgn2.6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
14:	/cgn2.6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	DB ID	Description
1	612	100.0	117	8	US-08-790-540A-6	Sequence 6, Appli
2	612	100.0	117	8	US-08-791-391A-6	Sequence 6, Appli
3	552	90.2	117	8	US-08-790-540A-2	Sequence 2, Appli
4	552	90.2	117	8	US-08-791-391A-2	Sequence 2, Appli
5	497	81.2	245	9	US-09-956-086-5	Sequence 5, Appli
6	497	81.2	245	9	US-09-956-087-5	Sequence 5, Appli
7	497	81.2	265	9	US-09-985-442-5	Sequence 5, Appli
8	497	81.2	265	10	US-09-983-580-5	Sequence 46, Appli
9	485.5	79.3	137	9	US-09-423-800-46	Sequence 76, Appli
10	485.5	79.3	137	9	US-09-423-800-76	Sequence 2, Appli
11	476.5	77.9	240	10	US-09-968-561A-2	Sequence 2, Appli
12	476.5	77.9	240	10	US-09-192-854-2	Sequence 4, Appli
13	473	77.3	140	10	US-09-286-240-4	Sequence 12, Appli
14	472	77.1	144	10	US-09-881-823-12	Sequence 56, Appli
15	470.5	76.9	118	9	US-09-423-800-56	Sequence 77, Appli
16	470.5	76.9	137	9	US-09-423-800-77	Sequence 4, Appli
17	468.5	76.6	443	10	US-09-917-410-4	Sequence 3, Appli
18	468	76.5	119	10	US-09-811-123-3	Sequence 11, Appli
19	464	75.8	113	10	US-09-056-160B-11	

Query Match 100.0%; Score 612; DB 8; Length 117;
Best Local Similarity 100.0%; Pred. No. 9.8e-48;

ALIGNMENTS

RESULT 1

US-08-790-540A-6

; Sequence 6, Application US/08790540A

; Patent No. US2001011125A1

; GENERAL INFORMATION:

; APPLICANT: Huse, William D.

; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human

; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use

; NUMBER OF SEQUENCES: 24

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Campbell & Flores LLP

; STREET: 4370 La Jolla Village Drive, Suite 700

; CITY: San Diego

; STATE: California

; COUNTRY: United States

; ZIP: 92122

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/790,540A

; FILING DATE: 30-JAN-1997

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: Campbell, Cathryn A.

; REGISTRATION NUMBER: 31,815

; REFERENCE/DOCKET NUMBER: P-IX 2405

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (619) 535-9001

; TELEFAX: (619) 535-8949

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 117 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-790-540A-6

```

: NUMBER OF SEQUENCES: 24
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Campbell & Flores LLP
: STREET: 4370 La Jolla Village Drive, Suite 700
: CITY: San Diego
: STATE: California
: COUNTRY: United States
: ZIP: 92122
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/790,540A
: FILING DATE: 30-JAN-1997
: CLASSIFICATION: 424
: ATTORNEY/AGENT INFORMATION:
: NAME: Campbell, Cathryn A.
: REGISTRATION NUMBER: 31,815
: REFERENCE/DOCKET NUMBER: P-IX 2405
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (619) 535-9001
: TELEFAX: (619) 535-8949
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 117 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-790-540A-2

Query Match 90.2%; Score 552; DB 8; Length 117;
Best Local Similarity 88.0%; pred. No. 1.9e-42;
Matches 103; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVQGRSLRLSCAASGFAFSSYDSMWVRQIPEKRLIEWAKVSSGGSTYY 60
: QVQLVESGGGVQVQGRSLRLSCAASGFTFSSYDSMWVRQAPGKLEWAKVSSGGSTYY 60
Db- 1 QVQLVESGGGVQVQGRSLRLSCAASGFTFSSYDSMWVRQAPGKLEWAKVSSGGSTYY 60

Qy 61 LDTVGQRTISRDNKNTLYLQMSLNSDRTAMVYCARHNYGSPFAYWGQGLTVTVA 117
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Db 61 LDTVGQRTISRDNKNTLYLQMSLNSDRTAMVYCARHNYGSPFAYWGQGLTVTVSS 117

RESULT 4
US-08-791-391A-2
: Sequence 2, Application US/08791391A
: Patent No. US20010016645A1
: GENERAL INFORMATION:
: APPLICANT: Huse, William D.
: ATTORNEY/AGENT INFORMATION:
: NAME: Glaser, Scott M.
: TITLE OF INVENTION: Anti-Alpha v Beta 3 Recombinant Human
: TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
: NUMBER OF SEQUENCES: 32
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Campbell & Flores LLP
: STREET: 4370 La Jolla Village Drive, Suite 700
: CITY: San Diego
: STATE: California
: COUNTRY: United States
: ZIP: 92122
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/791,391A
: FILING DATE: 30-JAN-1997
: CLASSIFICATION: 424
: ATTORNEY/AGENT INFORMATION:
: NAME: Campbell, Cathryn A.

```

REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX 1482
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-791-391A-2

Query Match 90.2%; Score 552; DB 8; Length 117;
Best Local Similarity 88.0%; Pred. No. 1.9e-42;
Matches 103; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

Qy 1 EVLVESGGGLVKPGRSLRLSCAASGFAFSSYDMSWVRQIPEKRLWAKVSSGGGSTYY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 QVLVESGGGVQVGRSLRLSCAASGFTFSYDMSWVRQAPGKLEWAKVSSGGGSTYY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 61 LDTVOGRTISRDNKNTLYLQMSLSNSEDAMYCARHNYGSFAYWGGTLTVSA 117
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 LDTVOGRTISRDNKNTLYLQMSLSRAEDTAVVYCARHNYGSFAYWGGTTLTVSS 117
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 5
US-09-956-086-5
Sequence 5, Application US/09956086
Patent No. US20020155498A1
GENERAL INFORMATION:

APPLICANT: FILPULA, DAVID
WANG, MAOLIANG
SHORR, ROBERT
WHITLOW, MARC
LEE, LIHSYNG S.

TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS
CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF

NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC

COUNTRY: USA
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/956,086
FILING DATE: 20-Sep-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/069,821
FILING DATE: <Unknown>
APPLICATION NUMBER: US 60/063,074
FILING DATE: 27-OCT-1997
APPLICATION NUMBER: US 60/050,472
FILING DATE: 23-JUN-1997
APPLICATION NUMBER: US 60/044,449
FILING DATE: 30-APR-1997

ATTORNEY/AGENT INFORMATION:
NAME: KIM, JUDITH U.
REGISTRATION NUMBER: 40,679
REFERENCE/DOCKET NUMBER: 0977.2280003
TELEPHONE: (202)371-2600
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:

LENGTH: 245 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: No. US20020155498A1 Relevant
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-956-086-5

Query Match 81.2%; Score 497; DB 9; Length 245;
Best Local Similarity 81.9%; Pred. No. 2.7e-37;
Matches 95; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

Qy 1 EVLVESGGGLVKPGRSLRLSCAASGFAFSSYDMSWVRQIPEKRLWAKVSSGGGSTYY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 126 EVLVESGGGLVKPGRSLRLSCAASGFAFSTYDMSWVRQIPEKRLWATISSGGSTYY 185
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 61 LDTVOGRTISRDNKNTLYLQMSLSNSEDAMYCARHNYGSFAYWGGTLTVTS 116
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 186 LDSVKGRTISRDSARNTLYLQMSLSRSEDALYYCAPTTVVFPAYWGGTLTVTS 241
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 6

US-09-956-087-5
Sequence 5, Application US/09956087
Patent No. US20020161201A1
GENERAL INFORMATION:

APPLICANT: FILPULA, DAVID
WANG, MAOLIANG
SHORR, ROBERT
WHITLOW, MARC
LEE, LIHSYNG S.

TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS
CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF

NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC

COUNTRY: USA
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/956,087
FILING DATE: 20-Sep-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/069,821
FILING DATE: 1998-04-30
APPLICATION NUMBER: US 60/063,074
FILING DATE: 27-OCT-1997
APPLICATION NUMBER: US 60/050,472
FILING DATE: 23-JUN-1997
APPLICATION NUMBER: US 60/044,449
FILING DATE: 30-APR-1997

ATTORNEY/AGENT INFORMATION:
NAME: KIM, JUDITH U.
REGISTRATION NUMBER: 40,679
REFERENCE/DOCKET NUMBER: 0977.2280003
TELEPHONE: (202)371-2600
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:

LENGTH: 245 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide

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; SEQUENCE DESCRIPTION: SEQ ID NO: 5;
US-09-956-087-5
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Best Local Similarity 81.9%; Pred. No. 2.7e-37;
Matches 95; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

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QY 61 LDTVOGRFTISRDNKNTLYLQMSLSNSEDAMYCARHNYGSPAYWGQGLTVTS 116
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RESULT 7
US-09-985-442-5
; Sequence 5, Application US/09985442
; Patent No. US20020156248A1
; GENERAL INFORMATION:
; APPLICANT: Filpula, David R.
; APPLICANT: Wang, Maoliang
; APPLICANT: Whitlow, Marc D.
; TITLE OF INVENTION: No. US20020156248A1 Method for Targeted Delivery of Nucleic Acid
; FILE REFERENCE: 0977.2300003
; CURRENT APPLICATION NUMBER: US/09/985,442
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: 09/420,592
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/104,949
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 5
; LENGTH: 265
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: A33/218 sfv
US-09-985-442-5

Query Match      81.2%; Score 497; DB 9; Length 265;
Best Local Similarity 81.9%; Pred. No. 3e-37;
Matches 95; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

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Db 186 LDSVKGRFTISRDNKNTLYLQMSLSNSEDALYICAPTIVVPFAYWGQGLTVTS 241

RESULT 8
US-09-983-580-5
; Sequence 5, Application US/09983580
; Patent No. US20020151061A1
; GENERAL INFORMATION:
; APPLICANT: Filpula, David R.
; APPLICANT: Wang, Maoliang
; APPLICANT: Whitlow, Marc D.
; TITLE OF INVENTION: No. US20020151061A1 Method for Targeted Delivery of Nucleic Acid
; FILE REFERENCE: 0977.2300002
; CURRENT APPLICATION NUMBER: US/09/983,580
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: 09/420,592
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/104,949
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent In Ver. 2.1
US-09-983-580-5
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; SEQ ID NO 5
; LENGTH: 265
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: A33/218 sfv
US-09-983-580-5

Query Match      81.2%; Score 497; DB 10; Length 265;
Best Local Similarity 81.9%; Pred. No. 3e-37;
Matches 95; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

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QY 61 LDTVOGRFTISRDNKNTLYLQMSLSNSEDAMYCARHNYGSPAYWGQGLTVTS 116
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Db 186 LDSVKGRFTISRDNKNTLYLQMSLSNSEDALYICAPTIVVPFAYWGQGLTVTS 241

RESULT 9
US-09-423-800-46
; Sequence 46, Application US/09423800
; Patent No. US20020165363A1
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: TSUNENARI, TOSHIKI
; APPLICANT: ISHII, KIMIE
; TITLE OF INVENTION: CACHEXIA REMEDY
; FILE REFERENCE: 04853-0036
; CURRENT APPLICATION NUMBER: US/09/423,800
; CURRENT FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: PCT/JP98/02116
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: JP 125505/1997
; PRIOR FILING DATE: 1997-05-15
; PRIOR APPLICATION NUMBER: JP 194445/1997
; PRIOR FILING DATE: 1997-07-18
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 46
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-423-800-46

Query Match      79.3%; Score 485.5; DB 9; Length 118;
Best Local Similarity 80.5%; Pred. No. 1.4e-36;
Matches 95; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

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QY 61 LDTVOGRFTISRDNKNTLYLQMSLSNSEDAMYCARHNYGSPAYWGQGLTVTS 117
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RESULT 10
US-09-423-800-76
; Sequence 76, Application US/09423800
; Patent No. US20020165363A1
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: TSUNENARI, TOSHIKI
; APPLICANT: ISHII, KIMIE
; TITLE OF INVENTION: CACHEXIA REMEDY
; FILE REFERENCE: 04853-0036
; CURRENT APPLICATION NUMBER: US/09/423,800
; CURRENT FILING DATE: 1999-11-12
; SOFTWARE: Patent In Ver. 2.1
US-09-423-800-76
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; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: JP 125505/1997
; PRIOR FILING DATE: 1997-05-15
; PRIOR APPLICATION NUMBER: JP 194445/1997
; PRIOR FILING DATE: 1997-07-18
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 76
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-423-800-76

Query Match 79.3%; Score 485.5; DB 9; Length 137;
Best Local Similarity 80.5%; Pred. No. 1.6e-36;
Matches 95; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

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RESULT 11
US-09-968-561A-2
; Sequence 2, Application US/09968561A
; Patent No. US20020164642A1
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, Ian M
; APPLICANT: Winter, Gregory
; TITLE OF INVENTION: Method to Screen Phase Display Libraries with Different Ligands
; FILE REFERENCE: 8039/1073b
; CURRENT APPLICATION NUMBER: US/09/968,561A
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: GB 9722131.1
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/065,248
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/066,729
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: PCT/GB98/03135
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: US 09/511,939
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-968-561A-2

Query Match 77.9%; Score 476.5; DB 9; Length 240;
Best Local Similarity 76.9%; Pred. No. 1.7e-35;
Matches 90; Conservative 14; Mismatches 12; Indels 1; Gaps 1;

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RESULT 12
US-09-192-854-2
; Sequence 2, Application US/09192854
; Patent No. US20020068276A1
; GENERAL INFORMATION:

; APPLICANT: Winter, Greg
; APPLICANT: Tomlinson, Ian
; TITLE OF INVENTION: Methods for Selecting Functional Peptides
; FILE REFERENCE: 3789/72916
; CURRENT APPLICATION NUMBER: US/09/192,854
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/066,729
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-192-854-2

Query Match 77.9%; Score 476.5; DB 10; Length 240;
Best Local Similarity 76.9%; Pred. No. 1.7e-35;
Matches 90; Conservative 14; Mismatches 12; Indels 1; Gaps 1;

Qy 1 EVLVESGGGLVKPGSRRLSCAASGFAPSSYDMSWVRQIPEKRLWAKVSSGGSTYY 60
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RESULT 13
US-09-286-240-4
; Sequence 4, Application US/09286240
; Patent No. US20020010320A1
; GENERAL INFORMATION:
; APPLICANT: Felt, James W
; TITLE OF INVENTION: Chimeric and Humanized Antibodies to Angiogenin
; FILE REFERENCE: 10498/74073
; CURRENT APPLICATION NUMBER: US/09/286,240
; CURRENT FILING DATE: 1999-04-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-286-240-4

Query Match 77.3%; Score 473; DB 10; Length 140;
Best Local Similarity 77.7%; Pred. No. 2.1e-35;
Matches 94; Conservative 9; Mismatches 14; Indels 4; Gaps 2;

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Qy 117 A 117
; ;
Db 140 S 140

RESULT 14
US-09-881-823-12
; Sequence 12, Application US/09881823
; Patent No. US20020068066A1
; GENERAL INFORMATION:
; APPLICANT: SHI, WENYUAN
; APPLICANT: ANDERSON, MAXWELL
; APPLICANT: MORRISON, SHERIE
; APPLICANT: TRINH, RYAN

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:01 ; Search time 49.6103 Seconds
(without alignments)
69.390 Million cell updates/sec

Title: US-09-016-061-6
Perfect score: 612
Sequence: 1 EQVLVESGGGLVPGESRL.....RHNGSFAYWGQTLTVTSA 117

Scoring table: BLOSUM62

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	501	81.9	117	4	US-08-752-693A-3
2	501	81.9	136	4	US-08-976-183A-31
3	501	81.9	136	4	US-08-976-183A-32
4	501	81.9	136	4	US-08-976-183A-33
5	501	81.9	136	4	US-08-976-183A-34
6	497	81.2	237	2	US-08-224-591-16
7	497	81.2	237	2	US-08-926-789-16
8	497	81.2	241	2	US-08-224-591-18
9	497	81.2	241	2	US-08-926-789-18
10	497	81.2	245	4	US-09-069-821-5
11	497	81.2	265	4	US-09-420-592A-5
12	496	81.0	136	1	US-08-253-877C-57
13	496	81.0	136	2	US-08-452-164A-57
14	486	79.4	247	5	PCT-US94-07659-2
15	485.5	79.3	139	1	US-08-129-930B-96
16	485.5	79.3	139	4	US-08-134-346A-51
17	485.5	79.3	139	4	US-08-976-288A-96
18	484.5	79.2	118	4	US-08-487-761-15
19	477	77.9	119	1	US-08-053-171-14
20	477	77.9	119	1	US-08-053-171-17
21	477	77.9	119	3	US-08-615-190A-13
22	476	77.8	119	2	US-08-475-000-16
23	476	77.8	119	2	US-08-483-199-16
24	476	77.8	119	2	US-08-484-508-16
25	476	77.8	125	1	US-08-331-398A-65
26	476	77.8	125	2	US-08-331-397B-65
27	476	77.8	125	2	US-08-759-804A-64

28 476 77.8 138 1 US-08-053-171-7 Sequence 7, Appli
29 476 77.8 138 1 US-08-053-171-11 Sequence 11, Appl
30 474 77.5 119 1 US-08-053-171-13 Sequence 13, Appl
31 473 77.3 117 4 US-08-752-693A-4 Sequence 4, Appl
32 473 77.3 150 4 US-08-976-183A-55 Sequence 55, Appl
33 469.5 76.7 135 4 US-08-579-378A-16 Sequence 16, Appl
34 468.5 76.6 135 4 US-08-579-378A-20 Sequence 20, Appl
35 468.5 76.6 443 5 PCT-US96-13152-4 Sequence 4, Appl
36 465 76.0 119 1 US-08-053-171-12 Sequence 12, Appl
37 464 75.8 113 3 US-08-974-899-6 Sequence 6, Appl
38 464 75.8 118 2 US-08-379-057-30 Sequence 30, Appl
39 463 75.7 117 4 US-09-025-769B-24 Sequence 24, Appl
40 463 75.7 158 2 US-08-653-402B-6 Sequence 6, Appl
41 463 75.7 158 2 US-08-653-402B-10 Sequence 10, Appl
42 462 75.5 138 2 US-08-379-057-14 Sequence 14, Appl
43 461.5 75.4 122 3 US-07-934-373C-21 Sequence 21, Appl
44 461.5 75.4 122 3 US-08-437-642B-21 Sequence 21, Appl
45 461.5 75.4 122 4 US-08-146-206C-21 Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-08-752-693A-3
; Sequence 3, Application US/08752693A
; Patent No. 6190640
; GENERAL INFORMATION:
; APPLICANT: Sydney Welt
; Gerd Ritter
; Leonard Cohen
; Clarence William Jr.
; Elizabeth Carswell Richards
; Mary John
; TITLE OF INVENTION: METHOD FOR TREATING NEOPLASIA
; USING HUMANIZED ANTIBODIES WHICH
; BIND TO ANTIGEN A33
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski LLP
; STREET: 666 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
; COMPUTER: IBM PAULINE STASIAK, PH.D./2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/752.693A
; FILING DATE: 19-No. 6190640-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/07321
; FILING DATE: May 21, 1996
; APPLICATION NUMBER: 08/020.223
; FILING DATE: February 16, 1993
; APPLICATION NUMBER: 07/673.153
; FILING DATE: March 18, 1991
; APPLICATION NUMBER: 07/327.765
; FILING DATE: March 23, 1989
; APPLICATION NUMBER: 07/118.411
; FILING DATE: No. 6190640ember 6, 1987
; APPLICATION NUMBER: 06/724.991
; FILING DATE: April 19, 1985
; ATTORNEY/AGENT INFORMATION:
; NAME: Mary Anne Schofield
; REGISTRATION NUMBER: 36,669
; REFERENCE/DOCKET NUMBER: LUD 5381.1 CIP - JEL/MAS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000


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;
; TELEFAX: (212) 318-3400
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: <Unknown>
; ORIGINAL SOURCE:
; ORGANISM: Mice A33
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-08-752-693A-3

Query Match      81.9%; Score 501; DB 4; Length 117;
Best Local Similarity 82.1%; Pred. No. 1.7e-43;
Matches 96; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

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Db 1 EVKLVESGGGLVPGGSLKLSCAASGFAFSTYDMSWVRQTPKRLWVATISSGGSTYY 60
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Db 61 LDSVKGRFTISRDSARNTLYQMSSLSRSED TALYYCAPTVVPFAYWGQGLTVTVA 117

RESULT 2
US-08-976-183A-31
; Sequence 31, Application US/08976183A
; Patent No. 6307026
; GENERAL INFORMATION:
; APPLICANT: King, David J.
; APPLICANT: Adair, John R.
; APPLICANT: Owens, Raymond J.
; TITLE OF INVENTION: HUMANISED ANTIBODIES DIRECTED AGAINST A33
; TITLE OF INVENTION: ANTIGEN
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K. Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/976,183A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/595,848
; FILING DATE: 02-FEB-1996
; APPLICATION NUMBER: PCT/GB93/02529
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9225853.2
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9315249.4
; FILING DATE: 22-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Bernhard D. Saxe
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 40283/151/CARA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 136 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; INFORMATION FOR SEQ ID NO: 31:
US-08-976-183A-32
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;
; LENGTH: 136 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-976-183A-31

Query Match      81.9%; Score 501; DB 4; Length 136;
Best Local Similarity 82.1%; Pred. No. 2e-43;
Matches 96; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVPGGSLRLSCAASGFAFSSYDMSWVRQIPEKRLWVAKVSSGGSTYY 60
Db 20 EVKLVESGGGLVPGGSLKLSCAASGFAFSTYDMSWVRQTPKRLWVATISSGGSTYY 79
QY 61 LDTVQGRFTISRDAKNTLYQMSSLSNEDTAMYYCARHNYGSFAYWGQGLTVTVA 117
Db 80 LDSVKGRFTISRDSARNTLYQMSSLSRSED TALYYCAPTVVPFAYWGQGLTVTVA 136

RESULT 3
US-08-976-183A-32
; Sequence 32, Application US/08976183A
; Patent No. 6307026
; GENERAL INFORMATION:
; APPLICANT: King, David J.
; APPLICANT: Adair, John R.
; APPLICANT: Owens, Raymond J.
; TITLE OF INVENTION: HUMANISED ANTIBODIES DIRECTED AGAINST A33
; TITLE OF INVENTION: ANTIGEN
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K. Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/976,183A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/595,848
; FILING DATE: 02-FEB-1996
; APPLICATION NUMBER: PCT/GB93/02529
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9225853.2
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9315249.4
; FILING DATE: 22-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Bernhard D. Saxe
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 40283/151/CARA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 136 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; INFORMATION FOR SEQ ID NO: 32:
US-08-976-183A-32
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Query Match 81.9%; Score 501; DB 4; Length 136;
Best Local Similarity 82.1%; Pred. No. 2e-43;
Matches 96; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVPGKSLRLSCAASGFAFSSYDMSWVRQIPEKRLWYAKVSSGGSTYY 60
Db 20 EVKLVESGGGLVPGKSLRLSCAASGFAFSSYDMSWVRQIPEKRLWYAKVSSGGSTYY 79

Qy 61 LDTVGRTTISRDNKNTLYLQMSLSNSEDATMYICARHNYGSFAYWGQGLTVTVSA 117
Db 80 LDSVKGRTTISRDSARNTLYLQMSLSRSEDATLYICAPTTPVVPFAYWGQGLTVTVSA 136

RESULT 4

US-08-976-183A-33
; Sequence 33, Application US/08976183A
; Patent No. 6307026
; GENERAL INFORMATION:
; APPLICANT: King, David J.
; APPLICANT: Adair, John R.
; APPLICANT: Owens, Raymond J.
; TITLE OF INVENTION: HUMANISED ANTIBODIES DIRECTED AGAINST A33
; TITLE OF INVENTION: ANTIGEN
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K. Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/976,183A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/595,848
; FILING DATE: 02-FEB-1996
; APPLICATION NUMBER: PCT/GB93/02529
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9225853.2
; FILING DATE: 10-DEC-1993
; APPLICATION NUMBER: 9315249.4
; FILING DATE: 22-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Bernhard D. Saxe
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 40283/151/CARA
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 136 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-976-183A-33

Query Match 81.9%; Score 501; DB 4; Length 136;
Best Local Similarity 82.1%; Pred. No. 2e-43;
Matches 96; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVPGKSLRLSCAASGFAFSSYDMSWVRQIPEKRLWYAKVSSGGSTYY 60
Db 20 EVKLVESGGGLVPGKSLRLSCAASGFAFSSYDMSWVRQIPEKRLWYAKVSSGGSTYY 79

Qy 61 LDTVGRTTISRDNKNTLYLQMSLSNSEDATMYICARHNYGSFAYWGQGLTVTVSA 117
Db 80 LDSVKGRTTISRDSARNTLYLQMSLSRSEDATLYICAPTTPVVPFAYWGQGLTVTVSA 136

RESULT 5

US-08-976-183A-34
; Sequence 34, Application US/08976183A
; Patent No. 6307026
; GENERAL INFORMATION:
; APPLICANT: King, David J.
; APPLICANT: Adair, John R.
; APPLICANT: Owens, Raymond J.
; TITLE OF INVENTION: HUMANISED ANTIBODIES DIRECTED AGAINST A33
; TITLE OF INVENTION: ANTIGEN
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K. Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/976,183A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/595,848
; FILING DATE: 02-FEB-1996
; APPLICATION NUMBER: PCT/GB93/02529
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9225853.2
; FILING DATE: 10-DEC-1993
; APPLICATION NUMBER: 9315249.4
; FILING DATE: 22-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Bernhard D. Saxe
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 40283/151/CARA
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 136 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-976-183A-34

Query Match 81.9%; Score 501; DB 4; Length 136;
Best Local Similarity 82.1%; Pred. No. 2e-43;
Matches 96; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVPGKSLRLSCAASGFAFSSYDMSWVRQIPEKRLWYAKVSSGGSTYY 60
Db 20 EVKLVESGGGLVPGKSLRLSCAASGFAFSSYDMSWVRQIPEKRLWYAKVSSGGSTYY 79

Qy 61 LDTVGRTTISRDNKNTLYLQMSLSNSEDATMYICARHNYGSFAYWGQGLTVTVSA 117
Db 80 LDSVKGRTTISRDSARNTLYLQMSLSRSEDATLYICAPTTPVVPFAYWGQGLTVTVSA 136

RESULT 6

US-08-224-591-16
; Sequence 16, Application US/08224591
; Patent No. 5856456
; GENERAL INFORMATION:
; APPLICANT: Whitlow, Marc
; APPLICANT: Filpula, David
; TITLE OF INVENTION: Linker For Linked Fusion Polypeptides
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/224,591
; FILING DATE: Herewith
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/002,845
; FILING DATE: 15-JAN-1993
; APPLICATION NUMBER: US 07/980,529
; FILING DATE: 20-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldstein, Jorge A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0977.1920002/JAG
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 237 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-224-591-16

Query Match 81.2%; Score 497; DB 2; Length 237;
Best Local Similarity 81.9%; Pred. No. 9,6e-43;
Matches 95; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVPGKSRLLSCAASGFAFSDYMSVWRQIPEKRLWVAKVSSGGSTYY 60
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 122 EVKLVESGGGLVPGKSLKLSCAASGFAFSDYMSVWRQIPEKRLWVATISSGGSTYY 181

Qy 61 LDTVGRTISRDNKNTLYLQMSLSNSEDYMYCARHNYGSFAYWGQGLTVTS 116
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 182 LDSVKGRFTISRDSRNTLYLQMSLSRSEDYALYYCAPTVVVPFAYWGQGLTVTS 237

RESULT 7
US-08-926-789-16
; Sequence 16, Application US/08926789
; Patent No. 5990275
; GENERAL INFORMATION:
; APPLICANT: Whitlow, Marc
; APPLICANT: Filpula, David
; TITLE OF INVENTION: Linker For Linked Fusion Polypeptides
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/926,789
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/224,591
; FILING DATE:
; APPLICATION NUMBER: US 08/002,845
; FILING DATE: 15-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/980,529
; FILING DATE: 20-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldstein, Jorge A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0977.1920002/JAG
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 237 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-926-789-16

Query Match 81.2%; Score 497; DB 2; Length 237;
Best Local Similarity 81.9%; Pred. No. 9,6e-43;
Matches 95; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVPGKSRLLSCAASGFAFSDYMSVWRQIPEKRLWVAKVSSGGSTYY 60
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 122 EVKLVESGGGLVPGKSLKLSCAASGFAFSDYMSVWRQIPEKRLWVATISSGGSTYY 181

Qy 61 LDTVGRTISRDNKNTLYLQMSLSNSEDYMYCARHNYGSFAYWGQGLTVTS 116
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 182 LDSVKGRFTISRDSRNTLYLQMSLSRSEDYALYYCAPTVVVPFAYWGQGLTVTS 237

RESULT 8
US-08-224-591-18
; Sequence 18, Application US/08224591
; Patent No. 5856456
; GENERAL INFORMATION:
; APPLICANT: Whitlow, Marc
; APPLICANT: Filpula, David
; TITLE OF INVENTION: Linker For Linked Fusion Polypeptides
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/224,591
; FILING DATE: Herewith
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/002,845
; FILING DATE: 15-JAN-1993

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;
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-926-789-18

Query Match      81.2%; Score 497; DB 2; Length 241;
Best Local Similarity 81.9%; Pred. NO. 9.7e-43;
Matches 95; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

QY    1 EVLVESGGGLVPGRLSLRSCAASGFAFSYDMSWVRQIPEKRLEWAKVSSGGSTYY 60
      II::IIIIIIIIII II::IIIIIIIIII:IIIIIIIIII:IIIIIIIIII:IIII III
Db    126 EVKLVESGGGLVPGKSGLKLSCAASGAFFATYDMSWVRQTPEKRLEWAVTISGGSYTY 185
      II::IIIIIIIIII:IIIIIIIIII:IIIIIIIIII:IIIIIIIIII:IIIIIIIIII
QY    61 LDTVOGRFTISRDNAKNTLYLOMSSLNSDETAMYICARHNYGSFAYQGQGLTVTS 116
      II::IIIIIIIIII:IIIIIIIIII:IIIIIIIIII:IIIIIIIIII:IIIIIIIIII
Db    186 LDSVKGRFTIRDSARNLTLYLQMSSLRSDELTALYYCAPTTVPFYAQGQGLTVTS 241
      II::IIIIIIIIII:IIIIIIIIII:IIIIIIIIII:IIIIIIIIII:IIIIIIIIII

RESULT 10
US-09-069-821-5
; Sequence 5, Application US/09069821
; Patent No. 6323322
; GENERAL INFORMATION:
; APPLICANT: FILPUILA, DAVID
; APPLICANT: WANG, MAOLIANG
; APPLICANT: SHORR, ROBERT
; APPLICANT: WHITLOW, MARC
; APPLICANT: LEE, LIHSYNG S.
; TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS
; TITLE OF INVENTION: CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/069,821
; FILING DATE: 30-APR-1998
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/067,341
; FILING DATE: 02-DEC-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/063,074
; FILING DATE: 27-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/050,472
; FILING DATE: 23-JUN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/044,449
; FILING DATE: 30-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: KIM, JUDITH U.
; REGISTRATION NUMBER: 40,679
; REFERENCE/DOCKET NUMBER: 0977.2280003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)371-2600
; TELEFAX: (202)371-2540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 245 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
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Job time : 50.6103 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:01 ; Search time 52.451 Seconds
(without alignments)
196.114 Million cell updates/sec

Title: US-09-016-061-8
Perfect score: 561
Sequence: 1 DIVLTQSPATLSVTPGDVS.....CQSGSWPHTFGGKLEIK 107

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	528	94.3	107	2 A45722	anti-glycoprotein
2	528	94.1	107	2 B45722	anti-glycoprotein
3	523	93.2	123	2 S35479	Ig kappa chain pre
4	513	91.4	106	2 PL0267	Ig kappa chain v r
5	507	90.4	138	2 A26471	Ig kappa chain pre
6	499	88.9	102	2 S26346	Ig kappa chain v r
7	497	88.6	104	2 B43413	Ig kappa chain v r
8	482	85.9	107	2 C45722	anti-glycoprotein
9	434	77.4	108	2 C30502	Ig kappa chain v r
10	424	75.6	103	2 S19375	Ig kappa chain v r
11	420	74.9	128	2 PN0445	Ig kappa chain pre
12	402	71.7	96	2 G33730	Ig kappa chain v r
13	379	67.6	115	1 KVMSL7	Ig kappa chain pre
14	378	67.4	144	2 PL0106	Ig kappa chain pre
15	374	66.7	111	2 S23628	Ig kappa chain v r
16	374	66.7	117	2 S40362	Ig kappa chain - h
17	374	66.7	128	2 S40379	Ig kappa chain v r
18	373.5	66.6	114	2 S54905	Ig kappa chain v r
19	372	66.3	108	2 S19674	Ig kappa chain v r
20	372	66.3	128	2 A56701	Ig kappa chain v r
21	368	65.6	106	2 PC4282	Ig kappa chain (an
22	368	65.6	108	2 G44151	Ig kappa chain v r
23	367	65.4	107	2 S34005	Ig kappa chain v r
24	365.5	65.2	215	2 JE0244	Ig kappa chain NIG
25	365	65.1	128	2 S40343	Ig kappa chain v r
26	364	64.9	128	1 K3HU41	Ig kappa chain pre
27	360.5	64.3	109	2 A30808	Ig kappa chain v r
28	360.5	64.3	129	2 A32274	Ig kappa chain pre
29	359	64.0	111	2 S09963	Ig kappa chain v r

30	359	64.0	128	2 S40345	Ig kappa chain v r
31	358.5	63.9	109	2 G30607	Ig kappa chain v r
32	357.5	63.7	108	2 B30608	Ig kappa chain v r
33	356.5	63.5	109	1 K3HUPM	Ig kappa chain v r
34	355.5	63.4	116	2 B26555	Ig kappa chain v r
35	355	63.3	108	2 S36279	Ig lambda chain v
36	354.5	63.2	109	2 H30601	Ig kappa chain v r
37	354	63.1	125	2 S40344	Ig kappa chain v r
38	354	63.1	129	2 S29627	Ig kappa chain v r
39	353	62.9	108	2 B49047	Ig kappa chain v r
40	352.5	62.8	109	2 G30601	Ig kappa chain v r
41	352	62.7	107	2 S36264	Ig lambda chain v
42	351	62.6	107	2 S57444	Ig kappa chain v r
43	350.5	62.5	108	2 C30608	Ig kappa chain v r
44	350.5	62.5	109	1 K3HUTI	Ig kappa chain v r
45	349.5	62.3	109	2 D30601	Ig kappa chain v r

ALIGNMENTS

RESULT 1
A45722
anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 5) - mouse (C:Species: Mus musculus (house mouse))
C:Date: 03-Mar-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: A45722
R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Va J. Virol. 67, 489-496, 1993
A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on A:Reference number: A45722; MUID:93100833; PMID:7677958
A:Accession: A45722
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-107 <SIM>
A:Note: sequence extracted from NCBI backbone (NCBIP:120589)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: glycoprotein
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match	94.3%	Score 529;	DB 2;	Length 107;
Best Local Similarity	93.5%	Pred: No. 7e-41;		
Matches 100;	Conservative 3;	Mismatches 4;	Indels 0;	Gaps 0;
Qy	1	DIVLTQSPATLSVTPGDVSLSQASQSI	NHLHWYQKSHESPRLLIKYRSQISGIPS	60
Db	1	DIVLTQSPATLSVTPGDVSLSQASQSI	NHLHWYQKSHESPRLLIKYASQISGIPS	60
Qy	61	RFGSGSGTDFALSNVETEDFGMYFCQ	SGSWPHTFGGKLEIK	107
Db	61	RFGSGSGTDFTLVNGVETEDFGMYFC	QSGNSWPHTFGGKLEIK	107

RESULT 2
B45722
anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 33) - mouse (C:Species: Mus musculus (house mouse))
C:Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: B45722
R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Va J. Virol. 67, 489-496, 1993
A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on A:Reference number: A45722; MUID:93100833; PMID:7677958
A:Accession: B45722
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-107 <SIM>
A:Note: sequence extracted from NCBI backbone (NCBIP:120590)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: glycoprotein
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 94.1%; Score 528; DB 2; Length 107;


```

Best Local Similarity 93.5%; Pred. No. 8.6e-41;
Matches 100; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIVLTQSPATLSVTPGDSVSLSCQASQISNHLHWYQOKSHSPRLLIKYSQISGIPS 60
|||||
Db 1 DIVLTQSPATLSVTPGDSVSLSCRASQISNNLHWYQOKSHSPRLLIKVASQISGIPS 60
|||||

QY 61 RFGSGSGTDFALSINSVETEDFGMYFCQOQSGSWPHTFGGTTKLEIK 107
|||||
Db 61 RFGSGSGTDFTLTINSVETEDFGMYFCQQTNSWPHTFGGTTKLEIK 107
|||||

RESULT 3
S35479
Ig kappa chain precursor V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-Mar-1997 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: S35479
R:Takeda, Y.; Wise, K.S.; Hoffman, R.W.
Nucleic Acids Res. 20, 4099, 1992
A:Title: Nucleotide sequences of immunoglobulin heavy and light chain V-regions from a m
A:Reference number: S35479; MUID:92375706; PMID:1387203
A:Accession: S35479
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-123 <TAK>
A:Cross-references: EMBL:M93959; NID:g197572; PIDN:AAA39079.1; PID:g554148
C:Genetics:
A:Map position: 6
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-12/Domain: signal sequence (fragment) #status predicted <SIG>
F:13-123/Product: Ig kappa chain V region (fragment) #status predicted <MAT>
F:28-102/Domain: immunoglobulin homology <IMM>

Query Match 93.2%; Score 523; DB 2; Length 123;
Best Local Similarity 93.5%; Pred. No. 2.8e-40;
Matches 100; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIVLTQSPATLSVTPGDSVSLSCQASQISNHLHWYQOKSHSPRLLIKYSQISGIPS 60
|||||
Db 13 DIVLTQSPATLSVTPGDKVSLSCRASQISNNLHWYQOKSHSPRLLIKVSQISGIPS 72
|||||

QY 61 RFGSGSGTDFALSINSVETEDFGMYFCQOQSGSWPHTFGGTTKLEIK 107
|||||
Db 73 RFGSGSGTDFTLTINSVETEDFGMYFCQOQSNWPHTFGGTTKLEIK 119
|||||

RESULT 4
PL0267
Ig kappa chain V region (anti-DNA, DP12VK) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C:Accession: PL0267
R:Shlomchik, M.; Masei, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A
J. Exp. Med. 171, 265-297, 1990
A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
A:Reference number: PL0231; MUID:90111618; PMID:2104919
A:Accession: PL0267
A:Molecule type: mRNA
A:Residues: 1-106 <SHL>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-23/Region: framework 1
F:16-90/Domain: immunoglobulin homology <IMM>
F:24-34/Region: complementarity-determining 1
F:35-49/Region: framework 2
F:50-56/Region: complementarity-determining 2
F:57-88/Region: framework 3
F:89-97/Region: complementarity-determining 3
F:98-106/Region: framework 4

Query Match 91.4%; Score 513; DB 2; Length 106;

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Best Local Similarity 92.5%; Pred. No. 1.9e-39;
Matches 98; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIVLTQSPATLSVTPGDSVSLSCQASQISNHLHWYQOKSHSPRLLIKYSQISGIPS 60
|||||
Db 1 DIVLTQSPATLSVTPGDRVSLSCRASQISNNLHWYQOKSHSPRLLIKVASQISGIPS 60
|||||

QY 61 RFGSGSGTDFALSINSVETEDFGMYFCQOQSGSWPHTFGGTTKLEIK 106
|||||
Db 61 RFGSGSGTDFTLTINSVETEDFGMYFCQOQSNWPHTFGGTTKLEIK 106
|||||

RESULT 5
A26471
Ig kappa chain precursor V region (MAK33) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 23-Jul-1999
C:Accession: A26471
R:Buckel, P.; Hubner-Parajsz, C.; Mattes, R.; Lenz, H.; Haug, H.; Beaucamp, K.
Gene 51, 13-19, 1987
A:Title: Cloning and nucleotide sequence of heavy- and light-chain cDNAs from a creat
A:Reference number: A91572; MUID:87248058; PMID:3110009
A:Accession: A26471
A:Molecule type: mRNA
A:Residues: 1-138 <BUC>
A:Cross-references: GB:M1612; NID:g196893; PIDN:AAA38823.1; PID:g196894
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-138/Product: Ig kappa chain V region #status predicted <MAT>

Query Match 90.4%; Score 507; DB 2; Length 138;
Best Local Similarity 91.6%; Pred. No. 8.8e-39;
Matches 98; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIVLTQSPATLSVTPGDSVSLSCQASQISNHLHWYQOKSHSPRLLIKYSQISGIPS 60
|||||
Db 21 DIVLTQSPATLSVTPRDSVSLSCRASQISNNLHWYQOKSHSPRLLIKVASQISGIPS 80
|||||

QY 61 RFGSGSGTDFALSINSVETEDFGMYFCQOQSGSWPHTFGGTTKLEIK 107
|||||
Db 81 RFGSGSGTDFTLTINSVETEDFGMYFCQOQSNWPHTFGAGTTKLEIK 127
|||||

RESULT 6
S26346
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C:Accession: S26346
R:Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A:Title: Antibodies that are specific for a single amino acid interchange in a protei
A:Reference number: S26309; MUID:91341421; PMID:1908510
A:Accession: S26346
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-102 <STA>
A:Cross-references: EMBL:X59211; NID:g52338; PIDN:CAA41921.1; PID:g1334075
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:14-88/Domain: immunoglobulin homology <IMM>

Query Match 88.9%; Score 499; DB 2; Length 102;
Best Local Similarity 93.1%; Pred. No. 3.3e-38;
Matches 95; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 VLTQSPATLSVTPGDSVSLSCQASQISNHLHWYQOKSHSPRLLIKYSQISGIPS 62
|||||
Db 1 VLTQSPATLSVTPGDSVSLSCRASQISNNLHWYQOKSHSPRLLIKVSQISGIPS 60
|||||

QY 63 SGSGSGTDFALSINSVETEDFGMYFCQOQSGSWPHTFGGTTKLEIK 104
|||||

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Db 61 GSGSGTDFTLINSVETEDFGMYFCQSQSNTPYTFGGGTKL 102
RESULT 7
B43413
Ig kappa chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: B43413
R:Tomiyama, Y.; Brojer, E.; Ruggeri, Z.M.; Shattil, S.J.; Smiltneck, J.; Gorski, J.; Kum
J. Biol. Chem. 267, 18085-18092, 1992
A:Title: A molecular model of RGD ligands. Antibody D gene segments that direct specific
A:Reference number: A43413; MUID:92388177; PMID:1517241
A:Accession: B43413
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-104 <ROM>
A:Note: sequence extracted from NCBI backbone (NCBIP:112818)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:13-87/Domain: immunoglobulin homology <IMM>
Query Match 88.6%; Score 497; DB 2; Length 104;
Best Local Similarity 91.3%; Pred. No. 5.1e-38;
Matches 95; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
QY 4 LTQSPATLSVTPGDSVSLSCQASQISNHLHWYQOKSHSPRLLIKYRSQISGIPSRFS 63
DB 1 LTQSPATLSVTPGDSVSLSCRASQISNHLHWYQOKSHSPRLLIKYASQISGIPSRFS 60
QY 64 GSGSGTDFALINSVETEDFGMYFCQSQSNTPYTFGGGTKLEIK 107
DB 61 GSGSGTDFTLINSVETEDFGMYFCQSQSNWPLTFGAGSKLEIK 104
RESULT 8
C45722
anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 115) - mouse (f
C:Species: Mus musculus (house mouse)
C>Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: C45722
R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Vasqu
J. Virol. 67, 489-496, 1993
A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on hu
A:Reference number: A45722; MUID:93100833; PMID:7677958
A:Accession: C45722
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-107 <SIM>
A:Note: sequence extracted from NCBI backbone (NCBIP:120591)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: glycoprotein
F:16-90/Domain: immunoglobulin homology <IMM>
Query Match 85.9%; Score 482; DB 2; Length 107;
Best Local Similarity 85.8%; Pred. No. 1.2e-36;
Matches 91; Conservative 8; Mismatches 7; Indels 0; Gaps 0;
QY 2 IVLTQSPATLSVTPGDSVSLSCQASQISNHLHWYQOKSHSPRLLIKYRSQISGIPSR 61
DB 2 VVLTQSPATLSVTPGDSVSLSCRASQISNHLHWYQOKSHGSPRLLIKYASQISGIPSR 61
QY 62 FSGSGTDFALINSVETEDFGMYFCQSQSNTPYTFGGGTKLEIK 107
DB 62 FSGSGTDFTLINSVETEDLGMVFCQSQSNWPLTFGAGTKLEIK 107
RESULT 9
C30502
Ig kappa chain V region (D444) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 03-Nov-1988 #sequence_revision 03-Nov-1988 #text_change 21-Jan-2000
C:Accession: C30502
R:Eilat, D.; Webster, D.M.; Rees, A.R.
J. Immunol. 141, 1745-1753, 1988
A:Title: V region sequences of anti-DNA and anti-RNA autoantibodies from NZB/NZW F-1
A:Reference number: A30502; MUID:88315787; PMID:2457627
A:Accession: C30502
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-108 <ETL>
A:Cross-references: GB:M21907; NID:g197071; PIDN:AAA38907.1; PID:g197072
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>
Query Match 77.4%; Score 434; DB 2; Length 108;
Best Local Similarity 76.6%; Pred. No. 2.5e-32;
Matches 82; Conservative 11; Mismatches 14; Indels 0; Gaps 0;
QY 1 DIVTQSPATLSVTPGDSVSLSCQASQISNHLHWYQOKSHSPRLLIKYRSQISGIPSRFS 60
DB 1 DILLTQSPAILSVSPGERVFSRCRASQISGTLHWYQORTNGSPRLLIKYASESISGIPSRFS 60
QY 61 RFGSGSGTDFALINSVETEDFGMYFCQSQSNTPYTFGGGTKLEIK 107
DB 61 RFGSGSGTDFTLINSVETEDVADYQQTNSWPRTFEGGTKLEIK 107
RESULT 10
S19975
Ig kappa chain V region (M-T408) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C:Accession: S19975
R:Weissenhorn, W.; Riethmuller, G.; Weiss, E.M.; Rieber, E.P.
submitted to the EMBL Data Library, March 1992
A:Description: Structural characterization of CD4 mAb.
A:Reference number: S19963
A:Accession: S19975
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-103 <WEI>
A:Cross-references: EMBL:X65097; NID:g52296; PIDN:CAA46225.1; PID:g52297
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:11-85/Domain: immunoglobulin homology <IMM>
Query Match 75.6%; Score 424; DB 2; Length 103;
Best Local Similarity 77.5%; Pred. No. 1.9e-31;
Matches 79; Conservative 14; Mismatches 9; Indels 0; Gaps 0;
QY 6 QSPATLSVTPGDSVSLSCQASQISNHLHWYQOKSHSPRLLIKYRSQISGIPSRFS 65
DB 1 QSPATLSLSPGERATLSCRASQISDYLHWYQOKSHSPRLLIREFVSQISGIPSRFS 60
QY 66 GSGTDFALINSVETEDFGMYFCQSQSNTPYTFGGGTKLEIK 107
DB 61 GSGSDFTLINSVETEDGVVYVYQNGHSPFYTFGGGTKLEIK 102
RESULT 11
PN0445
Ig kappa chain precursor V-I region - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C:Accession: PN0445
R:Kaluza, B.; Betzl, G.; Shao, H.; Diamantstein, T.; Weidle, U.H.
Gene 122, 321-328, 1992
A:Title: A general method for chimerization of monoclonal antibodies by inverse polym
A:Reference number: PN0444; MUID:93138402; PMID:1339379
A:Accession: PN0445
A:Molecule type: mRNA
A:Residues: 1-128 <KAL>
A:Cross-references: GB:L02347
C:Superfamily: immunoglobulin V region; immunoglobulin homology
```

F:36-110/Domain: immunoglobulin homology <IMM>
F:43-108/Disulfide bonds: #status predicted

Query Match 67.6%; Score 379; DB 1; Length 115;
Best Local Similarity 74.7%; Pred. No. 2.3e-27;
Matches 71; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY 1 DIVLTQSPATLSVTPGDVSLSCQASQISNHLHWYQOKSHSPRLLIKYRSQISGIPS 60
|||:||||| |||:|: |||:||||| :|||||: ||||||| |:|||||
Db 21 DILLTQSPAILSVSPGERVFSQASQISGTSIHVYQRTNGSPRLLIKYASISGIPS 80

QY 61 RFGSGSGTDFALINSVETEDFGMYFCQSGSWP 95
|||||:||||| ||||||:|: |||:||||| |||

Db 81 RFGSGSGTDFTLINSVESEDIADYYCQSGNSWP 115

RESULT 14

PL0106
Ig kappa chain precursor V-J-C region (Lsl) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C:Accession: PL0106
R:Silberstein, L.E.; Litwin, S.; Carmack, C.E.
J. Exp. Med. 169, 1631-1643, 1989
A:Title: Relationship of variable region genes expressed by a human B cell lymphoma
A:Reference number: PL0106; MUID:89235583; PMID:2541221
A:Accession: PL0106
A:Molecule type: mRNA
A:Residues: 1-144 <SIL>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-115/Domain: V region <VRE>
F:36-110/Domain: immunoglobulin homology <IMM>
F:44-54/Region: complementarity-determining 1
F:70-76/Region: complementarity-determining 2
F:109-115/Region: complementarity-determining 3
F:116-127/Domain: J region <JRG>
F:128-144/Domain: C region (fragment) <CRE>

Query Match 67.4%; Score 378; DB 2; Length 144;
Best Local Similarity 64.3%; Pred. No. 3.7e-27;
Matches 69; Conservative 21; Mismatches 17; Indels 0; Gaps 0;

QY 1 DIVLTQSPATLSVTPGDVSLSCQASQISNHLHWYQOKSHSPRLLIKYRSQISGIPS 60
:|||||:|||||:|: |||:|||||:|: |||:|: |||:|: |||:|: |||:
Db 21 EIVLTQSPATLSVSPGERVFSQASQISGTSIHVYQRTNGSPRLLIKYASISGIPS 80

QY 61 RFGSGSGTDFALINSVETEDFGMYFCQSGSWPHTFGGKTLEIK 107
|||||:|||||:|: |||:|: |||:|: |||:|: |||:|: |||:|: |||:
Db 81 RFGSGSGTDFTLTISLEPEDFAVYVCQQRNWPHTFGGKTVEIK 127

RESULT 15

S23628
Ig kappa chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C:Accession: S23628
R:Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Defetos, M.; Kozin, F.; Carson, D.A.
J. Exp. Med. 175, 831-842, 1992
A:Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors fro
A:Reference number: S23623; MUID:92156804; PMID:1740665
A:Accession: S23628
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-111 <OLE>
A:Cross-references: EMBL:X59705; NID:g34022; PIDN:CAA42226.1; PID:g1335190
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 66.7%; Score 374; DB 2; Length 111;

Best Local Similarity 64.5%; Pred. No. 6.4e-27;
Matches 69; Conservative 20; Mismatches 18; Indels 0; Gaps 0;

Qy	1	DIVLTQSPATLSVTPGDVSVLSLCOASQSI	SNHLHWYQOKSHESPELLIKYRSQISGIPS	60
Db	1	EIVLTQSPATLSLSPGERATLSCRASQSV	SYLAWYQOKPGQAPRLLIYDASNRATGIPA	60
Qy	61	RFSGSGGTDFALSI	NSVETEDFGMYFCQQSGSWPHTFGG	107
Db	61	RFSGSGGTDFTLTI	SSLEPEDFAVYYCQQRSNWPWTFGQ	107

Search completed: November 18, 2002, 17:46:59
Job time : 53.451 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:00 ; Search time 26.2255 Seconds
(without alignments)
169.223 Million cell updates/sec

Title: US-09-016-061-8
Perfect score: 561
Sequence: 1 DIVLTQSPATLSVTPGDSVS.....CQSGSWPHTFGGKLEIK 107

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	%	Match	Length	DB	ID	Description
1	379	67.6	115	1	KV5I_MOUSE		P01642	mus musculus
2	364	64.9	128	1	KV3K_HUMAN		P06311	homo sapien
3	356.5	63.5	109	1	KV3F_HUMAN		P01624	homo sapien
4	351.5	62.7	129	1	KV3H_HUMAN		P04207	homo sapien
5	350.5	62.5	109	1	KV3D_HUMAN		P01622	homo sapien
6	347.5	61.9	109	1	KV3B_HUMAN		P01620	homo sapien
7	346.5	61.8	129	1	KV3L_HUMAN		P18135	homo sapien
8	344	61.3	108	1	KV5K_MOUSE		P01644	mus musculus
9	342	61.0	108	1	KV5Q_MOUSE		P01648	mus musculus
10	341.5	60.9	109	1	KV3E_HUMAN		P01623	homo sapien
11	341.5	60.9	129	1	KV3M_HUMAN		P18136	homo sapien
12	339	60.4	108	1	KV5L_MOUSE		P01645	mus musculus
13	339	60.4	108	1	KV5M_MOUSE		P01646	mus musculus
14	336.5	60.0	108	1	KV3A_HUMAN		P01619	homo sapien
15	336	59.9	108	1	KV5N_MOUSE		P01647	mus musculus
16	334	59.5	108	1	KV1_CANFA		P01618	canis famil
17	334	59.5	111	1	KV3D_MOUSE		P03977	mus musculus
18	334	59.5	111	1	KV3H_MOUSE		P01660	mus musculus
19	333	59.4	111	1	KV3L_MOUSE		P01664	mus musculus
20	333	59.4	111	1	KV3R_MOUSE		P01670	mus musculus
21	332	59.2	108	1	KV1M_HUMAN		P01605	homo sapien
22	330	58.8	108	1	KV1C_HUMAN		P01595	homo sapien
23	330	58.8	111	1	KV3A_MOUSE		P01654	mus musculus
24	330	58.8	115	1	KV3L_HUMAN		P04433	homo sapien
25	329	58.6	108	1	KV5P_MOUSE		P01649	mus musculus
26	328	58.5	108	1	KV1S_HUMAN		P01611	homo sapien
27	328	58.5	111	1	KV3T_MOUSE		P01672	mus musculus
28	327	58.3	108	1	KV5J_MOUSE		P01643	mus musculus
29	327	58.3	111	1	KV3C_MOUSE		P01656	mus musculus
30	326.5	58.2	113	1	KV2G_MOUSE		P01631	mus musculus
31	326.5	58.2	117	1	KV2E_MOUSE		P06309	homo sapien
32	324	57.8	108	1	KV1H_HUMAN		P01600	homo sapien
33	324	57.8	111	1	KV3M_MOUSE		P01665	mus musculus

ALIGNMENTS

RESULT 1

KV5I_MOUSE

ID KV5I_MOUSE STANDARD; PRT; 115 AA.

AC P01642;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig kappa chain V-V region L7 precursor (Fragment).

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Cranata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=81220975; PubMed=6264318;

RA Pech M., Hochl J., Schnell H., Zachau H.G.;

RT "Differences between germ-line and rearranged immunoglobulin V kappa

RT coding sequences suggest a localized mutation mechanism.";

RL Nature 291:668-670(1981).

CC -! MISCELLANEOUS: THERE APPEAR TO BE TWO POSSIBLE SPLICING JUNCTIONS AT

CC THE 3' END OF THE INTRON. THE ALTERNATE WOULD CODE FOR A PROTEIN

CC LACKING RESIDUES 17-19.

DR HSP: A01925; KVM5L7.

DR HSP: P80362; 1M7L.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_V.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IGV; 1.

KW Immunoglobulin V region; Signal.

FT SIGNAL 1 20

FT CHAIN 21 >115 IG KAPPA CHAIN V-V REGION L7.

FT DOMAIN 21 43 FRAMEWORK-1.

FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING-1.

FT DOMAIN 55 69 FRAMEWORK-2.

FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING-2.

FT DOMAIN 77 108 FRAMEWORK-3.

FT DOMAIN 109 >115 COMPLEMENTARITY-DETERMINING-3.

FT DISULFID 43 108 BY SIMILARITY.

FT NON_TER 115 115

SQ SEQUENCE 115 AA; 12615 MW; C17BEC758C577E00 CRC64;

Query Match 67.6%; Score 379; DB 1; Length 115;

Best Local Similarity 74.7%; Pred. No. 1.8e-33;

Matches 71; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

Oy 1 DIVLTQSPATLSVTPGDSVSLSQASQSTSNHLHWQOKSHSPRLIKYRSQISGIPS 60

Db 21 DLLLTQSPATLSVTPGDSVSLSQASQSTSNHLHWQOKSHSPRLIKYRSQISGIPS 80

Oy 61 RFGSGSGTDFALSINSVETDFGMVFCQSGSWP 95

Db 81 RFGSGSGTDFALSINSVETDFGMVFCQSGSWP 115

RESULT 2

KV3K_HUMAN

```

ID  KV3K_HUMAN  STANDARD;  PRT;  128 AA.
AC  P06311;
DT  01-JAN-1988 (Rel. 06, Created)
DT  01-JAN-1988 (Rel. 06, Last sequence update)
DT  15-JUL-1999 (Rel. 38, Last annotation update)
DE  Ig kappa chain V-III region IARC/BL41 precursor.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=86041852; PubMed=2997711;
RA  Klobbeck H.G., Meindl A., Combratio G., Solomon A., Zachau H.G.;
RT  "Human immunoglobulin kappa light chain genes of subgroups II and
RT  III.";
RL  Nucleic Acids Res. 13:6499-6513(1985).
CC  -----
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CC  or send an email to license@isb-sib.ch).
CC  -----
CC  EMBL; Z00021; CAA77316.1; -.
DR  PIR; A01899; K3HU41.
DR  HSP; P01607; IREI.
DR  InterPro; IPR003006; Ig_MHC.
DR  InterPro; IPR003596; Ig_v.
DR  Pfam; PF00047; Ig; 1.
DR  SMART; SM00406; Igv; 1.
DR  Immunoglobulin V region; Signal.
KW  Immunoglobulin V region; Signal.
FT  SIGNAL 1 20
FT  CHAIN 21 128 IG KAPPA CHAIN V-III REGION IARC/BL41.
FT  DOMAIN 21 43 FRAMEWORK-1.
FT  DOMAIN 44 54 COMPLEMENTARITY-DETERMINING-1.
FT  DOMAIN 55 69 FRAMEWORK-2.
FT  DOMAIN 70 76 COMPLEMENTARITY-DETERMINING-2.
FT  DOMAIN 77 108 FRAMEWORK-3.
FT  DOMAIN 109 117 COMPLEMENTARITY-DETERMINING-3.
FT  DOMAIN 118 128 JK1 SEGMENT.
FT  DISULFID 43 108 BY SIMILARITY.
FT  NON_TER 128 128
SQ  SEQUENCE 128 AA; 14070 MW; CC8957F0FE3B9012 CRC64;

Query Match 64.9%; Score 364; DB 1; Length 128;
Best Local Similarity 64.5%; Pred. No. 8e-32;
Matches 69; Conservative 18; Mismatches 20; Indels 0; Gaps 0;

QY 1 DIVLTQSPATLSVTPGDSVLSQASQISNHLHWYQOKSHSPRLTIKYRSQSISGIPS 60
DB 21 EIVLTQSPGTLSPGDSATLSQASQSVSSNLAWYQOKRQSPRLTIKRDASSRANGIPD 80
QY 61 RFSGSGGTDFALSINSVETEDFGMYFCQSGSWPHTFGGKLEIK 107
DB 81 RFSGSGGTDFLLISRLPEFAVYVCQYSTSPYFGGKLEIK 127

RESULT 3
KV3F_HUMAN  STANDARD;  PRT;  109 AA.
ID  KV3F_HUMAN
AC  P01624;
DT  21-JUL-1986 (Rel. 01, Created)
DT  21-JUL-1986 (Rel. 01, Last sequence update)
DT  16-OCT-2001 (Rel. 40, Last annotation update)
DE  Ig kappa chain V-III region POM.
OS  Homo sapiens (Human)
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]

```

```

RP  SEQUENCE.
RA  MEDLINE=76276460; PubMed=60899;
RA  Klapper D.G., Capra J.D.;
RT  "The amino acid sequence of the variable regions of the light chains
RT  from two idiotypically cross reactive IgM anti-gamma globulins.";
RL  Ann. Immunol. (Paris) 127C:261-271(1976).
CC  -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC  GLOBULIN ACTIVITY.
DR  PIR; A01897; K3HUPM.
DR  HSP; P80362; IWTL.
DR  InterPro; IPR003006; Ig_MHC.
DR  InterPro; IPR003596; Ig_v.
DR  Pfam; PF00047; Ig; 1.
DR  SMART; SM00406; Igv; 1.
DR  Immunoglobulin V region.
KW  DISULFID 23 89
FT  NON_TER 109 109 BY SIMILARITY.
SQ  SEQUENCE 109 AA; 11922 MW; 62821DDC6A8ABA86 CRC64;

Query Match 63.5%; Score 356.5; DB 1; Length 109;
Best Local Similarity 63.0%; Pred. No. 4.1e-31;
Matches 68; Conservative 20; Mismatches 19; Indels 1; Gaps 1;

QY 1 DIVLTQSPATLSVTPGDSVLSQASQISNHLHWYQOKSHSPRLTIKYRSQSISGIP 59
DB 1 EIVLTQSPVTLSPGGERATLSQASQISNSYLAQYQKSPGSLIYGASTRATGIP 60
QY 60 SRFGSGGTDFALSINSVETEDFGMYFCQSGSWPHTFGGKLEIK 107
DB 61 ARFGSGSGTFTLTISLQSEDFAVYVCQYNNWPTFGGTRVEIK 108

RESULT 4
KV3H_HUMAN  STANDARD;  PRT;  129 AA.
ID  KV3H_HUMAN
AC  P04207;
DT  20-MAR-1987 (Rel. 04, Created)
DT  01-NOV-1990 (Rel. 16, Last sequence update)
DT  15-JUL-1999 (Rel. 38, Last annotation update)
DE  Ig kappa chain V-III region CLL precursor (Rheumatoid factor).
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=86177570; PubMed=3083417;
RA  Jirik F.R., Sorge J., Fong S., Heitzmann J.G., Curd J.G., Chen P.P.,
RA  Goldfien R., Carson D.A.;
RT  "Cloning and sequence determination of a human rheumatoid factor
RT  light-chain gene.";
RL  Proc. Natl. Acad. Sci. U.S.A. 83:2195-2199(1986).
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
CC  EMBL; M12740; AAA58992.1; -.
DR  PIR; A01898; K3HUCI.
DR  HSP; P80362; IWTL.
DR  InterPro; IPR003006; Ig_MHC.
DR  InterPro; IPR003596; Ig_v.
DR  Pfam; PF00047; Ig; 1.
DR  SMART; SM00406; Igv; 1.
DR  Immunoglobulin V region; Signal.
KW  SIGNAL 1 20
FT  CHAIN 21 129 IG KAPPA CHAIN V-III REGION CLL.
FT  DOMAIN 21 43 FRAMEWORK-1.
FT  DOMAIN 44 54 COMPLEMENTARITY-DETERMINING-1.

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FT DOMAIN 55 69 FRAMEWORK-2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 77 108 FRAMEWORK-3.
FT DOMAIN 109 118 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 119 129 JKI SEGMENT.
FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14275 MW; 5C13B411BE60CC14 CRC64;

Query Match 62.7%; Score 351.5; DB 1; Length 129;
Best Local Similarity 61.1%; Pred. No. 1.7e-30;
Matches 66; Conservative 22; Mismatches 19; Indels 1; Gaps 1;

QY 1 DIVLTQSPATLSVTPGDGVSLSQASQISN-HLHWYQKSHSPRLTIKYRSQSISGIP 60
Db 21 EIVLTQSPGTLSPGERATLSCRASQSVNSLAWYQKPGQAPRLIIYGASTRATGIPA 80
QY 61 RFSGSGSGTDFTLISRLEPEDFAVYCYQYNNWPTFGQGRVLEIK 107
Db 81 RFSGSGSGTEFTLISRLEPEDFAVYCYQYNNWPTFGQGRVLEIK 128

RESULT 5
KV3D_HUMAN
ID KV3D_HUMAN STANDARD; PRT; 109 AA.
AC P01622;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region TI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72188439; PubMed=5027703;
RA Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein
Ti). IV. The complete amino acid sequence and its significance for
the mechanism of antibody production."
RL Hoppe-Sevler's Z. Physiol. Chem. 353:189-208 (1972).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR; A01895; K3HUTI.
DR HSSP; P80362; IWTU.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Ig; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DISULFID 23 89 BY SIMILARITY.
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11788 MW; 8C35058DCD7749BC CRC64;

Query Match 62.5%; Score 350.5; DB 1; Length 109;
Best Local Similarity 63.0%; Pred. No. 1.8e-30;
Matches 68; Conservative 17; Mismatches 22; Indels 1; Gaps 1;

QY 1 DIVLTQSPATLSVTPGDGVSLSQASQISN-HLHWYQKSHSPRLTIKYRSQSISGIP 59
Db 1 EIVLTQSPGTLSPGERATLSCRASQSVNSLAWYQKPGQAPRLIIYVASSRATGIP 60
QY 60 SRFGSGSGTDFTLISRLEPEDFAVYCYQYNNWPTFGGKLEIK 107
Db 61 DRFGSGSGTDFTLISRLEPEDFAVYCYQYNNWPTFGGKLEIK 108

RESULT 6
KV3B_HUMAN
ID KV3B_HUMAN STANDARD; PRT; 109 AA.
AC P01620;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region SIE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=82046598; PubMed=6794615;
RA Andrews D.W., Capra J.D.;
RT "Amino acid sequence of the variable regions of light chains from two
idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
group."
RL Biochemistry 20:5816-5822 (1981).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
GLOBULIN ACTIVITY.
DR PIR; A01892; K3HUTI.
DR HSSP; P80362; IWTU.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Ig; 1.
KW Immunoglobulin V region.
FT DISULFID 23 89 BY SIMILARITY.
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11775 MW; 7689C3ECD646FFB4 CRC64;

Query Match 61.9%; Score 347.5; DB 1; Length 109;
Best Local Similarity 62.0%; Pred. No. 3.7e-30;
Matches 67; Conservative 19; Mismatches 21; Indels 1; Gaps 1;

QY 1 DIVLTQSPATLSVTPGDGVSLSQASQISN-HLHWYQKSHSPRLTIKYRSQSISGIP 59
Db 1 EIVLTQSPGTLSPGERATLSCRASQSVNSLAWYQKPGQAPRLIIYVASSRATGIP 60
QY 60 SRFGSGSGTDFTLISRLEPEDFAVYCYQYNNWPTFGGKLEIK 107
Db 61 DRFGSGSGTDFTLISRLEPEDFAVYCYQYNNWPTFGGKLEIK 108

RESULT 7
KV3L_HUMAN
ID KV3L_HUMAN STANDARD; PRT; 129 AA.
AC P18135;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region HAH precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88171307; PubMed=3127527;
RA Kipps T.J., Tomhave E., Chen P., Carson D.A.;
RT "Autoantibody-associated kappa light chain variable region gene
expressed in chronic lymphocytic leukemia with little or no somatic
mutation. Implications for etiology and immunotherapy."
RL J. Exp. Med. 167:840-852 (1988).
CC -!- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
LEUKEMIA.
DR PIR; LE0022; K3HUHA.
DR HSSP; P80362; IWTU.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
```



```
RA Andrews D.W., Capra J.D.;
RT "Amino acid sequence of the variable regions of light chains from two
RT idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
RT group.";
RL Biochemistry 20:5816-5822(1981).
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
DR PIR: A01896; K3HUW1.
DR HSSP: P80362; 1WTL.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IgV; 1.
KW Immunoglobulin V region.
FT DISULFID 23 89 BY SIMILARITY.
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11746 MW; 566C115E6B9CBEE CRC64;

Query Match 60.9%; Score 341.5; DB 1; Length 109;
Best Local Similarity 62.0%; Pred. No. 1.6e-29;
Matches 67; Conservative 18; Mismatches 22; Indels 1; Gaps 1;

QY 1 DIVLTQSPATLSVTPGDSVLSQASQSI-NHLHWYQOKSHSPRLLIKYSQISGIP 59
:|||||:||||: :|||||: :|||||: :|||||: :|||||: :|||||: :|||||
Db 1 EIVLTQSPGTLSPGERATLSCRASQSVSSGYLGMWYQKPGQAPRLIYGASSRATGIP 60
:|||||:||||: :|||||: :|||||: :|||||: :|||||: :|||||: :|||||
QY 60 SRFGSGSGTDFALSINSVETDFGMVFCQSGSWPHFTGGGKLEIK 107
:|||||:||||: :|||||: :|||||: :|||||: :|||||: :|||||: :|||||
Db 61 DRFGSGSGTDFLTISRLEPDAVYVYCOQYGLRFTGGGKVEIK 108
:|||||:||||: :|||||: :|||||: :|||||: :|||||: :|||||: :|||||

RESULT 11
KV3M_HUMAN STANDARD; PRT; 129 AA.
ID KV3M_HUMAN
AC P18136;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region HIC precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=88171307; PubMed=3127527;
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Autoantibody-associated kappa light chain variable region gene
RT expressed in chronic lymphocytic leukemia with little or no somatic
RT mutation. Implications for etiology and immunotherapy.";
RL J. Exp. Med. 167:840-852(1988).
CC -I- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
CC AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
CC LEUKEMIA.
DR PIR: PLO021; K3HUH1.
DR HSSP: P80362; 1WTL.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IgV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HIC.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 56 70 FRAMEWORK-2.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 78 109 FRAMEWORK-3.
FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 119 129 JK1 SEGMENT.
FT DISULFID 43 109 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14070 MW; 7395528EA2BB74D6 CRC64;

Andrews D.W., Capra J.D.;
RT "Amino acid sequence of the variable regions of light chains from two
RT idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
RT group.";
RL Biochemistry 20:5816-5822(1981).
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
DR PIR: A01896; K3HUW1.
DR HSSP: P80362; 1WTL.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IgV; 1.
KW Immunoglobulin V region.
FT DISULFID 23 89 BY SIMILARITY.
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11746 MW; 566C115E6B9CBEE CRC64;

Query Match 60.9%; Score 341.5; DB 1; Length 109;
Best Local Similarity 62.0%; Pred. No. 1.6e-29;
Matches 67; Conservative 18; Mismatches 22; Indels 1; Gaps 1;

QY 1 DIVLTQSPATLSVTPGDSVLSQASQSI-NHLHWYQOKSHSPRLLIKYSQISGIP 59
:|||||:||||: :|||||: :|||||: :|||||: :|||||: :|||||: :|||||
Db 1 EIVLTQSPGTLSPGERATLSCRASQSVSSGYLGMWYQKPGQAPRLIYGASSRATGIP 60
:|||||:||||: :|||||: :|||||: :|||||: :|||||: :|||||: :|||||
QY 60 SRFGSGSGTDFALSINSVETDFGMVFCQSGSWPHFTGGGKLEIK 107
:|||||:||||: :|||||: :|||||: :|||||: :|||||: :|||||: :|||||
Db 61 DRFGSGSGTDFLTISRLEPDAVYVYCOQYGLRFTGGGKVEIK 108
:|||||:||||: :|||||: :|||||: :|||||: :|||||: :|||||: :|||||

RESULT 12
KV5L_MOUSE STANDARD; PRT; 108 AA.
ID KV5L_MOUSE
AC P01645;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-V region HP 93G7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=82150934; PubMed=6801658;
RA Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived
RT from five monoclonal anti-p-azophenylarsenate antibodies differing
RT with respect to a crossreactive idiotype.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -I- MISCELLANEOUS: ANTI-ARSONATE HYBRIDOMA PROTEIN.
DR PIR: A01927; KYNSAR.
DR HSSP: P01607; IREI.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IgV; 1.
KW Immunoglobulin V region; Antiarsenate antibody.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 108 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11954 MW; 22F4642C63EFF58E CRC64;

Query Match 60.4%; Score 339; DB 1; Length 108;
Best Local Similarity 59.8%; Pred. No. 2.9e-29;
Matches 64; Conservative 20; Mismatches 23; Indels 0; Gaps 0;

QY 1 DIVLTQSPATLSVTPGDSVLSQASQSI-NHLHWYQOKSHSPRLLIKYSQISGIP 60
:|||||:||||: :|||||: :|||||: :|||||: :|||||: :|||||: :|||||
Db 1 DIQMTQTSSLSASLGRDVTISCRASQDISLNLYNQKPGDGTGKLLIYTSRLHSGVPS 60
:|||||:||||: :|||||: :|||||: :|||||: :|||||: :|||||: :|||||
QY 61 RFSGSGSGTDFALSINSVETDFGMVFCQSGSWPHFTGGGKLEIK 107
:|||||:||||: :|||||: :|||||: :|||||: :|||||: :|||||: :|||||
Db 61 RFSGSGSGTDFLTISRLEPDAVYVYCOQYGLRFTGGGKLEIK 107
:|||||:||||: :|||||: :|||||: :|||||: :|||||: :|||||: :|||||

RESULT 13
KV5M_MOUSE STANDARD; PRT; 108 AA.
ID KV5M_MOUSE
AC P01645;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
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DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-V region HP 123E6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=82150934; PubMed=6801658;
RA Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived
RT from five monoclonal anti-p-azophenylarsonate antibodies differing
RT with respect to a crossreactive idiotype.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -|- MISCELLANEOUS: ANTI-ARSONATE HYBRIDOMA PROTEIN.
DR PIR: A01927; KVMASR.
DR HSP: P01607; IREI.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IgV; 1.
KW Immunoglobulin V region; Antiarsenate antibody.
FT DOMAIN 1 23
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 108 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11989 MW; 4C98599C08EBA09A CRC64;

Query Match 60.4%; Score 339; DB 1; Length 108;
Best Local Similarity 60.7%; Pred. No. 2.9e-29;
Matches 65; Conservative 19; Mismatches 23; Indels 0; Gaps 0;

QY 1 DIVLTQSPATLSVTPGDSVLSQASQSI-SNHLHWYQOKSHSPRLLIKYSQISGIPS 60
Db 1 DIQMTQSTSSLSASLGDRVTISCRASQISNLYLNWYQOKPDGTVKLLIYTSRLHSGVPS 60

QY 61 RFSGSGSGTDFALSINSVETEDFGMYFCQSGSWPHTFGGKLEIK 107
Db 61 RFSGSGSGTDFALSINSVETEDFGMYFCQSGSWPHTFGGKLEIK 107

RESULT 14
KV3A_HUMAN STANDARD; PRT; 108 AA.
AC P01619;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region B6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA Milstein C.;
RT "The basic sequences of immunoglobulin kappa chains: sequence studies
RT of Bence Jones proteins Rad, Fr4 and B6.";
RL FEBS Lett. 2:301-304(1969).
CC -|- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR: A01891; K3H086.
DR HSP: P80362; 1WTL.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IgV; 1.
KW Immunoglobulin V region; Bence-Jones protein.

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FT DISULFID 23 89 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11635 MW; 8BC14FF07A419E3D CRC64;

Query Match 60.0%; Score 336.5; DB 1; Length 108;
Best Local Similarity 60.2%; Pred. No. 5.4e-29;
Matches 65; Conservative 20; Mismatches 22; Indels 1; Gaps 1;

QY 1 DIVLTQSPATLSVTPGDSVLSQASQSI-SNHLHWYQOKSHSPRLLIKYSQISGIP 59
Db 1 ZIVLTZSPGTLSPGZRAALSCRASQISNLYLNWYQOKPDGTVKLLIYTSRLHSGVPS 60

QY 60 RFSGSGSGTDFALSINSVETEDFGMYFCQSGSWPHTFGGKLEIK 107
Db 61 RFSGSGSGADFTLTISRLZPEDFAVYCYQYQSGSPFTFGGSKLEIK 108

RESULT 15
KV5N_MOUSE STANDARD; PRT; 108 AA.
ID KV5N_MOUSE
AC P01647;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-V region HP 124E1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=82150934; PubMed=6801658;
RA Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived
RT from five monoclonal anti-p-azophenylarsonate antibodies differing
RT with respect to a crossreactive idiotype.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -|- MISCELLANEOUS: ANTI-ARSONATE HYBRIDOMA PROTEIN.
DR PIR: A01927; KVMASR.
DR HSP: P01607; IREI.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IgV; 1.
KW Immunoglobulin V region; Antiarsenate antibody.
FT DOMAIN 1 23
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 108 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11965 MW; 39971BC653EFEFA2 CRC64;

Query Match 59.9%; Score 336; DB 1; Length 108;
Best Local Similarity 58.9%; Pred. No. 6.1e-29;
Matches 63; Conservative 22; Mismatches 22; Indels 0; Gaps 0;

QY 1 DIVLTQSPATLSVTPGDSVLSQASQSI-SNHLHWYQOKSHSPRLLIKYSQISGIPS 60
Db 1 DIQMTQSTSSLSASLGDRVTISCRASQISNLYLNWYQOKPDGTVKLLIYTSRLHSGVPS 60

QY 61 RFSGSGSGTDFALSINSVETEDFGMYFCQSGSWPHTFGGKLEIK 107
Db 61 RFSGSGSGTDFALSINSVETEDFGMYFCQSGSWPHTFGGKLEIK 107

Search completed: November 18, 2002, 17:33:17
Job time : 26.2255 secs

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Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
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2	358	63.8		108	4	Q9uL83	Q9uL83 homo
3	346.5	61.8		109	4	Q9uL78	Q9uL78 homo
4	336.5	60.0		107	4	Q96Sa9	Q96Sa9 homo
5	336	59.9		108	4	Q9uL77	Q9uL77 homo
6	336	59.9		298	11	Q9QYF0	Q9QYF0 mus
7	335	59.7		111	11	Q9Z0E9	Q9Z0E9 mus
8	334.5	59.6		238	11	Q8VC16	Q8VC16 mus
9	333	59.4		108	4	Q9uL79	Q9uL79 homo
10	333	59.4		109	11	Q9Z0E6	Q9Z0E6 mus
11	331	59.0		108	11	Q8V1J0	Q8V1J0 mus
12	327	58.3		234	11	Q91WF8	Q91WF8 mus
13	324.5	57.8		109	4	Q9uL86	Q9uL86 homo
14	324.5	57.8		134	11	Q8VDD0	Q8VDD0 mus
15	324	57.8		108	4	Q9uL70	Q9uL70 homo
16	323.5	57.7		239	11	Q8VC55	Q8VC55 mus

Qy	Db
1 DIVLTQSPATLSVTPGDSVSLSCQASQSI	1 EIVMTQSPATLSVTPGERATLSCWASQSI
SNHLHWYQKSHESPRLLIKYRSQSI	SNLWYQKPGQAPRLITYGASTRAT
GIPS 60	GIPA 60


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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035037; AAD56273.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Ig; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11738 MW; C05681716C4D16F3 CRC64;

Query Match 59.9%; Score 336; DB 4; Length 108;
Best Local Similarity 60.7%; Pred. No. 5.3e-30;
Matches 65; Conservative 20; Mismatches 22; Indels 0; Gaps 0;

QY 1 DIVLTQSPATLSVTPGDSVLSLCOASQISNHLHWYQOKSHSPRLLIKYRSQISGIPS 60
Db 1 DIQMTQSPSSLSASVGDRTVITCRASQSISSYLNWYQKPGKAPNLLIYAASLSQGVPS 60

QY 61 RFSGSGSGTDFTLTISSLQPEDFATYVCOQSYSTSWTFEGGTVKLEIK 107
Db 61 RFSGSGSGTDFTLTISSLQPEDFATYVCOQSYSTSWTFEGGTVKLEIK 107

RESULT 6
QYQYF0 PRELIMINARY; PRT; 298 AA.
AC QYQYF0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE CN 8 scFv.
GN CN 8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BALB/C; TISSUE=SPLEEN;
RX MEDLINE=20183931; PubMed=10706631;
RA Shinohara N., Demura T., Fukuda H.;
RT "Isolation of a vascular cell wall-specific monoclonal antibody
RT recognizing a cell polarity by using a phage display subtraction
RT method.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:2585-2590(2000).
DR EMBL; AB036341; BAA88633.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; Ig; 2.
SQ SEQUENCE 298 AA; 31867 MW; E0F96B8A17004317 CRC64;

Query Match 59.9%; Score 336; DB 11; Length 298;
Best Local Similarity 58.3%; Pred. No. 1.8e-29;
Matches 63; Conservative 26; Mismatches 17; Indels 2; Gaps 2;

QY 1 DIVLTQSPATLSVTPGDSVLSLCOASQISNHLHWYQOKSHSPRLLIKYRSQIS-GIP 59
Db 173 DIETLQSPASLSASVGEVTITCRASGNHNYLAWYQOKGKSPQLLV-YNAKTLADGVP 231

QY 60 SRFSGSGGTDFALSINSVETEDFGMYFCQSGSWPHFTFGGTVKLEIK 107
Db 232 SRFSGSGGTQYSLKINSIQPEDFGSYVQHFWTTPTPTFGGTVKLEIK 279
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RESULT 7
QY20E9 PRELIMINARY; PRT; 111 AA.
AC QY20E9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Pterin-mimicking anti-idiotope kappa chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Ackin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.;
RT "Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed
RT in Mammalian Cells.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307935; AAL09419.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
FT NON_TER 1
FT NON_TER 111
SQ SEQUENCE 111 AA; 12046 MW; 1E46988AA6858526 CRC64;

Query Match 59.7%; Score 335; DB 11; Length 111;
Best Local Similarity 58.6%; Pred. No. 7e-30;
Matches 65; Conservative 19; Mismatches 23; Indels 4; Gaps 1;

QY 1 DIVLTQSPATLSVTPGDSVLSLCOASQIS----NHLHWYQOKSHSPRLLIKYRSQIS 56
Db 1 DIVLTQSPASLSVSLGQRTATISCRASKSVSTSGSYNHWYQOKPGQPKLLIYASNL 60

QY 57 GIPSRFSGSGGTDFALSINSVETEDFGMYFCQSGSWPHFTFGGTVKLEIK 107
Db 61 GVPARFSGSGGTDFTLNIHPVEEDAATYVQHSRELPLPTFGGTVKLEIK 111

RESULT 8
QYQYI6 PRELIMINARY; PRT; 238 AA.
AC QYQYI6;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 26.2 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COLON;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019760; AAH19760.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IGC1; 1.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 238 AA; 26224 MW; 35EC08E3DE54114AD CRC64;

Query Match 59.6%; Score 334.5; DB 11; Length 238;
Best Local Similarity 58.0%; Pred. No. 2e-29;
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Matches 65; Conservative 16; Mismatches 26; Indels 5; Gaps 1;
QY 1 DIVLTQSPATLSVTPGDSVSLSCAQSQSI-----SNHLHWYQOKSHSPRLLIKYSQSII 55
Db 20 DIVMTQTPLSLVSLVDSQASISCRSSQVSHSNGNTLYHLWYLOKPGQSPKLLIYKVSNR 79
QY 56 SGIPRFSGSGGTDFALSNVETEDFGMYFCQOQSGSWPHTFGGKLEIK 107
Db 80 SGVPDRFSGSGGTDFTLKISRVEADLGVYFCQSQSTHVPPTFGGKLEIK 131
RESULT 9
Q9UL79 PRELIMINARY; PRT; 108 AA.
AC Q9UL79;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment)..
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus".
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035035; AAD56271.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724FB4E CRC64;
Query Match 59.4%; Score 333; DB 4; Length 108;
Best Local Similarity 59.8%; Pred. No. 1.le-29;
Matches 64; Conservative 19; Mismatches 24; Indels 0; Gaps 0;
QY 1 DIVLTQSPATLSVTPGDSVSLSCAQSQSI-SNHLHWYQOKSHSPRLLIKYSQSISGIPS 60
Db 1 DIVMTQSPSLLSASTGDRVTISCRMSQGISYLAWTQQKRAPELLIYAASLTQSGVPS 60
QY 61 RFGSGSGTDFALSNVETEDFGMYFCQOQSGSWPHTFGGKLEIK 107
Db 61 RFGSGSGTDFTLTISCLQSEDFATYCCQYYSFPPTFGGKVEIK 107
RESULT 10
Q920E6 PRELIMINARY; PRT; 109 AA.
AC Q920E6;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Pterin-mimicking anti-idiotope kappa chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Atkin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.;
RT "Definition of the idiotope of Pterin-Mimicking Antibodies Expressed
RT in Mammalian Cells.";
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RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307938; AAL09422.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
FT NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 11943 MW; DAD3F98E05DD1501 CRC64;
Query Match 59.4%; Score 333; DB 11; Length 109;
Best Local Similarity 58.3%; Pred. No. 1.2e-29;
Matches 63; Conservative 25; Mismatches 18; Indels 2; Gaps 2;
QY 1 DIVLTQSPATLSVTPGDSVSLSCAQSQSI-SNHLHWYQOKSHSPRLLIKYSQSIS-CIP 59
Db 1 DIQMTOSPASLSASVGETVITCRASGNIHNYLAWYQOKGKSPOLLV-YNAKTLADGVP 59
QY 60 SRFSGSGGTDFALSNVETEDFGMYFCQOQSGSWPHTFGGKLEIK 107
Db 60 SRFSGSGGTQYSLKINSIQPEDEFGSYCYQHFWSTPWTFGGKLEIK 107
RESULT 11
Q8VIJ0 PRELIMINARY; PRT; 108 AA.
AC Q8VIJ0;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Anti-DNA light chain (Fragment).
GN VK19.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/HEJ-LPR/LPR;
RX MEDLINE=96409289; PubMed=8814271;
RA Wloch M.K., Alexander A.L., Pippen A.M., Pisetsky D.S., Gilkeson G.S.;
RT "Differences in V kappa gene utilization and VH CDR3 sequence among
RT anti-DNA from C3H-lpr mice and lupus mice with nephritis.";
RL Eur. J. Immunol. 26:2225-2233(1996).
DR EMBL; U59155; AAB02917.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; IGV; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11859 MW; 68506D75613DBFBE CRC64;
Query Match 59.0%; Score 331; DB 11; Length 108;
Best Local Similarity 57.0%; Pred. No. 1.9e-29;
Matches 61; Conservative 21; Mismatches 25; Indels 0; Gaps 0;
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Db 1 DIVMTQSPFTNSTVSGDRVSVTKASQNVGTNVAVYQOKPGQSPKALIYSASYPSGVPH 60
QY 61 RFGSGSGTDFALSNVETEDFGMYFCQOQSGSWPHTFGGKLEIK 107
Db 61 RFTGSGSGTDFTLTISNVQSEDLAEYFCQYNSYPYTFGGGKLEIK 107
RESULT 12
Q91WF8 PRELIMINARY; PRT; 234 AA.
AC Q91WF8;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:21:57 ; Search time 147.912 Seconds
(without alignments)
96.394 Million cell updates/sec

Title: US-09-016-061-8

Perfect score: 561

Sequence: 1 DIVLQSPATLSVTFCDVS.....CQSGSWPHTFGGTTKLEIK 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
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23:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	561	100.0	107	22	AAW76004
3	561	100.0	107	22	AAW76004
4	530	94.5	109	20	AAW76004
5	529	94.3	107	22	AAW76004
6	529	94.3	127	22	AAW76004
7	526	93.8	127	15	AAW76004
8	519	92.5	108	12	AAW76004
9	519	92.5	109	15	AAW76004
10	519	92.5	240	12	AAW76004

11	516	92.0	107	14	AAW76004
12	516	92.0	107	19	AAW76004
13	501	89.3	108	20	AAW76004
14	498	88.8	108	17	AAW76004
15	496.5	88.5	114	22	AAW76004
16	491	87.5	259	21	AAW76004
17	490	87.3	127	21	AAW76004
18	486.5	86.7	109	20	AAW76004
19	470	83.8	107	19	AAW76004
20	470	83.8	107	22	AAW76004
21	467	83.2	107	22	AAW76004
22	465	82.9	128	20	AAW76004
23	465	82.9	128	23	AAW76004
24	465	82.9	214	20	AAW76004
25	465	82.9	214	23	AAW76004
26	464	82.7	107	19	AAW76004
27	464	82.7	107	22	AAW76004
28	464	82.7	107	22	AAW76004
29	459	81.8	108	17	AAW76004
30	451	80.4	107	21	AAW76004
31	438	78.1	107	20	AAW76004
32	438	78.1	112	20	AAW76004
33	432	77.0	107	13	AAW76004
34	432	77.0	107	22	AAW76004
35	432	77.0	107	22	AAW76004
36	429	76.5	107	21	AAW76004
37	426	75.9	107	15	AAW76004
38	426	75.9	107	20	AAW76004
39	423	75.4	107	21	AAW76004
40	423	75.4	107	22	AAW76004
41	423	75.4	107	22	AAW76004
42	422	75.2	242	22	AAW76004
43	422	75.2	244	20	AAW76004
44	422	75.2	244	22	AAW76004
45	421	75.0	127	21	AAW76004

ALIGNMENTS

RESULT 1

AAW76004
ID AAW76004 standard; Protein; 107 AA.

XX AAW76004;

XX 02-NOV-1998 (first entry)

DT LM609 antibody light chain variable region protein fragment.

DE Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis.

XX Mus sp.

OS WO9833919-A2.

PN 06-AUG-1998.

PD 30-JAN-1998; 98WO-US01826.

PF 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

PI Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

DR N-PSDB; AAW76004.

XX

CC demonstrate the method of the invention.

SQ Sequence 107 AA;

Query Match 94.3%; Score 529; DB 22; Length 107;

Best Local Similarity 93.5%; Pred. No. 3.6e-33;

Matches 100; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIVLTQSPATLSVTPGDSVSLSCASQSIHNLHWYQOKSHSPRLLIKYRSQISGIPS 60

||||| 1 DIVLTQSPATLSVTPGDSVSLSCASQSIHNLHWYQOKSHSPRLLIKYRSQISGIPS 60

Db 1 DIVLTQSPATLSVTPGDSVSLSCASQSIHNLHWYQOKSHSPRLLIKYRSQISGIPS 60

QY 61 RFSGSGGTDFALSIHNSVETDFGMVFCQSGSWPHTFGGKLEIK 107

||||| 61 RFSGSGGTDFALSIHNSVETDFGMVFCQSGSWPHTFGGKLEIK 107

Db 61 RFSGSGGTDFALSIHNSVETDFGMVFCQSGSWPHTFGGKLEIK 107

RESULT 6

AAB69687

ID AAB69687 standard; Protein; 127 AA.

XX AC AAB69687;

DT 30-APR-2001 (first entry)

XX DE Murine CMV5 antibody light chain SEQ ID NO: 83.

XX Humanised immunoglobulin; mouse; human; antibody; heavy chain; diabetes;
KW light chain; graft versus host disease; transplant; autoimmune disease;
KW multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus;
KW myasthenia gravis; herpes infection; myeloid leukaemia; CMV infection.

XX Mus sp.

XX US6180370-B1.

PN 30-JAN-2001.

XX 07-JUN-1995; 95US-0484537.

XX 28-DEC-1988; 88US-0290975.

PR 13-FEB-1989; 89US-0310252.

PR 28-SEP-1990; 90US-0590274.

PR 19-DEC-1990; 90US-0634278.

XX (PROT-) PROTEIN DESIGN LABS INC.

XX Queen CL, Selick HE;

XX WPI; 2001-190856/19.

DR N-PSDB; AAF58747.

XX Producing humanized immunoglobulin, involves producing a cell

PT containing DNA segments encoding humanized heavy and light chain

PT variable regions, and expressing the DNA segments in the cell -

XX Example 8; Fig 39; 145pp; English.

PS The present invention describes a method of producing humanised

XX immunoglobulins involving expressing in a cell a nucleic acid encoding a

CC humanised version of an immunoglobulin. This is obtained by comparing a

CC donor and human immunoglobulin and producing a combined antibody which

CC contains part of each. These are useful in the treatment of

CC graft-versus-host disease, transplant rejection, autoimmune diseases such

CC as diabetes, rheumatoid arthritis, myasthenia gravis, multiple sclerosis

CC and systemic lupus erythematosus, herpes infections, CMV virus infections

CC and myeloid leukaemia. The present sequence is an antibody used to

CC demonstrate the method of the invention.

XX Seqèncè 127 AA;

SQ Query Match 94.3%; Score 529; DB 22; Length 127;

Best Local Similarity 93.5%; Pred. No. 4.3e-33;

Matches 100; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIVLTQSPATLSVTPGDSVSLSCASQSIHNLHWYQOKSHSPRLLIKYRSQISGIPS 60

||||| 1 DIVLTQSPATLSVTPGDSVSLSCASQSIHNLHWYQOKSHSPRLLIKYRSQISGIPS 60

Db 21 DIVLTQSPATLSVTPGDSVSLSCASQSIHNLHWYQOKSHSPRLLIKYRSQISGIPS 80

QY 61 RFSGSGGTDFALSIHNSVETDFGMVFCQSGSWPHTFGGKLEIK 107

||||| 61 RFSGSGGTDFALSIHNSVETDFGMVFCQSGSWPHTFGGKLEIK 107

Db 81 RFSGSGGTDFALSIHNSVETDFGMVFCQSGSWPHTFGGKLEIK 127

RESULT 7

AAR54093

ID AAR54093 standard; Protein; 127 AA.

XX AC AAR54093;

XX DT 29-DEC-1994 (first entry)

XX DE Sequence of mouse V-kappa showing the sequences of recombinant

DE anti-FHV-1 antibody CDRs 1, 2 and 3.

XX KW Feline herpes virus; FHV-1; monoclonal antibody; CDR;

KW complementarity determining region.

XX OS Mus musculus.

XX FH Key Location/Qualifiers

FT Peptide 1..20

FT Region /label= leader

FT 21..43

FT /label= FR1

FT 44..54

FT /label= CDR1

FT 55..70

FT /label= FR2

FT 71..76

FT /label= CDR2

FT 77..108

FT /label= FR3

FT 109..117

FT /label= CDR3

FT 118..127

FT /label= FR4

XX WO9412661-A.

XX 09-JUN-1994.

XX 25-NOV-1993; 93WO-JP01724.

XX 28-NOV-1992; 92JP-0341255.

XX (KAGA) CHERO SERO THERAPEUTIC RES INST.

XX Kimachi K, Maeda H, Nishiyama K, Tokiyoshi S;

XX WPI; 1994-200288/24.

DR N-PSDB; AA064167.

XX Feline monoclonal antibody and recombinant antibodies specific

PT for FHV-1 - for detection, treatment and prevention of FHV-1

PT infection.

XX Disclosure; Page 18-19; 53pp; Japanese.

XX The inventors claim a monoclonal antibody against feline herpes

CC virus (FHV-1). They also claim a recombinant antibody against FHV-1

CC and fragments of VH and VL CDR1, CDR2 and CDR3. The antibodies are

CC used in the detection, treatment and prevention of FHV-1. The

CC sequences of the CDRs in the VH of the recombinant anti-FHV-1

CC antibody are given in AAR54092. The sequences of the CDRs in the VL of

CC the recombinant anti-FHV-1 antibody are given in AAR54093. These CDR

CC	sequences are claimed.	
XX		
SQ	Sequence 127 AA;	
	Query Match 93.8%; Score 526; DB 15; Length 127;	
	Best Local Similarity 93.5%; Pred. No. 7.2e-33;	
	Matches 100; Conservative 3; Mismatches 4; Indels 0; Gaps 0;	
QY	1 DIVLTQSPATLSVTPGDVSLSCQASQSIISNNLHWYQOKSHSPRLLIKYSQISGIPS 60	
DB	21 DIVLTQSPATLSVTPGDVSLSCRASQSIISNNLHWYQOKSHSPRLLIKYSQISGIPS 80	
QY	61 RFSGSGGTDFTLINSVETEDFGMYFCQOSGNSWPHTFGGTTKLEIK 107	
DB	81 RFSGSGGTDFTLINSVETEDFGMYFCQOSGNSWPHTFGGTTKLEIK 127	
RESULT 8		
AAR15438		
ID	AAR15438 standard; Protein; 108 AA.	
XX		
AC	AAR15438;	
XX		
DT	25-FEB-1992 (first entry)	
XX		
DE	Light chain variable region of MAb 1A6.	
XX		
XX	HRV; ICAM-1; antigen-binding fragment; inflammation;	
KW	auto-immune disease.	
KW		
XX		
OS	Homo sapiens.	
XX		
PN	EP459577-A.	
XX		
PD	04-DEC-1991.	
XX		
PF	25-MAY-1991; 91EP-0201243.	
XX		
PR	01-JUN-1990; 90US-0532001.	
XX		
XX	(MERI) MERCK & CO INC.	
XX		
PI	Colonna RJ, Condra JH, Tomassini JE, Sardana VV;	
XX		
DR	WPI; 1991-355850/49.	
XX		
PT	Microbially expressed portions of monoclonal antibody - can block	
PT	attachment of rhinovirus ligands to inter-cellular adhesion	
PT	molecule (ICAM-1)	
XX		
PS	Claim 1; Page 19; 28pp; English.	
XX		
CC	This is one of six antibody fragments from MAb's specific for domain	
CC	1 of ICAM-1. MAb 1A6 also specifically blocks the major group of	
CC	human rhinovirus from binding to and infecting HeLa cells. The	
CC	peptide fragments can be used to treat or prevent rhinovirus	
CC	infection. See AAR15437-R15443.	
XX		
SQ	Sequence 108 AA;	
	Query Match 92.5%; Score 519; DB 12; Length 108;	
	Best Local Similarity 92.5%; Pred. No. 2.1e-32;	
	Matches 99; Conservative 5; Mismatches 3; Indels 0; Gaps 0;	
QY	1 DIVLTQSPATLSVTPGDVSLSCQASQSIISNNLHWYQOKSHSPRLLIKYSQISGIPS 60	
DB	1 DIVLTQSPATLSVTPGDVSLSCRASQSIISNNLHWYQOKSHSPRLLIKHSQISGIPS 60	
QY	61 RFSGSGGTDFTLINSVETEDFGMYFCQOSGNSWPHTFGGTTKLEIK 107	
DB	61 RFSGSGGTDFTLINSVETEDFGMYFCQOSGNSWPHTFGGTTKLEIK 107	
RESULT 9		
AAR52033		
ID	AAR52033 standard; Protein; 109 AA.	
XX		
AC	AAR52033;	
XX		
DT	26-SEP-1996 (first entry)	
XX		
DE	Light chain variable region of murine antibody 3Hfm.	
XX		
XX	antibody; humanised; murine; human; heavy chain; light; variable;	
KW	framework region; complementarity determining region; reshaping;	
KW	modelling; surface residue; modify.	
XX		
OS	Mus sp.	
XX		
FH	Key	Location/Qualifiers
FT	Region	1..23
FT		/label= framework_region_1
FT		/note= "FR 1"
FT	Region	24..34
FT		/label= complementarity_determining_region_1
FT		/note= "CDR 1"
FT	Region	35..49
FT		/label= FR_2
FT	Region	50..56
FT		/label= CDR_2
FT	Region	57..88
FT		/label= FR_3
FT	Region	89..97
FT		/label= CDR_3
FT	Region	98..109
FT		/label= FR_4
XX		
PN	EP592106-A1.	
XX		
PD	13-APR-1994.	
XX		
PF	07-SEP-1993; 93EP-0307051.	
XX		
PR	09-SEP-1992; 92US-0942245.	
XX		
XX	(PEDE/) PEDERSEN J T.	
PA	(IMMU-) IMMUNOGEN INC.	
XX		
PI	Guild BC, Pedersen JT, Rees AR, Roguska MA, Searle SMJ;	
XX		
DR	WPI; 1994-120230/15.	
XX		
PT	Method of resurfacing of rodent antibodies to produce humanised	
PT	antibody forms - for producing non-human antibodies with improved	
PT	therapeutic efficiency by presenting human surface on V-region	
XX		
PS	Example 1; Fig 3A; 230pp; English.	
XX		
CC	The present sequence is that of the light chain variable (LC VR) region	
CC	of murine antibody 3Hfm. This sequence was aligned with 11 other known	
CC	antibody LC VRs and a set of framework positions of surface exposed amino	
CC	acid residues was determined. This information can be used in a method to	
CC	determine how to modify a rodent antibody or fragment by resurfacing in	
CC	order to produce a humanised rodent antibody. Residues (determined from	
CC	alignment) at positions 1, 3, 5, 9, 15, 18, 46, 47, 51, 63, 66, 73, 86,	
CC	87, 111, 115, 116 and 117 are accessible residues. None of the entire	
CC	combinations of surface residues in the murine sequences were found in	
CC	the human sequences and vice versa. However the residues in individual	
CC	positions appear to be conserved.	
XX		
SQ	Sequence 109 AA;	
	Query Match 92.5%; Score 519; DB 15; Length 109;	
	Best Local Similarity 92.5%; Pred. No. 2.1e-32;	
	Matches 99; Conservative 4; Mismatches 4; Indels 0; Gaps 0;	

```

QY 1 DIVLTQSPATLSVTPGDSVSLSCQASQSIINHLHWYQOKSHSPRLLIKYSQISGIPS 60
  |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 DIVLTQSPATLSVTPGDSVSLSCRASQSIINHLHWYQOKSHSPRLLIKYSQISGIPS 60
QY 61 RFSGSGGTDFTLSINSVETEDFGMYFCQSGSWPHTFGGKLEIK 107
  |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 RFSGSGGTDFTLSINSVETEDFGMYFCQSGSNWPYTFGGKLEIK 107

RESULT 10
AAR15443
ID AAR15443 standard; Protein; 240 AA.
XX
XX
AC AAR15443;
XX
XX 25-FEB-1992 (first entry)
XX
XX Single chain Fv from pSCV1 for blocking HRV binding to ICAM-1.
XX
XX antigen-binding fragment; inflammation; auto-immune disease.
XX
XX Homo sapiens.
XX
XX EP459577-A.
XX
XX 04-DEC-1991.
XX
XX 25-MAY-1991; 91EP-0201243.
XX
XX 01-JUN-1990; 90US-0532001.
XX
XX (MERI ) MERCK & CO INC.
XX
XX Colonna RJ, Condra JH, Tomassini JE, Sardana VV;
XX
XX WPI; 1991-355850/49.
XX
XX Microbially expressed portions of monoclonal antibody - can block
PT attachment of rhinovirus ligands to inter-cellular adhesion
PT molecule (ICAM-1)
XX
XX Claim 5; Page 21; 28pp; English.
XX
XX The Fv fragment encoded by pSCV1 was able to protect cells against
CC infection by HRV-14. It was less active than modified Fv fragments
CC which included a Gly-Gly-Gly-Ser flexible linker between the L
CC and H chains as either a monomer or a dimer.
CC See also AAR15437-R15442.
XX
XX Sequence 240 AA;
XX
Query Match 92.5%; Score 519; DB 12; Length 240;
Best Local Similarity 92.5%; Pred. No. 4.5e-32;
Matches 99; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIVLTQSPATLSVTPGDSVSLSCQASQSIINHLHWYQOKSHSPRLLIKYSQISGIPS 60
  |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 DIVLTQSPATLSVTPGDSVSLSCRASQSIINHLHWYQOKSHSPRLLIKHSQISGIPS 60
QY 61 RFSGSGGTDFTLSINSVETEDFGMYFCQSGSWPHTFGGKLEIK 107
  |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 RFSGSGGTDFTLSINSVETEDFGMEFCQSGSNWPYTFGGKLEIK 107

RESULT 11
AAR38601
ID AAR38601 standard; peptide; 107 AA.
XX
XX AAR38601;
XX
XX 28-OCT-1993 (first entry)
XX
XX HYH light chain.
XX

```

```

XX
XX Antibody; variable domain; light; L; heavy; H; consensus;
KW affinity; antigen; immunogenicity; humanisation; framework.
XX
XX Homo sapiens.
XX
XX WO9311794-A.
XX
XX 24-JUN-1993.
XX
XX 14-DEC-1992; 92WO-US10906.
XX
XX 13-DEC-1991; 91US-0808464.
XX
XX (XOMA ) XOMA CORP.
XX
XX Fishwild DM, Kohn FR, Little RG, Studnicka GM;
XX
XX WPI; 1993-213827/26.
XX
XX Antibodies prepn. used for treatment of auto-immune diseases - by
PT replacement of critical residues to reduce immunogenicity but
PT retain binding affinity, etc.
XX
XX Disclosure; Page 84; 160pp; English.
XX
XX The amino acid sequences of the light and heavy chains of the
CC variable domains from antibodies HYH (HYHEL-10 Fab-lysosome complex)
CC (AAR38601 and AAR38608, respectively), MCPC (IgA Fab
CC MCPC603-phosphocholine complex) (AAR38602-03 and AAR38609-10,
CC respectively), NEWM (Ig Fab' NEW) (AAR38604-05 and AAR38611,
CC respectively) and KOL (IgG1 KOL) (AAR38606-07 and AAR38612, respectively)
CC may be used to determine an alignment from which appropriate changes may
CC be made. Unlike other methods of humanisation, which advocate the
CC replacement of entire antibody framework regions with those of human
CC antibodies, this method involves only the introduction of human
CC residues into those positions not critical for antigen binding.
CC This ensures that the binding properties of the modified antibody
CC are not diminished.
XX
XX Sequence 107 AA;
XX
Query Match 92.0%; Score 516; DB 14; Length 107;
Best Local Similarity 91.6%; Pred. No. 3.5e-32;
Matches 98; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIVLTQSPATLSVTPGDSVSLSCQASQSIINHLHWYQOKSHSPRLLIKYSQISGIPS 60
  |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 DIVLTQSPATLSVTPGDSVSLSCRASQSIINHLHWYQOKSHSPRLLIKYSQISGIPS 60
QY 61 RFSGSGGTDFTLSINSVETEDFGMYFCQSGSWPHTFGGKLEIK 107
  |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 RFSGSGGTDFTLSINSVETEDFGMYFCQSGSNWPYTFGGKLEIK 107

RESULT 12
AAR58482
ID AAR58482 standard; protein; 107 AA.
XX
XX AAR58482;
XX
XX 18-AUG-1998 (first entry)
XX
XX Murine HYH antibody light chain variable domain.
XX
XX Humanised; human; mouse; CD5; anti-CD5 antibody; immunoglobulin;
KW depletion; cytotoxic; immunoconjugate; fusion protein; psoriasis;
KW autoimmune disease; rheumatoid arthritis; type I diabetes.
XX
XX Mus sp.
XX
XX US5770196-A.
XX

```

PD 23-JUN-1998.
 XX
 PF 07-JUN-1995; 95US-0472788.
 XX
 PR 23-JUN-1993; 93US-0082842.
 PR 13-DEC-1991; 91US-0808464.
 PR 14-DEC-1992; 92WO-US10906.
 PR 07-JUN-1995; 95US-0472788.
 XX
 PA (XOMA) XOMA CORP.
 XX
 XX Studnicka GM;
 XX
 XX WPI; 1998-376744/32.
 XX
 PT Depletion of CD5-positive cells in vivo - using anti-CD5 antibodies
 PT with humanised variable regions
 PT
 XX
 PS Disclosure; Column 43-44; 77pp; English.
 XX
 CC A method has been developed of depleting CD5+ cells in an animal. The
 CC method comprises administering a cytotoxic protein containing a modified
 CC immunoglobulin (Ig) variable domain, where the protein is an anti-CD5 Ig
 CC molecule or an immunoconjugate or fusion protein containing an anti-CD5
 CC Ig molecule, and where the modified Ig variable domain comprises at
 CC least one of (a) a modified light chain variable region (see AAW58478 or
 CC AAW58480), and (b) a modified heavy chain variable region (see AAW58479
 CC or AAW58481), where AAW58478 and AAW58479 are humanised forms of the H65
 CC light and heavy chain variable domains with low risk amino acid
 CC substitutions (i.e. low risk of reducing antigen-binding specificity.)
 CC and AAW58480 and AAW58481 are humanised forms of the H65 light and heavy
 CC chain variable domains with moderate risk amino acid substitutions and
 CC are present in humanised H65 antibody he3 (AFCC HB 11206). The method is
 CC useful for treating autoimmune diseases, especially systemic lupus
 CC erythematosus, rheumatoid arthritis, psoriasis or type 1 diabetes. The
 CC present sequence represents the murine HVH antibody light chain variable
 CC domain.
 XX
 XX Sequence 107 AA;
 SQ

Query Match 92.0%; Score 516; DB 19; Length 107;
 Best Local Similarity 91.6%; Pred. No. 3.5e-32;
 Matches 98; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIVLTQSPATLSVTPGDSVSLSCQASQISLNHLHWYQOKSHESPRLLIKYRSQISGIPS 60
 |||||
 DB 1 DIVLTQSPATLSVTPGDSVSLSCRASQISGNLHLHWYQOKSHESPRLLIKYASQISGIPS 60
 |||||

QY 61 RFSGSGGTDFALINSVETEDFGMYFCQSGSWPHTFGGTTKLEIK 107
 |||||
 DB 61 RFSGSGGTDFTLINSVETEDFGMYFCQSGSWPHTFGGTTKLDIK 107
 |||||

RESULT 13
 AAW84094
 ID AAW84094 standard; Protein; 108 AA.
 XX
 AC AAW84094;
 XX
 DT 15-MAR-1999 (first entry)
 XX
 DE Murine vitronectin alpha-v beta-3 receptor MAB VL region.
 XX
 KW Humanised antibody; monoclonal antibody; MAB; antibody engineering;
 KW mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;
 KW cancer; metastasis; rheumatoid arthritis; atherosclerosis;
 KW angiogenesis; diabetic retinopathy; inflammation;
 KW macular degeneration; osteoporosis; Paget's disease;
 KW hyperparathyroidism; hypercalcaemia; therapy; immunotherapy.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers

FT Region 24..34
 /label= CDR1
 FT Region 50..56
 /label= CDR2
 FT Region 89..97
 /label= CDR3
 XX
 PN WO9840488-A1.
 XX
 XX 17-SEP-1998.
 XX
 XX 12-MAR-1998; 98WO-US04987.
 XX
 XX 12-MAR-1997; 97US-0039609.
 XX
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 XX
 XX Johanson KO, Jonak ZL, Taylor AH;
 XX
 XX WPI; 1999-034590/03.
 DR N-PSDB; AAV71798.
 DR
 XX New anti alpha_v beta_3 vitronectin receptor antibodies - used for
 XX immunotherapeutic treatment of e.g. diabetic retinopathy.
 PT inflammatory disorders, atherosclerosis, restenosis, cancers or
 PT osteoporosis
 XX
 PS Example 13; Page 59-60; 97pp; English.
 XX
 CC This is the amino acid sequence of the light chain variable region
 CC (VL) of the anti-human alpha-v beta-3 vitronectin receptor murine
 CC monoclonal antibody D12, as deduced from isolated cDNA (see
 CC AAV71798). D12 VH (see AAW84093) and VL show sequence similarity to
 CC Kabat VH subgroup I (see AAW84093) and Kabat VK subgroup III (see
 CC AAW84096), respectively. Humanised VH (see AAW84097) and VL (see
 CC AAW84098) were constructed by combining the framework regions of the
 CC human V region consensus sequences with complementarity determining
 CC regions of D12 (keeping some preferred murine framework residues).
 CC The humanised antibodies are specifically reactive with the human
 CC alpha-v beta-3 protein receptor and capable of neutralising the
 CC receptor. They can be used for passive immunotherapy of a disorder
 CC mediated by the alpha-v beta-3 receptor, e.g. cardiovascular
 CC disorders or angiogenic-related disorders, such as angiogenesis
 CC associated with diabetic retinopathy, atherosclerosis and
 CC restenosis, chronic inflammatory disorders, macular degeneration,
 CC rheumatoid arthritis and cancer, e.g. solid tumour metastasis, and
 CC diseases where bone resorption is associated with pathology such as
 CC osteoporosis, hyperparathyroidism, Paget's disease, hypercalcaemia
 CC of malignancy, osteolytic lesions produced by bone metastasis, bone
 CC loss due to immobilisation or sex hormone deficiency. They can also
 CC be used for targeted drug therapy, and for detection and diagnosis.
 XX
 XX Sequence 108 AA;
 SQ

Query Match 89.3%; Score 501; DB 20; Length 108;
 Best Local Similarity 88.8%; Pred. No. 4.9e-31;
 Matches 95; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIVLTQSPATLSVTPGDSVSLSCQASQISLNHLHWYQOKSHESPRLLIKYRSQISGIPS 60
 |||||
 DB 1 DIVLTQSPATLSVTPGDSVSLSCRASQISLNHLHWYQOKSHESPRLLIKYASQISGIPS 60
 |||||

QY 61 RFSGSGGTDFALINSVETEDFGMYFCQSGSWPHTFGGTTKLEIK 107
 |||||
 DB 61 RFSGSGGTDFTLINILETEDEFGMYFCQSGSWPHTFGGTTNLEIK 107
 |||||

RESULT 14
 AAW00241
 ID AAW00241 standard; Protein; 108 AA.
 XX
 AC AAW00241;
 XX

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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:54:45 ; Search time 20.9804 Seconds
(without alignments)
76.811 Million cell updates/sec

Title: US-09-016-061-8
Perfect score: 561
Sequence: 1 DIVLTQSPATLSVTPGDSYS.....CQSGSNWPHFGGTTKLEIK 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 97044 seqs, 15060890 residues

Total number of hits satisfying chosen parameters: 97044

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
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2	561	100.0	107	8	US-08-791-391A-8
3	511	91.1	128	12	US-10-006-773-6
4	470	83.8	107	8	US-08-791-391A-4
5	464	82.7	107	8	US-08-790-540A-4
6	464	82.7	107	8	US-08-791-391A-32
7	422	75.2	244	10	US-09-940-391-1
8	409	72.9	107	10	US-09-756-301A-3
9	409	72.9	107	10	US-09-927-703-3
10	409	72.9	107	10	US-09-766-535A-3
11	409	72.9	107	10	US-09-756-161A-3
12	409	72.9	107	12	US-10-010-229-3
13	409	72.9	107	12	US-10-043-450-3
14	409	72.9	107	12	US-10-044-534-3
15	357.5	63.7	107	12	US-09-965-099-44
16	357.5	63.7	107	12	US-10-051-852-44
17	354	63.1	106	8	US-08-844-215-11
18	353	62.9	129	10	US-09-839-447A-2
19	350.5	62.5	109	12	US-10-025-687-10

20	350	62.4	108	10	US-09-905-243-68	Sequence 68, Appl
21	350	62.4	108	10	US-09-905-243-73	Sequence 73, Appl
22	349	62.2	240	9	US-09-968-561A-2	Sequence 2, Appl
23	349	62.2	240	10	US-09-192-854-2	Sequence 2, Appl
24	346.5	61.8	105	8	US-08-844-215-9	Sequence 9, Appl
25	345	61.5	108	10	US-09-056-160B-12	Sequence 12, Appl
26	345	61.5	109	10	US-09-811-123-6	Sequence 6, Appl
27	345	61.5	214	10	US-09-940-166A-2	Sequence 2, Appl
28	345	61.5	214	10	US-09-811-384-11	Sequence 11, Appl
29	345	61.5	237	10	US-09-940-166A-6	Sequence 6, Appl
30	344	61.3	107	10	US-09-056-160B-13	Sequence 13, Appl
31	343.5	61.2	109	9	US-09-144-886-97	Sequence 97, Appl
32	343	61.1	110	10	US-09-056-160B-103	Sequence 103, App
33	343	61.1	110	10	US-09-056-160B-107	Sequence 107, App
34	343	61.1	110	10	US-09-056-160B-117	Sequence 117, App
35	343	61.1	237	10	US-09-056-160B-100	Sequence 100, App
36	343	61.1	491	12	US-10-011-125-2	Sequence 2, Appl
37	342.5	61.1	107	8	US-08-844-215-10	Sequence 10, Appl
38	342.5	61.1	109	9	US-09-144-886-98	Sequence 98, Appl
39	341	60.8	107	10	US-09-056-160B-15	Sequence 15, Appl
40	341	60.8	107	10	US-09-850-165-93	Sequence 93, Appl
41	341	60.8	108	10	US-09-056-160B-8	Sequence 8, Appl
42	341	60.8	108	12	US-10-140-555-4	Sequence 4, Appl
43	340.5	60.7	107	10	US-09-965-099-57	Sequence 57, Appl
44	340.5	60.7	107	12	US-10-051-852-57	Sequence 57, Appl
45	340	60.6	110	10	US-09-056-160B-105	Sequence 105, App

ALIGNMENTS

RESULT 1
US-08-790-540A-8
; Sequence 8, Application US/08790540A
; Patent No. US20010011125A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,540A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9901
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-790-540A-8

Query Match 100.0%; Score 561; DB 8; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.3e-37;

	61	RFSGSGSCTDFALSINSVETEDFGMYFCQGSWSWPHTFGGCTKLEIK	107
Qy		: : :	
	61	RFSGSGSCTDFTLTISSLEPEDFAVVYCOOGSWSWPHTFGGCTKEIK	107
Dd		: : :	

RESULT 5

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US-08-790-540A-4
; Sequence 4, Application US/08790540A
; Patent No. US20010011125A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,540A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-790-540A-4

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Query Match	82.7%	Score 464;	DB 8;	Length 107;
Best Local Similarity	78.5%	Pred. No. 4.6e-30;		
Matches 84;	Conservative	15;	Mismatches 8;	Indels 0;
Gaps				

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Db	1	EVITQSPATLSLSPGERATLSCAQSQISNHLHWYQORPGQAPRLILXYRSQISGIPA	60
Qy	61	RFSGSGGTDFALINSVETEDFQYFCQSGSWPHTFGGKLEIK	107
Db	61	RFSGSGGTDFLLRISLPEDFAVYFCQSGSWPHTFGGKVEIK	107

RESULT 6

US-08-791-391A-32
; Sequence 32, Application US/08791391A
; Patent No. US20010016645A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego

STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/791,391A
FILING DATE: 30-JAN-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,615
REFERENCE/DOCKET NUMBER: P-IX 1482
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PIS-08-791-391A-32

Query Match	82.7%	Score 464;	DB 8;	Length 107;
Best Local Similarity	78.5%	Pred. No. 4.6e-30;		
Matches 84;	Conservative 15;	Mismatches 8;	Indels 0;	Gaps 0;

[illegible]

RESULT 7

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; Sequence 1, Application US/09940391
; Patent No. US20020035325A1
; GENERAL INFORMATION:
; APPLICANT: Barbera-Guillem, Emilio
; TITLE OF INVENTION: Method for detecting lymphoid tissue involved in tumor progres
; FILE REFERENCE: Phy-03
; CURRENT APPLICATION NUMBER: US/09/940,391
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: 09/244,369
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 60/077,970
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: 60/073,882
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Mus sp.
; US-09-940-391-1

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Query Match	75.2%	Score 422;	DB 10;	Length 244;
Best Local Similarity	72.9%	Pred. NO. 1.7e-26;		
Matches 78;	Conservative 14;	Mismatches 15;	Indels 0;	Gaps 0;

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		: :: : : : : :: :	
Db	135	DILLTQPALLSVPGRVSFSCRASQNIGTSIHYYQRTNGSPRLLIKYASESVSGIPS	194
Oy	61	RFGSGGSGDTFALINSVETEDFGMYFCOOSGSWPHTFGGTCKLEIK	107


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; PRIOR APPLICATION NUMBER: U.S. 08/192,102
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,861
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,093
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/010,406
; PRIOR FILING DATE: 1993-01-29
; PRIOR APPLICATION NUMBER: U.S. 08/013,413
; PRIOR FILING DATE: 1993-02-02
; PRIOR APPLICATION NUMBER: U.S. 07/943,852
; PRIOR FILING DATE: 1992-09-11
; PRIOR APPLICATION NUMBER: U.S. 07/853,606
; PRIOR FILING DATE: 1992-03-18
; PRIOR APPLICATION NUMBER: U.S. 07/670,827
; PRIOR FILING DATE: 1991-03-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus Balb/c
; US-09-766-535A-3

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	Best Local Similarity	70.1%;	Pred. No. 8.5e-26;		
	Matches	75;	Conservative	16;	Mismatches 0; Indels 0; Gaps 0;
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Db	1	DILLTQSPAILSVGGERVSPCRASQFVGSSIHWYQORTNGSPRLLIKYASEMSGIPS	60		
QY	61	RFSSGSGTDFALINSVETEDFCMYCQSGSWPHTFGGKTLEIK	107		
Db	61	RFSSGSGTDFTLINVTESDIADYTCQSHSWPFFFGSGTINLEVK	107		

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RESULT 11
US-09-756-161A-3
; Sequence 3, Application US/09756161A
; Patent No. US2002013207A1
; GENERAL INFORMATION:
; APPLICANT: Le, Junming
; APPLICANT: Viacek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Grayeb, John
; APPLICANT: Knight, David M.

```

```

; PRIOR APPLICATION NUMBER: U.S.07/670,827
; PRIOR FILING DATE: 1991-03-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus Balb/c
US-09-756-161A-3

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	Query Match	72.9%	Score 409;	DB 10;	Length 107;
	Best Local Similarity	70.1%;	Pred. No. 8.5e-26;		
	Matches	75;	Conservative 16;	Mismatches 16;	Indels 0; Gaps 0;
Qy	1	DIVTQSPATLSVTPGDSVLSQASQASISNHLHWYQOKSHESPRLLIKYRSQISGIPS	60		
Db	1	DILLTQPAILLSVSPGERVSPCRASQFVGSSIHMYQORTNGSPRLLIKYASMSGIPS	60		
Qy	61	RFSGSGGTDFALSIINSEYETEDFQWYFCQQSGSWPHTFGGKTLEIK	107		
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RESULT 12
US-10-010-229-3
; Sequence 3, Application US/10010229
; Patent No. US20020114805A1
; GENERAL INFORMATION:
; APPLICANT: Le, Junming
; APPLICANT: Vilecek, Jan
; APPLICANT: Dadona, Peter
; APPLICANT: Ghraayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antib
; TITLE OF INVENTION: Human Tumor N
; FILE REFERENCE: 0975.1005-013
; CURRENT APPLICATION NUMBER: US/10/
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US/09/92
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Vers
; SEQ ID NO 3
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus Balb/c
; US-10-010-229-3

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[illegible]

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RESULT 13
US-10-043-450-3
; Sequence 3, Application US/10043450
; Patent No. US20020141996A1
; GENERAL INFORMATION:
; APPLICANT: Le, Junming
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Graybe, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott

```

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; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
; TITLE OF INVENTION: Human Tumor Necrosis Factor
; FILE REFERENCE: 0975.1005-013
; CURRENT APPLICATION NUMBER: US/10/043,450
; CURRENT FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: 09/927,703
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: U.S. 09/756,398
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: U.S. 09/133,119
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1994-10-18
; PRIOR APPLICATION NUMBER: U.S. 08/192,102
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,861
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,093
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/010,406
; PRIOR FILING DATE: 1993-01-29
; PRIOR APPLICATION NUMBER: U.S. 08/013,413
; PRIOR FILING DATE: 1993-02-02
; PRIOR APPLICATION NUMBER: U.S. 07/943,852
; PRIOR FILING DATE: 1992-09-11
; PRIOR APPLICATION NUMBER: U.S. 07/853,606
; PRIOR FILING DATE: 1992-03-18
; PRIOR APPLICATION NUMBER: U.S. 07/670,827
; PRIOR FILING DATE: 1991-03-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus Balb/c
; UNK: 0
US-10-043-450-3

Query Watch 72.9%; Score 409; DB 12; Leng
Best Local Similarity 70.1%; Pred. No. 8.5e-26; Ind
Matches 75; Conservative 16; Mismatches 16; Ind

QY 1 DIVLTQSPTATLSVTCDSVSLSQASQSIHNLHWYQQKSHSPRLII
||| ||| ||| ||| ||| ||| ||| : ||| ||| : ||| ||| : ||| |||
Db 1 DILLTQSPAILSVSPGERVSFCRASQIFGVGSSIHWWYQQRINGSRPLII
||| ||| ||| ||| ||| ||| ||| : ||| ||| ||| ||| ||| ||| |||

QY 61 RFSGSGGTDFALSNISVETEDFGMYFQQQSGSWPHFTGGTKLEIK
||||||| ||| ||| ||| ||| ||| : ||| ||| ||| ||| ||| ||| |||
Db 61 RFSGSGSGTDFTLNTIIVSESDIADYYCQQSHWPFITFGSGTNLEVK
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RESULT 14
US-10-044-534-3
; Sequence 3, Application US/10044534
; Patent No. US20020146419A1
; GENERAL INFORMATION:
; APPLICANT: Le, Junming
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Grayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
; TITLE OF INVENTION: Human Tumor Necrosis Factor
; FILE REFERENCE: 0975.1005-013
; CURRENT APPLICATION NUMBER: US/10/044,534
; CURRENT FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: 09/927,703
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: U.S. 09/756,398
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: U.S. 09/133,119

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NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50438-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX: <Unknown>
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 44:
US-09-965-099-44

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Query Match      63.7%; Score 357.5; DB 10; Length 107;
Best Local Similarity 63.6%; Pred. No. 8.5e-22;
Matches 68; Conservative 19; Mismatches 19; Indels 1; Gaps 1;

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DB      1 EIVLTOSPATLSLSPGERATLSGRASSV-NYMHWTQRPQAPRLLIYATSNLASCIPA 59

QY      61 RFSGSGGTDFAISINSVETEDFGVYCOQSGSWPHTFGGGKLEIK 107
DB      60 RFSGSGGTDFTLTSSLEPEDFAVYTCQOWSINPRTFGGKVEIK 106

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Search completed: November 18, 2002, 18:45:12
Job time : 20.9804 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:01 : Search time 45.3701 Seconds
(without alignments)
69.390 Million cell updates/sec

Title: US-09-016-061-8
Perfect score: 561
Sequence: 1 DIVLTQSPATLSVTPGDSVS.....CQSGSWPHTFGGCKLEIK 107

Scoring table: BLOSUM62

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Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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 - 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
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 - 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	529	94.3	107	1	US-07-634-278-62
2	529	94.3	107	1	US-08-477-728-62
3	529	94.3	107	1	US-08-474-040-62
4	529	94.3	107	1	US-08-487-200-62
5	529	94.3	107	4	US-08-484-537-62
6	529	94.3	127	1	US-07-634-278-83
7	529	94.3	127	1	US-08-477-728-83
8	529	94.3	127	1	US-08-474-040-83
9	529	94.3	127	1	US-08-487-200-83
10	529	94.3	127	4	US-08-484-537-83
11	526	93.8	127	1	US-08-436-463-4
12	519	92.5	107	1	US-08-436-463-20
13	519	92.5	109	1	US-07-942-245-4
14	516	92.0	107	1	US-08-107-669D-1
15	516	92.0	107	1	US-08-472-788A-1
16	516	92.0	107	2	US-08-477-531B-1
17	516	92.0	107	2	US-08-082-842A-1
18	507	90.4	127	1	US-08-436-463-18
19	494	88.1	100	1	US-08-436-463-19
20	465	82.9	108	4	US-09-247-352-1
21	465	82.9	108	4	US-09-466-635-1
22	465	82.9	214	4	US-09-247-352-4
23	465	82.9	214	4	US-09-466-635-4
24	459	81.8	108	2	US-08-737-560A-11
25	453	80.7	103	1	US-08-436-463-21
26	451	80.4	107	4	US-09-438-954-38
27	432	77.0	107	1	US-07-634-278-63

28	432	77.0	107	1	US-07-634-278-87	Sequence 87, Appl
29	432	77.0	107	1	US-08-477-728-63	Sequence 63, Appl
30	432	77.0	107	1	US-08-477-728-87	Sequence 87, Appl
31	432	77.0	107	1	US-08-474-040-63	Sequence 63, Appl
32	432	77.0	107	1	US-08-474-040-87	Sequence 87, Appl
33	432	77.0	107	1	US-08-487-200-63	Sequence 63, Appl
34	432	77.0	107	1	US-08-487-200-87	Sequence 87, Appl
35	432	77.0	107	4	US-08-484-537-63	Sequence 63, Appl
36	432	77.0	107	4	US-08-484-537-87	Sequence 87, Appl
37	429	76.5	107	4	US-09-438-954-1	Sequence 1, Appl
38	426	75.9	107	2	US-08-476-176B-4	Sequence 4, Appl
39	426	75.9	107	3	US-08-127-721A-4	Sequence 4, Appl
40	426	75.9	107	3	US-08-485-246A-4	Sequence 4, Appl
41	422	75.2	244	4	US-09-244-369B-1	Sequence 1, Appl
42	419	74.7	107	4	US-09-438-954-3	Sequence 3, Appl
43	418	74.5	107	2	US-08-232-081B-40	Sequence 40, Appl
44	418	74.5	240	2	US-07-956-399-2	Sequence 2, Appl
45	415	74.0	106	2	US-08-800-198-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-07-634-278-62
; Sequence 62, Application US/07634278
; Patent No. 5530101
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO. Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/634,278
; FILING DATE: 19-DEC-1990
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-634-278-62

Query Match 94.3%; Score 529; DB 1; Length 107;
Best Local Similarity 93.5%; Pred. No. 9e-44;
Matches 100; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIVLTQSPATLSVTPGDSVSLSCASQASISNHLHWYQOKSHSPRLLIKYSQISGIPS 60
|||||
Db 1 DIVLTQSPATLSVTPGDSVSLSCASQASISNHLHWYQOKSHSPRLLIKYSQISGIPS 60
|||||
QY 61 RFSGSGTGDFALINSVETEDFGMYFCQSGSWPHTFGGKLEIK 107
|||||
Db 61 RFSGSGTGDFALINSVETEDFGMYFCQSGSWPHTFGGKLEIK 107
|||||

RESULT 2

US-08-477-728-62
; Sequence 62, Application US/08477728
; Patent No. 5585089
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,728
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

Query Match 94.3%; Score 529; DB 1; Length 107;
Best Local Similarity 93.5%; Pred. No. 9e-44;
Matches 100; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Matches 100; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 DIVLTQSPATLSVTPGDSVSLSCASQASISNHLHWYQOKSHSPRLLIKYSQISGIPS 60
|||||
Db 1 DIVLTQSPATLSVTPGDSVSLSCASQASISNHLHWYQOKSHSPRLLIKYSQISGIPS 60
|||||
QY 61 RFSGSGTGDFALINSVETEDFGMYFCQSGSWPHTFGGKLEIK 107
|||||
Db 61 RFSGSGTGDFALINSVETEDFGMYFCQSGSWPHTFGGKLEIK 107
|||||

RESULT 3

US-08-474-040-62
; Sequence 62, Application US/08474040
; Patent No. 5693761
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELING, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,040
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-474-040-62

Query Match 94.3%; Score 529; DB 1; Length 107;
Best Local Similarity 93.5%; Pred. No. 9e-44;
Matches 100; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIVLTQSPATLSVTPGDSVSLSCASQASISNHLHWYQOKSHSPRLLIKYSQISGIPS 60
|||||

Db 1 DIVLTQSPATLSVTPGDSVSLSCRASQSISSNNLHWYQKSHESPRLLIKYASQISGIPS 60
QY 61 RFSGSGSGTDFALSINSVETEDFGMYFCQSGSWPHTFGGKLEIK 107
Db 61 RFSGSGSGTDFTLVNGVETEDFGMYFCQSGSNWPHTFGGKLEIK 107

RESULT 4
US-08-487-200-62
; Sequence 62, Application US/08487200
; Patent No. 5693762
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,200
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-487-200-62

Query Match 94.3%; Score 529; DB 1; Length 107;
Best Local Similarity 93.5%; Pred. No. 9e-44;
Matches 100; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIVLTQSPATLSVTPGDSVSLSCRASQSISSNNLHWYQKSHESPRLLIKYASQISGIPS 60
Db 1 DIVLTQSPATLSVTPGDSVSLSCRASQSISSNNLHWYQKSHESPRLLIKYASQISGIPS 60
QY 61 RFSGSGSGTDFALSINSVETEDFGMYFCQSGSWPHTFGGKLEIK 107
Db 61 RFSGSGSGTDFTLVNGVETEDFGMYFCQSGSNWPHTFGGKLEIK 107

Db 61 RFSGSGSGTDFTLVNGVETEDFGMYFCQSGSNWPHTFGGKLEIK 107

RESULT 5
US-08-484-537-62
; Sequence 62, Application US/08484537
; Patent No. 6180370
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,537
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-484-537-62

Query Match 94.3%; Score 529; DB 4; Length 107;
Best Local Similarity 93.5%; Pred. No. 9e-44;
Matches 100; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIVLTQSPATLSVTPGDSVSLSCRASQSISSNNLHWYQKSHESPRLLIKYASQISGIPS 60
Db 1 DIVLTQSPATLSVTPGDSVSLSCRASQSISSNNLHWYQKSHESPRLLIKYASQISGIPS 60
QY 61 RFSGSGSGTDFALSINSVETEDFGMYFCQSGSWPHTFGGKLEIK 107
Db 61 RFSGSGSGTDFTLVNGVETEDFGMYFCQSGSNWPHTFGGKLEIK 107

ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,040
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-474-040-83

Query Match 94.3%; Score 529; DB 1; Length 127;
Best Local Similarity 93.5%; Pred. No. 1.le-43;
Matches 100; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIVLTQSPATLSVTPGDVSLSCQASQSIHNLHWYQOKSHSPRLLIKYSQISGIPS 60
|||||
Db 21 DIVLTQSPATLSVTPGDVSLSCQASQSIHNLHWYQOKSHSPRLLIKYSQISGIPS 80
|||||

QY 61 RFGSGSGTDFALINSVETEDFGMYFCQSQSNWPHTFGGKLEIK 107
|||||
Db 81 RFGSGSGTDFTLVNGVETEDFGMYFCQSQSNWPHTFGGKLEIK 127

RESULT 9
US-08-487-200-83
Sequence 83, Application US/08487200
Patent No. 5693762
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US

ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,200
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002610
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-487-200-83

Query Match 94.3%; Score 529; DB 1; Length 127;
Best Local Similarity 93.5%; Pred. No. 1.le-43;
Matches 100; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIVLTQSPATLSVTPGDVSLSCQASQSIHNLHWYQOKSHSPRLLIKYSQISGIPS 60
|||||
Db 21 DIVLTQSPATLSVTPGDVSLSCQASQSIHNLHWYQOKSHSPRLLIKYSQISGIPS 80
|||||

QY 61 RFGSGSGTDFALINSVETEDFGMYFCQSQSNWPHTFGGKLEIK 107
|||||
Db 81 RFGSGSGTDFTLVNGVETEDFGMYFCQSQSNWPHTFGGKLEIK 127

RESULT 10
US-08-484-537-83
Sequence 83, Application US/08484537
Patent No. 6180370
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 28-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
FILING DATE: 28-SEP-1990
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US/07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-484-537-83

Query Match 94.3%; Score 529; DB 4; Length 127;
Best Local Similarity 93.5%; Pred. No. 1.1e-43;
Matches 100; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIVLTQSPATLSVTPGDVSLSCQASQSSINHLHWYQOKSHSPRLLIKYRSQISGIPS 60
|||||
DB 21 DIVLTQSPATLSVTPGDVSLSCQASQSSINHLHWYQOKSHSPRLLIKYRSQISGIPS 80
|||||
QY 61 RFGSGSGTDFALSINSVETEDFGMYFCQSGSWPHTFGGKLEIK 107
|||||
DB 81 RFGSGSGTDFLSVNGVETEDFGMYFCQSGSWPHTFGGKLEIK 127

RESULT 11
US-08-436-463-4
Sequence 4, Application US/08436463
Patent No. 5760185
GENERAL INFORMATION:
APPLICANT: KIMACHI, Kazuhiko
APPLICANT: MAEDA, Hiroaki
APPLICANT: NISHIYAMA, Kiyoto
APPLICANT: TOKIYOSHI, Sachio
TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT
TITLE OF INVENTION: ANTIBODY AND GENE FRAGMENT CODING FOR SAID ANTIBODY
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street, N.W., Suite 400
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,463
FILING DATE: 26-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 341255/1992
FILING DATE: 28-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: KIMACHI-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 341255/1992
FILING DATE: 28-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: KIMACHI-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-436-463-4

Query Match 93.8%; Score 526; DB 1; Length 127;
Best Local Similarity 93.5%; Pred. No. 2.1e-43;
Matches 100; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIVLTQSPATLSVTPGDVSLSCQASQSSINHLHWYQOKSHSPRLLIKYRSQISGIPS 60
|||||
DB 21 DIVLTQSPATLSVTPGDVSLSCQASQSSINHLHWYQOKSHSPRLLIKYRSQISGIPS 80
|||||
QY 61 RFGSGSGTDFALSINSVETEDFGMYFCQSGSWPHTFGGKLEIK 107
|||||
DB 81 RFGSGSGTDFLSVNGVETEDFGMYFCQSGSWPHTFGGKLEIK 127

RESULT 12
US-08-436-463-20
Sequence 20, Application US/08436463
Patent No. 5760185
GENERAL INFORMATION:
APPLICANT: KIMACHI, Kazuhiko
APPLICANT: MAEDA, Hiroaki
APPLICANT: NISHIYAMA, Kiyoto
APPLICANT: TOKIYOSHI, Sachio
TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT
TITLE OF INVENTION: ANTIBODY AND GENE FRAGMENT CODING FOR SAID ANTIBODY
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street, N.W., Suite 400
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,463
FILING DATE: 26-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 341255/1992
FILING DATE: 28-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: KIMACHI-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid

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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-436-463-20

Query Match          92.5%; Score 519; DB 1; Length 107;
Best Local Similarity 92.5%; Pred. No. 8.2e-43;
Matches 99; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIVLTQSPATLSVTPGDSVSLSCASQSIHNLHWYQOKSHSPRLLIKYSQISGIPS 60
   |||||
Db 1 DIVLTQSPATLSVTPGDSVSLSCASQSIHNLHWYQOKSHSPRLLIKYSQISGIPS 60
   |||||

QY 61 RFSGSGSGTDFALINSVETEDFGMYFCQSGSWPHTFGGKLEIK 107
   |||||
Db 61 RFSGSGSGTDFALINSVETEDFGMYFCQSGSWPHTFGGKLEIK 107
   |||||

RESULT 13
US-07-942-245-4
; Sequence 4, Application US/07942245
; Patent No. 5639641
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, Jan T.
; APPLICANT: SEARLE, Stephen M.J.
; APPLICANT: REES, Anthony R.
; APPLICANT: ROGUSKA, Michael A.
; APPLICANT: GUILD, Braydon C.
; TITLE OF INVENTION: SURFACE RESIDUE VENERING OF RODENT
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 522
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: HP 9000/700 workstation
; OPERATING SYSTEM: UNIX
; SOFTWARE: In house
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/942,245
; FILING DATE: 09-SEP-1992
; CLASSIFICATION: 530
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 293-7060
; TELEFAX: (202) 293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-942-245-4

Query Match          92.5%; Score 519; DB 1; Length 109;
Best Local Similarity 92.5%; Pred. No. 8.3e-43;
Matches 99; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIVLTQSPATLSVTPGDSVSLSCASQSIHNLHWYQOKSHSPRLLIKYSQISGIPS 60
   |||||
Db 1 DIVLTQSPATLSVTPGDSVSLSCASQSIHNLHWYQOKSHSPRLLIKYSQISGIPS 60
   |||||

QY 61 RFSGSGSGTDFALINSVETEDFGMYFCQSGSWPHTFGGKLEIK 107
   |||||
Db 61 RFSGSGSGTDFALINSVETEDFGMYFCQSGSWPHTFGGKLEIK 107
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RESULT 14
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US-08-107-669D-1
; Sequence 1, Application US/08107669D
; Patent No. 5766886
; GENERAL INFORMATION:
; APPLICANT: Studnicka, Gary M.
; TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States of America
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/107.669D
; FILING DATE: 13-AUG-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10906
; FILING DATE: 14-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/808,464
; FILING DATE: 13-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Michele A. Cimbala
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 0610.1000001/MAC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/371-2600
; TELEFAX: 202/371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-107-669D-1

Query Match          92.0%; Score 516; DB 1; Length 107;
Best Local Similarity 91.6%; Pred. No. 1.6e-42;
Matches 98; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIVLTQSPATLSVTPGDSVSLSCASQSIHNLHWYQOKSHSPRLLIKYSQISGIPS 60
   |||||
Db 1 DIVLTQSPATLSVTPGDSVSLSCASQSIHNLHWYQOKSHSPRLLIKYSQISGIPS 60
   |||||

QY 61 RFSGSGSGTDFALINSVETEDFGMYFCQSGSWPHTFGGKLEIK 107
   |||||
Db 61 RFSGSGSGTDFALINSVETEDFGMYFCQSGSWPHTFGGKLEIK 107
   |||||

RESULT 15
US-08-472-788A-1
; Sequence 1, Application US/08472788A
; Patent No. 5770196
; GENERAL INFORMATION:
; APPLICANT: Studnicka, Gary M.
; TITLE OF INVENTION: Modified Antibody Variable Domains
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,788A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/082,842
FILING DATE: 23-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10906
FILING DATE: 14-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/808,464
FILING DATE: 13-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Cimbala, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0610.1000003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/371-2600
TELEFAX: 202/371-2540
TELEX:

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-472-788A-1

Query Match 92.0%; Score 516; DB 1; Length 107;
Best Local Similarity 91.6%; Pred. No. 1.6e-42;
Matches 98; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
QY 1 DIVLTQSPATLSVTPGDSVSLSCQASQISNHLHWYQKSHSPRLLIKYRSQISGIPS 60
|||||
Db 1 DIVLTQSPATLSVTPGNSVSLSCRASQISGNLHLHWYQKSHSPRLLIKYASQISGIPS 60
|||||
QY 61 RFSGSGSGTDFALINSVETEDFGMYFCQSGSWPHTFGGTTKLEIK 107
|||||
Db 61 RFSGSGSGTDFTLINSVETEDFGMYFCQSGNSWPYTFGGGTKLDIK 107
|||||

Search completed: November 18, 2002, 17:43:32
Job time : 46.3701 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:01 ; Search time 4.90196 Seconds
(without alignments)
196.114 Million cell updates/sec

Title: US-09-016-061-48

Perfect score: 52

Sequence: 1 GTTFSSYDMS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: - 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_73:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	ID	Description
1	45	86.5	94	2 S14580	Ig heavy chain V r
2	41	78.8	97	2 S26890	Ig heavy chain V r
3	40	76.9	113	2 S26468	Ig heavy chain V r
4	40	76.9	117	1 HVMS34	Ig heavy chain pre
5	40	76.9	121	2 D27888	Ig heavy chain V r
6	40	76.9	124	2 C27888	Ig heavy chain V r
7	39	75.0	548	2 S38864	Ig epsilon chain C
8	38	73.1	40	2 S33406	Ig heavy chain V r
9	38	73.1	83	2 C25913	Ig heavy chain V r
10	38	73.1	98	2 S26891	Ig heavy chain V r
11	38	73.1	108	2 PL0248	Ig heavy chain V r
12	38	73.1	108	2 PL1006	Ig heavy chain V r
13	38	73.1	114	1 AVDGM	Ig heavy chain V r
14	38	73.1	117	1 HVMS84	Ig heavy chain pre
15	38	73.1	117	2 PL0249	Ig heavy chain V r
16	38	73.1	117	2 PL0252	Ig heavy chain V r
17	38	73.1	119	2 F27888	Ig heavy chain V r
18	38	73.1	122	2 E27888	Ig heavy chain V r
19	38	73.1	138	2 S09258	Ig heavy chain V r
20	37	71.2	92	2 S56009	Ig heavy chain var
21	37	71.2	92	2 S56008	Ig heavy chain var
22	37	71.2	97	1 HVMS91	Ig heavy chain V r
23	37	71.2	97	2 PH0872	Ig heavy chain V r
24	37	71.2	98	2 S26889	Ig heavy chain V r
25	37	71.2	100	2 D48223	Ig heavy chain V r
26	37	71.2	102	2 S14581	Ig heavy chain V r
27	37	71.2	108	2 PH1648	Ig heavy chain V r
28	37	71.2	108	2 PH1011	Ig heavy chain V r
29	37	71.2	109	2 PH1649	Ig heavy chain V r

30	37	71.2	111	2 PH1659	Ig heavy chain V r
31	37	71.2	111	2 S40090	Ig heavy chain - m
32	37	71.2	111	2 PH1007	Ig heavy chain V r
33	37	71.2	112	2 S26327	Ig heavy chain V r
34	37	71.2	112	2 PH1647	Ig heavy chain V r
35	37	71.2	113	2 S25571	Ig heavy chain V r
36	37	71.2	117	1 H3HU26	Ig heavy chain pre
37	37	71.2	117	2 A45953	Ig heavy chain pre
38	37	71.2	117	2 B34964	Ig heavy chain pre
39	37	71.2	117	2 S34012	Ig heavy chain V r
40	37	71.2	118	2 S31121	Ig heavy chain - h
41	37	71.2	119	2 C36005	Ig heavy chain V r
42	37	71.2	119	2 D36005	Ig heavy chain V r
43	37	71.2	119	2 S31107	Ig heavy chain - h
44	37	71.2	119	2 S31108	Ig heavy chain - h
45	37	71.2	120	2 S48798	Ig heavy chain V r

ALIGNMENTS

RESULT 1

S14580

Ig heavy chain V region - mouse

C;Species: Mus musculus (house mouse)

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999

C;Accession: S14580

R;Chen, Q.; Stenzel-Poore, M.; Rittenberg, M.B.

submitted to the EMBL Data Library, March 1991

A;Description: Natural polyreactive antibodies differ from Ag-induced antibodies in V

A;Reference number: S14484

A;Accession: S14580

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-94 <CHE>

A;Cross-references: EMBL:X58652; NID:g51293; PIDN:CAA41509.1; PID:g51294

C;Superfamily: Immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;7-90/Domain: immunoglobulin homology <IMM>

Query Match 86.5%; Score 45; DB 2; Length 94;

Best Local Similarity 90.0%; Pred. No. 0.086; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10

I | | | | | | | |

Db 18 GTTFSSYDMS 27

RESULT 2

S26890

Ig heavy chain V region (DP-48) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C;Accession: S26890

R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.

J. Mol. Biol. 227, 776-798, 1992

A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups o

A;Reference number: S26885; MUID:93021117; PMID:1404388

A;Accession: S26890

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-97 <TOM>

A;Cross-references: EMBL:Z12348; NID:g32916; PIDN:CAA78218.1; PID:g32917

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-97/Domain: immunoglobulin homology <IMM>

Query Match 78.8%; Score 41; DB 2; Length 97;

Best Local Similarity 88.9%; Pred. No. 0.55; Indels 0; Gaps 0;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTFSSYDM 9

Db 26 GTTFSSYDM 34
| | | | | | | |

RESULT 3

S26468
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S26468

R:Kavaler, J.
submitted to the EMBL Data Library, April 1991

A:Reference number: S26459
A:Accession: S26468
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-113 <KAV>
A:Cross-references: EMBL:X59107; NID:g51944; PIDN:CAA41833.1; PID:g51945
C:Superfamily: immunoglobulin V region, immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:11-94/Domain: immunoglobulin homology <IMM>

Query Match 76.9%; Score 40; DB 2; Length 113;
Best Local Similarity 80.0%; Pred. No. 1;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
| | | | | | | |

Db 22 GFAFSSYDMS 31

RESULT 4

HVMS34
Ig heavy chain precursor V region (345) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 31-Mar-1997
C:Accession: J0502

R:Levy, M.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.
J. Exp. Med. 169, 2007-2019, 1989

A:Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary
A:Reference number: J0501; MUID:89279149; PMID:2499654
A:Accession: J0502

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-117 <LEV>

A:Experimental source: strain BALB/cJ
A:Note: this sequence belongs to the VH7183 subfamily
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-117/Product: Ig heavy chain V region (345) #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>
F:41-115/Disulfide bonds: #status predicted

Query Match 76.9%; Score 40; DB 1; Length 117;
Best Local Similarity 80.0%; Pred. No. 1.1;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
| | | | | | | |

Db 45 GFAFSSYDMS 54

RESULT 5

D27888
Ig heavy chain V region (H37-60) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996
C:Accession: D27888

R:Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
EMBO J. 5, 1577-1587, 1986

A:Title: Structural and functional implications of a restricted antibody response to a
A:Reference number: A91043; MUID:86300658; PMID:2427335

A:Accession: D27888
A:Molecule type: DNA
A:Residues: 1-121 <CAT>

A:Experimental source: strain Balb/c

A:Note: this sequence was determined from the germline gene

C:Comment: This chain was isolated from a hybridoma protein that binds influenza virus

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 76.9%; Score 40; DB 2; Length 121;
Best Local Similarity 80.0%; Pred. No. 1.1;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
| | | | | | | |

Db 26 GFAFSSYDMS 35

RESULT 6

C27888
Ig heavy chain V region (H37-62) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996.

C:Accession: C27888

R:Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.

EMBO J. 5, 1577-1587, 1986

A:Title: Structural and functional implications of a restricted antibody response to

A:Reference number: A91043; MUID:86300658; PMID:2427335

A:Accession: C27888

A:Molecule type: DNA

A:Residues: 1-124 <CAT>

A:Experimental source: strain Balb/c

A:Note: this sequence was determined from the germline gene

C:Comment: This chain was isolated from a hybridoma protein that binds influenza virus

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 76.9%; Score 40; DB 2; Length 124;
Best Local Similarity 80.0%; Pred. No. 1.1;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
| | | | | | | |

Db 26 GFAFSSYDMS 35

RESULT 7

S38864
Ig epsilon chain C region - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 24-May-2001

C:Accession: S38864

R:Kipp, B.; Becker, W.; Schlaak, M.

submitted to the EMBL Data Library, November 1993

A:Description: Combination of a defined specificity and desired isotype by cloning of

A:Reference number: S38864

A:Accession: S38864

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-548 <KIP>

A:Cross-references: EMBL:Z27397; NID:g416537; PIDN:CAA81788.1; PID:g940782
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:353-421/Domain: immunoglobulin homology <IMM>

Query Match 75.0%; Score 39; DB 2; Length 548;
Best Local Similarity 80.0%; Pred. No. 8.9;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
| | | | | | | |

Db 26 GLUTSSYDMS 35

RESULT 8
S33406
Ig heavy chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-Mar-1997 #sequence_revision 24-Jul-1997 #text_change 17-Jul-1998
C:Accession: S33406
R:Kettleborough, C.A.; Saldanha, J.; Ansell, K.H.; Bendig, M.M.
Eur. J. Immunol. 23, 206-211, 1993
A:Title: Optimization of primers for cloning libraries of mouse immunoglobulin genes using a PCR strategy
A:Reference number: S33391; MUID:93122092; PMID:8419173
A:Accession: S33406
A:Molecule type: mRNA
A:Residues: 1-40 <RET>
A:Cross-references: EMBL:X73009
A:Experimental source: strain BALE/c
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-40/Domain: immunoglobulin homology (fragment) <IMM>

Query Match 73.1%; Score 38; DB 2; Length 40;
Best Local Similarity 80.0%; Pred. No. 0.83;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
Db 26 GTTFSSYTMS 35

RESULT 9
C25913
Ig heavy chain V region (BFL14) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 16-Aug-1996
C:Accession: C25913
R:Lawler, A.M.; Lin, P.S.; Gearhart, P.J.
Proc. Natl. Acad. Sci. U.S.A. 84, 2454-2458, 1987
A:Title: Adult B-cell repertoire is biased toward two heavy-chain variable-region genes
A:Reference number: A94148; MUID:87175692; PMID:3104915
A:Accession: C25913
A:Molecule type: DNA
A:Residues: 1-83 <LAW>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 73.1%; Score 38; DB 2; Length 83;
Best Local Similarity 80.0%; Pred. No. 1.8;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
Db 11 GTTFSSYDMS 20

RESULT 10
S26891
Ig heavy chain V region (DP-58) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S26891
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V(H) segments
A:Reference number: S26885; MUID:93021117; PMID:1404388
A:Accession: S26891
A>Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-98 <TOM>
A:Cross-references: EMBL:Z12358; NID:g32935; PIDN:CAA78228.1; PID:g32936
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 73.1%; Score 38; DB 2; Length 98;
Best Local Similarity 70.0%; Pred. No. 2.2;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
Db 26 GTTFSSYEMN 35

RESULT 11
PL0248
Ig heavy chain V region (anti-DNA, DP12VH) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996
C:Accession: PL0248
R:Shlönchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, J. Exp. Med. 171, 265-297, 1990
A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic hypermutation
A:Reference number: PL0231; MUID:9011618; PMID:2104919
A:Accession: PL0248
A:Molecule type: mRNA
A:Residues: 1-108 <SHL>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-24/Region: framework 1
F:9-92/Domain: immunoglobulin homology <IMM>
F:25-29/Region: complementarity-determining 1
F:30-43/Region: framework 2
F:44-60/Region: complementarity-determining 2
F:61-92/Region: framework 3
F:93-95/Region: complementarity-determining 3
F:100-108/Region: framework 4

Query Match 73.1%; Score 38; DB 2; Length 108;
Best Local Similarity 80.0%; Pred. No. 2.4;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
Db 20 GTTFSSYTMS 29

RESULT 12
PH1006
Ig heavy chain V region (Clone 202.33) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PH1006
R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective hypermutation
A:Reference number: PH0571; MUID:92381444; PMID:1512540
A:Accession: PH1006
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-108 <TIL>
A:Experimental source: B cell, strain [NZB x NZW]F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:10-93/Domain: immunoglobulin homology <IMM>

Query Match 73.1%; Score 38; DB 2; Length 108;
Best Local Similarity 80.0%; Pred. No. 2.4;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
Db 21 GTTFSSYDMS 30

RESULT 13
AVDGGM

Ig heavy chain V region (Gom) - dog (tentative sequence)
 C:Species: Canis lupus familiaris (dog)
 C:Date: 31-May-1979 #sequence_revision 31-May-1979 #text_change 31-Mar-2000
 C:Accession: A02067
 R:Wasserman, R.L.; Capra, J.D.
 Biochemistry 16, 3160-3168, 1977
 A:Title: Primary structure of the variable regions of two canine immunoglobulin heavy chain
 A:Reference number: A90403; MUID:77242268; PMID:407924
 A:Accession: A02067
 A:Molecule type: protein
 A:Residues: 1-114 <WAS>
 C:Comment: This chain was isolated from a myeloma protein.
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>
 F:22-96/Disulfide bonds: #status predicted

Query Match 73.1%; Score 38; DB 1; Length 114;

Best Local Similarity 77.8%; Pred. No. 2.6; Mismatches 0; Indels 2; Gaps 0;

QY 1 GTTFSSYDM 9
 I I I I I I I
 Db 26 GITFSGYDM 34

RESULT 14

HVMS84

Ig heavy chain precursor V region (5-84) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 31-Mar-1997
 C:Accession: J070505
 R:Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.
 J. Exp. Med. 169, 2007-2019, 1989
 A:Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary
 A:Reference number: J070501; MUID:89279149; PMID:2499654
 A:Accession: J070505
 A>Status: translation not shown

A:Molecule type: mRNA
 A:Residues: 1-117 <LEV>
 A:Experimental source: strain BALB/cJ
 A:Note: this sequence belongs to the VH7183 subfamily
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-117/Product: Ig heavy chain V region (5-84) #status predicted <MAT>
 F:34-117/Domain: immunoglobulin homology <IMM>
 F:41-115/Disulfide bonds: #status predicted

Query Match 73.1%; Score 38; DB 1; Length 117;

Best Local Similarity 80.0%; Pred. No. 2.7; Mismatches 0; Indels 2; Gaps 0;

QY 1 GTTFSSYDMS 10
 I I I I I I I I
 Db 45 GTTFSSYTMS 54

RESULT 15

PL0249

Ig heavy chain V region (anti-DNA, 3E12VH) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996
 C:Accession: PL0249
 R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.
 J. Exp. Med. 171, 265-297, 1990
 A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
 A:Reference number: PL0231; MUID:90111618; PMID:2104919
 A:Accession: PL0249
 A:Molecule type: mRNA
 A:Residues: 1-117 <SHL>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

F:1-30/Region: framework 1
 F:15-98/Domain: immunoglobulin homology <IMM>
 F:31-35/Region: complementarity-determining 1
 F:36-49/Region: framework 2
 F:50-66/Region: complementarity-determining 2
 F:67-98/Region: framework 3
 F:99-108/Region: complementarity-determining 3
 F:109-117/Region: framework 4

Query Match 73.1%; Score 38; DB 2; Length 117;

Best Local Similarity 80.0%; Pred. No. 2.7; Mismatches 0; Indels 2; Gaps 0;

QY 1 GTTFSSYDMS 10
 I I I I I I I I
 Db 26 GTTFSSYTMS 35

Search completed: November 18, 2002, 17:46:59

Job time : 4.90196 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:00 : Search time 2.45098 Seconds
(without alignments)
169.223 Million cell updates/sec

Title: US-09-016-061-48
Perfect score: 52
Sequence: 1 GTTFSSYDMS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	76.9	117	1 HV55_MOUSE	P18526 mus musculus
2	38	73.1	114	1 HV01_CANFA	P01784 canis famil
3	38	73.1	117	1 HV54_MOUSE	P18525 mus musculus
4	37	71.2	97	1 HV56_MOUSE	P18527 mus musculus
5	37	71.2	117	1 HV33_HUMAN	P01764 homo sapien
6	36	69.2	117	1 HV53_MOUSE	P18524 mus musculus
7	35	67.3	117	1 HV52_MOUSE	P06327 mus musculus
8	35	67.3	117	1 HV59_MOUSE	P18530 mus musculus
9	35	67.3	569	1 AMY_STRVL	P22998 streptomyce
10	35	67.3	1177	1 SP97_DICDI	Q95293 dictyosteli
11	34	65.4	114	1 HV00_MOUSE	P01741 mus musculus
12	34	65.4	153	1 RISC_METTH	O26237 methanobact
13	34	65.4	153	1 RISC_METTH	O59587 methanobact
14	34	65.4	191	1 SC21_RICPR	Q92eb4 rickettsia
15	34	65.4	199	1 SC21_RICCN	Q92jms rickettsia
16	34	65.4	527	1 GUAD_SCHPO	O14057 schizosacch
17	34	65.4	641	1 FIB2_PETMA	P33573 petromyzon
18	34	65.4	703	1 CDGT_BACS2	P31746 bacillus sp
19	34	65.4	704	1 CDGT_BACOH	P27036 bacillus oh
20	33	63.5	94	1 RP0L_HALNI	Q9hr53 halobacteri
21	33	63.5	115	1 HV3D_HUMAN	P01765 homo sapien
22	33	63.5	650	1 RAEI_RAT	P37727 rattus norv
23	33	63.5	710	1 CDGT_THETU	P26827 thermoanaer
24	33	63.5	1024	1 RIP3_MOUSE	P97434 mus musculus
25	33	63.5	1029	1 RIP3_RAT	Q9ere6 rattus norv
26	33	63.5	2211	1 FA5_BOVIN	Q28107 bos taurus
27	32	61.5	130	1 CRCB_HELPJ	Q92k01 helicobacte
28	32	61.5	130	1 CRCB_HELPJ	O25823 helicobacte
29	32	61.5	258	1 Y789_TREPA	O83768 treponema p
30	32	61.5	314	1 RHRA_RHIME	O923q6 rhizobium m
31	32	61.5	441	1 DNB2_ADEGL	O64759 avian adeno
32	32	61.5	444	1 CIAH_STRPN	O54955 streptococc
33	32	61.5	576	1 RICI_RICCO	P02879 ricinus com

ALIGNMENTS

RESULT 1

HV55_MOUSE
ID HV55_MOUSE STANDARD; PRT; 117 AA.
AC P18526;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 345 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RT the primary immune response";
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; JT0502; HYMS34.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 345.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12902 MW; 49380E4627AC99A CRC64;

Query Match 76.9%; Score 40; DB 1; Length 117;

Best Local Similarity 80.0%; Pred. No. 0.37;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10

1 | | | | | | | | | |

DB 45 GFAFSSYDMS 54

RESULT 2

HV01_CANFA
ID HV01_CANFA STANDARD; PRT; 114 AA.
AC P01784;
DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig heavy chain V region GOM.

OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=77242268; PubMed=407924;
 RA Wasserman R.L., Capra J.D.;
 RT "Primary structure of the variable regions of two canine
 immunoglobulin heavy chains.";
 RL Biochemistry 16:3160-3168(1977).
 CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
 DR PIR: A02067; AVDGM.
 DR HSP; P01772; 2FB4.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; Igv; 1.
 KW Immunoglobulin V region.
 FT NON_TER 114 114
 SQ SEQUENCE 114 AA; 12430 MW; BID47452C4E13C4 CRC64;
 Query Match 73.1%; Score 38; DB 1; Length 114;
 Best Local Similarity 77.8%; Pred. No. 0.9;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GTTFSSYDM 9
 I I I I I I I
 DB 26 GTTFSSYDM 34
 RESULT 3
 ID HV54_MOUSE STANDARD; PRT; 117 AA.
 AC P18525;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V region 5-84 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/CJ;
 RX MEDLINE=89279149; PubMed=2499654;
 RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
 RT "Early onset of somatic mutation in immunoglobulin VH genes during
 the primary immune response.";
 RL J. Exp. Med. 169:2007-2019(1989).
 CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
 DR PIR: J70505; HVMS84.
 DR HSP; P01810; 2FBJ.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; Igv; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 CHAIN 20 117
 IG HEAVY CHAIN V REGION 5-84.
 FT CHAIN 20 49
 FRAMEWORK-1.
 FT DOMAIN 20 49
 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 50 54
 FRAMEWORK-2.
 FT DOMAIN 55 68
 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 69 85
 FRAMEWORK-3.
 FT DOMAIN 86 117
 BY SIMILARITY.
 FT NON_TER 41 115
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12872 MW; 234055CB6A469861 CRC64;
 Query Match 73.1%; Score 38; DB 1; Length 117;
 Best Local Similarity 80.0%; Pred. No. 0.92;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
 I I I I I I I
 DB 45 GTTFSSYTMS 54
 RESULT 4
 ID HV56_MOUSE STANDARD; PRT; 97 AA.
 AC P18527;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V region 914.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/CJ;
 RX MEDLINE=89279149; PubMed=2499654;
 RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
 RT "Early onset of somatic mutation in immunoglobulin VH genes during
 the primary immune response.";
 RL J. Exp. Med. 169:2007-2019(1989).
 CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
 DR PIR: J70504; HVMS91.
 DR HSP; P01810; 2FBJ.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; Igv; 1.
 KW Immunoglobulin V region.
 FT NON_TER 97 97
 SQ SEQUENCE 97 AA; 10661 MW; C23CB33FF55DA893 CRC64;
 Query Match 71.2%; Score 37; DB 1; Length 97;
 Best Local Similarity 80.0%; Pred. No. 1.2;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GTTFSSYDMS 10
 I I I I I I I
 DB 26 GTTFSSYAMS 35
 RESULT 5
 ID HV3C_HUMAN STANDARD; PRT; 117 AA.
 AC P01764;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V-III region VH26 precursor.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81101090; PubMed=6450418;
 RA Matthysens G., Rabbitts T.H.;
 RT "Structure and multiplicity of genes for the human immunoglobulin
 heavy chain variable region.";
 RL Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).
 CC -----
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CC EMBL; J00236; AAA53516.1; -
DR EMBL; M35415; AAA58735.1; -
DR PIR; A02047; H3HU26.
DR HSSP; P01772; 2FB4.
DR Genew; HGNC:5545; IGHV6.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin V region; Signal.
KW CHAIN 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V-III REGION VH26.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12582 MW; E826733F1A3CB0F1 CRC64;

Query Match 71.2%; Score 37; DB 1; Length 117;
Best Local Similarity 80.0%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTFSSYDMS 10
Db 45 GTTFSSYAMS 54

RESULT 6
HV53_MOUSE
ID HV53_MOUSE STANDARD; PRT; 117 AA.
AC P18524;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region RF precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=BALB/CJ;
RT MEDLINE=89279149; PubMed=2499654;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response.";
RC J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY..
DR PIR; J0503; HVMSRF.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin V region; Hybridoma; Signal.
KW CHAIN 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION RF.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12866 MW; 2CE3295F390F725B CRC64;

Query Match 69.2%; Score 36; DB 1; Length 117;
Best Local Similarity 80.0%; Pred. No. 2.3;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTFSSYDMS 10
Db 45 GTTFSSYAMS 54

-----
CC EMBL; J00236; AAA53516.1; -
DR EMBL; M35415; AAA58735.1; -
DR PIR; A02047; H3HU26.
DR HSSP; P01772; 2FB4.
DR Genew; HGNC:5545; IGHV6.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin V region; Signal.
KW CHAIN 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V-III REGION VH26.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12582 MW; E826733F1A3CB0F1 CRC64;

Query Match 71.2%; Score 37; DB 1; Length 117;
Best Local Similarity 80.0%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTFSSYDMS 10
Db 45 GTTFSSYAMS 54

RESULT 7
HV52_MOUSE
ID HV52_MOUSE STANDARD; PRT; 117 AA.
AC P06327;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region VH58 A1/A4 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Yancopoulos G.D., Alt F.W.;
RA "Developmentally controlled and tissue-specific expression of
unrearranged VH gene segments.";
RT Cell 40:271-281(1985).
CC -----
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CC -----
DR EMBL; M13787; AAA38499.1; -
DR PIR; A02029; HVMSAL.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin V region; Signal.
KW CHAIN 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION VH58 A1/A4.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12971 MW; 8B0BC138856DFC9D CRC64;

Query Match 67.3%; Score 35; DB 1; Length 117;
Best Local Similarity 60.0%; Pred. No. 3.7;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTFSSYDMS 10
Db 45 GTTFSSYDIN 54

RESULT 8
HV59_MOUSE
ID HV59_MOUSE STANDARD; PRT; 117 AA.
AC P18530;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 7-39 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=BALB/CJ;
RT MEDLINE=89279149; PubMed=2499654;
RT Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
```

RT "Early onset of somatic mutation in immunoglobulin VH genes during the primary immune response.";
 RL J. Exp. Med. 169:2007-2019(1989).
 CC -1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.

DR PIR: JT0507; HVMS39.
 DR HSSP: P01810; 2FBJ

DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_v.

DR Pfam: PF00047; Ig_1.
 DR SMART: SM00406; IGV; 1.

KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 19

FT CHAIN 20 117 IG HEAVY CHAIN V REGION 7-39.
 FT DOMAIN 20 49 FRAMEWORK-1.

FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 55 68 FRAMEWORK-2.

FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 86 117 FRAMEWORK-3.

FT DISULFID 41 115 BY SIMILARITY.
 FT NON_TER 117 117

SQ SEQUENCE 117 AA; 12972 MW; DSCA4167D0F1774F CRC64;

Query Match 67.3%; Score 35; DB 1; Length 117;
 Best Local Similarity 70.0%; Pred. No. 3.7; Indels 2; Gaps 0;

Matches 7; Conservative 1; Mismatches 1; Indels 2; Gaps 0;

Qy 1 GTTFSSYDMS 10
 I I I I I I I

Db 45 GTTFSSYDMS 54

RESULT 9

AMY_STRVL STANDARD; PRT; 569 AA.

AC P22998;
 DT 01-AUG-1991 (Rel. 19, Created)

DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DE 01-APR-1993 (Rel. 25, Last annotation update)

DE Alpha-amylase precursor (EC 3.2.1.1) (1.4-alpha-D-glucan
 glucanohydrolase).

DE AML.
 GN Streptomyces violaceus (Streptomyces venezuelae).

OS Bacteria; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.

CC NCBI_TaxID=1936;
 CC [1]

RN SEQUENCE FROM N.A.
 RC STRAIN=ATCC 15068;

RX MEDLINE=8923724; PubMed=3266752;
 RA Virolle M.-J., Long C.M., Chang S., Bibb M.J.;

RT "Cloning, characterisation and regulation of an alpha-amylase gene
 from Streptomyces venezuelae.";

RL Gene 74:321-334(1988)

CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
 linkages in oligosaccharides and polysaccharides.

CC -1- INDUCTION: BY MALTOSYL AND REPRESSOR BY GLUCOSE.
 CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
 KNOWN AS THE ALPHA-AMYLASE FAMILY.

CC -----
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 or send an email to license@isb-sib.ch).

CC -----
 CC EMBL; M25263; AAB36561.1; --
 DR PIR: JS0101; JS0101.

DR HSSP; P22957; 1AQM.
 DR InterPro: IPR000461; Alpha_amylase.

DR InterPro: IPR002044; CBD_4.
 DR Pfam; PF00128; alpha-amylase; 1.

DR Pfam; PF00686; CBM_20; 1.
 DR Pfam; PF02806; alpha-amylase_C; 1.

DR PRINTS; PR00110; ALPHAAMYLASE.
 DR ProDom; PD001568; CBD_4; 1.

KW Hydrolase; Glycosidase; Carbohydrate metabolism; Signal.
 FT SIGNAL 1 28 POTENTIAL.

FT CHAIN 29 569 ALPHA-AMYLASE.
 FT ACT_SITE 205 205 BY SIMILARITY.

FT ACT_SITE 209 209 BY SIMILARITY.
 FT ACT_SITE 296 296 BY SIMILARITY.

SQ SEQUENCE 569 AA; 60637 MW; 14CA5B1D56720043 CRC64;

Query Match 67.3%; Score 35; DB 1; Length 569;
 Best Local Similarity 75.0%; Pred. No. 22;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTFSSYD 8
 I I I I I I I

Db 132 GTTFSSYD 139

RESULT 10

SP97_DICDI STANDARD; PRT; 1177 AA.

ID SP97_DICDI
 AC Q95ZG3;

DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Spindle pole body component 97 (Spc97) (DdSpc97).

GN SPC97.
 OS Dictyostelium discoideum (Slime mold).

OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
 OX NCBI_TaxID=44689;

RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=AX2;
 RX PubMed=12018385;

RA Daudeker C., Graf R.O.;

RT "Molecular analysis of the cytosolic Dictyostelium gamma-tubulin
 complex.";

RL Eur. J. Cell Biol. 81:175-184(2002).

CC -1- FUNCTION: May be involved in microtubule nucleation.
 CC -1- SUBCELLULAR LOCATION: Centrosome, and also found in the cytoplasm.

CC -1- SIMILARITY: BELONGS TO THE GCP FAMILY.
 CC -----

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 or send an email to license@isb-sib.ch).

CC -----
 CC EMBL; AJ318508; CAC47949.1; --

DR Microtubules.
 KW DOMAIN 29 39 POLY-THR.

FT DOMAIN 54 119 ASN-RICH.

FT DOMAIN 95 100 POLY-THR.

FT DOMAIN 164 171 POLY-ASP.

FT DOMAIN 529 532 POLY-GLN.

FT DOMAIN 538 545 POLY-ASN.

FT DOMAIN 554 559 POLY-LEU.

FT DOMAIN 563 569 POLY-GLN.

FT DOMAIN 708 745 THR-RICH.

FT DOMAIN 988 991 POLY-SER.

FT DOMAIN 1008 1096 GLN-RICH.

FT DOMAIN 1068 1077 POLY-GLN.

FT DOMAIN 1103 1106 POLY-THR.

SQ SEQUENCE 1177 AA; 136812 MW; C458848B016A94ED CRC64;

Query Match 67.3%; Score 35; DB 1; Length 1177;
 Best Local Similarity 75.0%; Pred. No. 48;

Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 GTTFSSYD 8
DB 72 GTTFNSYN 79

RESULT 11
HV00_MOUSE
ID HV00_MOUSE STANDARD; PRT; 114 AA.
AC P01741;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 21-JUL-1986 (Rel. 01, Last annotation update)
DE Ig heavy chain V region (Anti-arsenate antibody).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=79195438; PubMed=109536;
RA Capra J.D., Nisonoff A.;
RT "Structural studies on induced antibodies with defined idiotypic
RT specificities. VII. The complete amino acid sequence of the heavy
RT chain variable region of anti-p-azophenylarsenate antibodies from A/J
RT mice bearing a cross-reactive idotype.";
RL J. Immunol. 123:279-284(1979).
CC -I- MISCELLANEOUS: ANTIBODY ISOLATED FROM TEN MICE WAS EXCLUSIVELY OF
CC THE IGG1 SUBCLASS. THERE WAS NO HETEROGENEITY IN THE HEAVY CHAIN V
CC REGION SEQUENCE.
DR PIR; A02022; GIMSAA.
DR HSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Antiarsenate antibody.
FT NON_TER 114
SQ SEQUENCE 114 AA; 12555 MW; 99DD8F0B6A69F4BE CRC64;

Query Match 65.4%; Score 34; DB 1; Length 114;
Best Local Similarity 66.7%; Pred. No. 5.7;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTFSSYDM 9
DB 26 GYTFSSYEL 34

RESULT 12
RISC_METTH
ID RISC_METTH STANDARD; PRT; 153 AA.
AC O26237;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Riboflavin synthase (EC 2.5.1.9).
GN RIBC OR MTHL34.
OS Methanobacterium thermoautotrophicum.
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriaceae; Methanothermobacter.
OX NCBI_TaxID=187420;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Delta H;
RX MEDLINE=98037514; PubMed=9371463;
RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,
RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
RA Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
RA Spadafora R., Vicare R., Wang F., Wierzbowski J., Gibson R.,
RA Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
RA McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,

Danieles C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
"Complete genome sequence of Methanobacterium thermoautotrophicum
deltaH: functional analysis and comparative genomics.";
J. Bacteriol. 179:7133-7153(1997).
RL -I- CATALYTIC ACTIVITY: 2 6,7-dimethyl-8-(1-D-ribityl)lumazine =
riboflavin + 4-(1-D-ribitylamino)-5-amino-2,6-dihydroxypyrimidine.
CC -I- COFACTOR: MAGNESIUM (By similarity).
CC -I- ENZYME REGULATION: INHIBITED BY EDTA (BY SIMILARITY).
CC -I- PATHWAY: Riboflavin biosynthesis; last step.
CC -I- SUBUNIT: HOMODIGOMER (BY SIMILARITY).
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CC or send an email to license@isb-sib.ch).
EMBL; AE000802; AAB84640.1; -
DR InterPro; IPR002180; DMRL_synthase.
DR Pfam; PF00885; DMRL_synthase; 1.
KW Riboflavin biosynthesis; Transferase; Magnesium; Complete proteome.
SQ SEQUENCE 153 AA; 16908 MW; 79DD08CCBABB785 CRC64;

Query Match 65.4%; Score 34; DB 1; Length 153;
Best Local Similarity 75.0%; Pred. No. 7.9;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 TTFSSYDM 9
DB 9 TTFARYDM 16

RESULT 13
RISC_METTH
ID RISC_METTH STANDARD; PRT; 153 AA.
AC Q59587;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Riboflavin synthase (EC 2.5.1.9).
GN RIBC.
OS Methanobacterium thermoautotrophicum (strain Marburg / DSM 2133).
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriaceae; Methanothermobacter.
OX NCBI_TaxID=79929;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-42 AND 129-151.
RX MEDLINE=97284497; PubMed=9139911;
RA Eberhardt S., Korn S., Lottspeich F., Bacher A.;
RT "Biosynthesis of riboflavin: an unusual riboflavin synthase of
RT Methanobacterium thermoautotrophicum.";
RL J. Bacteriol. 179:2938-2943(1997).
CC -I- FUNCTION: THE RELATIVELY LOW ACTIVITY OF THIS ENZYME SUGGESTED
CC THAT 6,7-DIMETHYL-8-RIBITYLLUMAZINE MIGHT NOT BE ITS NATURAL
CC SUBSTRATE.
CC -I- CATALYTIC ACTIVITY: 2 6,7-dimethyl-8-(1-D-ribityl)lumazine =
riboflavin + 4-(1-D-ribitylamino)-5-amino-2,6-dihydroxypyrimidine.
CC -I- COFACTOR: MAGNESIUM.
CC -I- ENZYME REGULATION: INHIBITED BY EDTA.
CC -I- PATHWAY: Riboflavin biosynthesis; last step.
CC -I- SUBUNIT: HOMODIGOMER.
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EMBL; X94292; CAA63959.1; -

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DR InterPro: IPR002180; DMRL_synthase.
DR Pfam: PF00885; DMRL_synthase; 1.
KW Riboflavin biosynthesis; Transferrase; Magnesium.
SQ SEQUENCE 153 AA; 16969 MW; CAAE34FDA348F534 CRC64;

Query Match 65.4%; Score 34; DB 1; Length 153;
Best Local Similarity 75.0%; Pred. No. 7.9;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 2 TTFSSYDM 9
    |||: |||
Db 9 TTFARYDM 16

RESULT 14
SC21_RICCPR STANDARD; PRT; 191 AA.
AC Q9ZEB4;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE SC02-like protein RP031.
GN RP031.
OS Rickettsia prowazekii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsieae; Rickettsia.
OX NCBI_TaxID=782;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=Madrid E;
RX MEDLINE=99039499; PubMed=9823893;
RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,
RA Sacheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
RT "The genome sequence of Rickettsia prowazekii and the origin of
RT mitochondria";
RL Nature 396:133-140(1998).
CC -!- SIMILARITY: BELONGS TO THE SC01/2 FAMILY.
-----
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-----
EMBL: AJ235270; CAAL4502.1; -.
DR InterPro: IPR003782; SC01_SenC.
DR Pfam: PF02630; SC01_SenC; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 191 AA; 22254 MW; 74B8EAD74CED2698 CRC64;

Query Match 65.4%; Score 34; DB 1; Length 191;
Best Local Similarity 75.0%; Pred. No. 10;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GTTFSSYD 8
    |||: |||
Db 77 GTTISLYD 84

RESULT 15
SC21_RICCN STANDARD; PRT; 199 AA.
AC Q9ZJM5;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE SC02-like protein RC0042.
GN RC0042.
OS Rickettsia conorii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
```

```
OC Rickettsiaceae; Rickettsieae; Rickettsia.
OX NCBI_TaxID=781;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=Malish 7;
RX MEDLINE=21442074; PubMed=11557893;
RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
RA Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
RA Raoult D.;
RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
RL Science 293:2093-2098(2001).
CC -!- SIMILARITY: BELONGS TO THE SC01/2 FAMILY.
-----
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-----
EMBL: AE008572; AAL02580.1; -.
DR InterPro: IPR003782; SC01_SenC.
DR Pfam: PF02630; SC01_SenC; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 199 AA; 23101 MW; 80CACB0D4FD0FCB4 CRC64;

Query Match 65.4%; Score 34; DB 1; Length 199;
Best Local Similarity 75.0%; Pred. No. 11;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GTTFSSYD 8
    |||: |||
Db 80 GTTISLYD 87

Search completed: November 18, 2002, 17:33:18
Job time : 3.45098 secs
```

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:01 ; Search time 10.4412 Seconds
(without alignments):
197.341 Million cell updates/sec

Title: US-09-016-061-48
Perfect score: 52
Sequence: 1 GTTFSSYDMS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL.21.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archheap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	38	73.1	119	11 Q920E7	Q920E7 mus musculus
2	38	73.1	258	16 Q8XKB0	Q8XKB0 clostridium
3	38	73.1	370	2 Q52474	Q52474 pseudomonas
4	38	73.1	486	11 Q91207	Q91207 mus musculus
5	37	71.2	437	11 Q9R1A4	Q9R1A4 mus musculus
6	37	71.2	487	11 Q99KA4	Q99KA4 mus musculus
7	36	69.2	104	16 Q8RBV1	Q8RBV1 thermoanaer
8	36	69.2	118	4 Q9UL91	Q9UL91 homo sapien
9	36	69.2	471	4 Q8TC77	Q8TC77 homo sapien
10	36	69.2	478	16 Q8RDG1	Q8RDG1 thermoanaer
11	36	69.2	478	16 Q8RCA8	Q8RCA8 thermoanaer
12	36	69.2	478	16 Q8RC71	Q8RC71 thermoanaer
13	36	69.2	478	16 Q8RBF9	Q8RBF9 thermoanaer
14	36	69.2	478	16 Q8REG4	Q8REG4 thermoanaer
15	36	69.2	478	16 Q8RAT9	Q8RAT9 thermoanaer
16	36	69.2	478	16 Q8RAM0	Q8RAM0 thermoanaer

17	36	69.2	478	16 Q8R9E4	Q8R9E4 thermoanaer
18	36	69.2	478	16 Q8R9A3	Q8R9A3 thermoanaer
19	36	69.2	478	16 Q8R8L1	Q8R8L1 thermoanaer
20	36	69.2	502	10 Q9FW15	Q9FW15 oryza sativ
21	35	67.3	95	4 Q9ULB6	Q9ULB6 homo sapien
22	35	67.3	125	16 Q9RZR0	Q9RZR0 deinococcus
23	35	67.3	142	16 Q92BD1	Q92BD1 listeria in
24	35	67.3	147	4 Q9Y509	Q9Y509 homo sapien
25	35	67.3	479	11 Q9LWP5	Q9LWP5 mus musculu
26	35	67.3	677	12 Q8V3Q6	Q8V3Q6 swinepox vi
27	35	67.3	892	5 P91644	P91644 drosophila
28	35	67.3	894	5 Q9VKG1	Q9VKG1 drosophila
29	35	67.3	1177	5 Q95ZG3	Q95ZG3 dictyosteli
30	34	65.4	92	7 Q9MAB2	Q9MAB2 barbus inte
31	34	65.4	113	4 Q9UL90	Q9UL90 homo sapien
32	34	65.4	140	10 Q9ARP0	Q9ARP0 oryza sativ
33	34	65.4	217	12 Q91IH6	Q91IH6 frog adenov
34	34	65.4	234	17 Q9HRD9	Q9HRD9 halobacteri
35	34	65.4	314	5 Q97279	Q97279 plasmodium
36	34	65.4	481	2 Q9X405	Q9X405 streptococc
37	34	65.4	613	4 Q8WUK1	Q8WUK1 homo sapien
38	34	65.4	692	2 Q30565	Q30565 bacillus br
39	34	65.4	704	2 Q82984	Q82984 bacillus sp
40	34	65.4	725	2 Q59239	Q59239 bacillus sp
41	34	65.4	855	5 Q15797	Q15797 plasmodium
42	34	65.4	1892	11 Q9QT40	Q9QT40 mus musculu
43	34	65.4	2325	10 Q41743	Q41743 zea mays (m
44	33	63.5	116	4 Q9UL93	Q9UL93 homo sapien
45	33	63.5	116	4 Q9UL89	Q9UL89 homo sapien

ALIGNMENTS

RESULT 1

Q920E7 PRELIMINARY; PRT; 119 AA.

AC Q920E7; AC Q920E7; (TREMREL. 19, Created)
DT 01-DEC-2001 (TREMREL. 19, Last sequence update)
DT 01-DEC-2001 (TREMREL. 19, Last sequence update)
DT 01-MAR-2002 (TREMREL. 20, Last annotation update)
DE Pterin-mimicking anti-idiotope heavy chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Atkin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.;
RT "Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed
in Mammalian Cells."
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307937; AAL09421.1;
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig; 1.
FT NON_TER 1
FT NON_TER 119 119
SQ SEQUENCE 119 AA; 13025 MW; F6E904044381CA7C CRC64;

Query Match 73.1%; Score 38; DB 11; Length 119;
Best Local Similarity 80.0%; Pred. No. 7.7;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10

Db 26 GTTFSSYDMS 35

RESULT 2

Q8XKB0 PRELIMINARY; PRT; 258 AA.
AC Q8XKB0;

```

DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Hypothetical protein CPE1490.
GN CPE1490.
OS Clostridium perfringens.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC Clostridiales; Clostridiaceae; Clostridium.
OX NCBI_TaxID=1502;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=13 / TYPE A;
RX PubMed=11792842;
RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
RT "Complete genome sequence of Clostridium perfringens, an anaerobic
RT flesh-eater.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
DR EMBL; AP003190; BAB81196.1; -.
DR InterPro; IPR002781; DUF81.
DR Pfam; PF01925; DUF81; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 258 AA; 27786 MW; 5DAE60FC71FECD1D CRC64;

Query Match 73.1%; Score 38; DB 16; Length 258;
Best Local Similarity 70.0%; Pred. No. 17;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
  |||||
DB 198 GTGFGYDLS 207

RESULT 3
Q52474 Q52474 PRELIMINARY; PRT; 370 AA.
ID AC Q52474;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE HrpZ.
DE HrpZ.
GN HrpZ.
OS Pseudomonas syringae (pv. tomato).
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=323;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DC3000;
RX MEDLINE=96025089; PubMed=7579616;
RA Preston G., Huang H.C., He S.Y., Collmer A.;
RT "The HrpZ proteins of Pseudomonas syringae pvs. syringae, glycinea,
RT and tomato are encoded by an operon containing Yersinia ysc homologs
RT and elicit the hypersensitive response in tomato but not soybean.";
RL Mol. Plant Microbe Interact. 8:717-732(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=DC3000;
RA Ramos A.R., Rehm A.H., Collmer A.R.;
RT "Pseudomonas syringae pv. tomato DC3000 hrpL through hrpC.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF232004; AAB00127.1; -.
SQ SEQUENCE 370 AA; 36584 MW; D22E4378ACD1E51 CRC64;

Query Match 73.1%; Score 38; DB 2; Length 370;
Best Local Similarity 88.9%; Pred. No. 25;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTFSSYDM 9
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DB 159 GTTFSSDDM 167

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RESULT 4
Q91207 Q91207 PRELIMINARY; PRT; 486 AA.
ID AC Q91207;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Hypothetical 52.7 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC010324; RAH10324.1; -.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00408; Igc2; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein; Immunoglobulin domain.
SQ SEQUENCE 486 AA; 52682 MW; 4FEF835125DA870B CRC64;

Query Match 73.1%; Score 38; DB 11; Length 486;
Best Local Similarity 70.0%; Pred. No. 34;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
  |:::|
DB 45 GFSFYSYDMS 54

RESULT 5
Q9RIA4 Q9RIA4 PRELIMINARY; PRT; 437 AA.
ID AC Q9RIA4;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Gammal heavy chain of Mab7 (Fragment).
GN IGH-4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT antibody (Mab 7, its light and heavy chains) and construction of a
RT single chain antibody (scFv).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF152372; AAD40243.1; -.
DR HSP; P01842; 7FAB.
DR MGD; MGI:96446; Igh-4.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; Igv; 1.
DR SMART; SM00410; IG_like; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 437
SQ SEQUENCE 437 AA; 48142 MW; 5C3A7BB3EE7D697C CRC64;

Query Match 71.2%; Score 37; DB 11; Length 437;
Best Local Similarity 80.0%; Pred. No. 48;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10

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Db      25 GTTSSYAMS 34
      1 | | | | | | | |
RESULT 6
Q99KA4 PRELIMINARY; PRT; 487 AA.
AC Q99KA4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical 52.6 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC004786; AA04786.1;
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003600; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; Ig; 3.
DR SMART; SM00407; IG1; 3.
DR SMART; SM00406; IG; 1.
DR SMART; SM00410; IG-like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 487 AA; 52554 MW; 7DC8E96DB333077B CRC64;

Query Match 71.2%; Score 37; DB 11; Length 487;
Best Local Similarity 80.0%; Pred. No. 53;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTSSYDMS 10
      1 | | | | | | | |
Db 45 GTTSSYAMS 54

RESULT 7
Q8RBV1 PRELIMINARY; PRT; 104 AA.
AC Q8RBV1;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical protein TTE0707.
GN TTE0707.
OS Thermoanaerobacter tengcongensis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC Thermoanaerobacteriales; Thermoanaerobacteriaceae; Thermoanaerobacter.
OX NCBI_TaxID=119072;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=MB4T / JCM11007;
RX MEDLINE=21992816; PubMed=11997336;
RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
RA Tan H., Chen R., Wang J., Yu J., Yang H.;
RT "A complete sequence of T. tengcongensis genome.";
RL Genome Res. 12:689-700(2002).
DR EMBL; AE013039; AAM23969.1;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 104 AA; 11798 MW; 338454248C277952 CRC64;

Query Match 69.2%; Score 36; DB 16; Length 104;
Best Local Similarity 75.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GTTSSYD 8
      1 | | | | | | | |
Db 35 GTTSSYD 42

RESULT 8
Q9UL91 PRELIMINARY; PRT; 118 AA.
AC Q9UL91;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035023; AAD56259.1;
DR HSSP; P01772; 2PBA.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IG; 1.
DR NON_TER 1
FT NON_TER 118
SQ SEQUENCE 118 AA; 12843 MW; D0633949F2AC149D CRC64;

Query Match 69.2%; Score 36; DB 4; Length 118;
Best Local Similarity 70.0%; Pred. No. 19;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTSSYDMS 10
      1 | | | | | | | |
Db 26 GTTSSYSMN 35

RESULT 9
Q8TC77 PRELIMINARY; PRT; 471 AA.
AC Q8TC77;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 51.8 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=SPLEEN;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC024289; AAH24289.1;
KW Hypothetical protein.
SQ SEQUENCE 471 AA; 51791 MW; 388F7F4CF588660E CRC64;

Query Match 69.2%; Score 36; DB 4; Length 471;
Best Local Similarity 70.0%; Pred. No. 81;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTSSYDMS 10

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Db 45 GTTSSYSMN 54
||||| |
RESULT 10
Q8RDC1 PRELIMINARY; PRT; 478 AA.
ID Q8RDG1
AC Q8RDG1;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DE Hypothetical protein TTE0071.
GN TTE0071.
OS Thermoanaerobacter tengcongensis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC Thermoanaerobacteriales; Thermoanaerobacteriaceae; Thermoanaerobacter.
OX NCBI_TaxID=119072;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MB4T / JCM11007;
RX MEDLINE=21992816; PubMed=11997336;
RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
RA Tan H., Chen R., Wang J., Yu J., Yang H.;
RT "A complete sequence of T. tengcongensis genome.";
RL Genome Res. 12:689-700(2002).
DR EMBL; AE012981; AAM23378.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 478 AA; 55378 MW; A7D02733575CA3DC CRC64;

Query Match 69.2%; Score 36; DB 16; Length 478;
Best Local Similarity 75.0%; Pred. No. 82;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTSSYD 8
|||||
Db 434 GTSFSTYD 441

RESULT 11
Q8RCB8 PRELIMINARY; PRT; 478 AA.
ID Q8RCB8;
AC Q8RCB8;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DE Hypothetical protein TTE0528.
GN TTE0528.
OS Thermoanaerobacter tengcongensis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC Thermoanaerobacteriales; Thermoanaerobacteriaceae; Thermoanaerobacter.
OX NCBI_TaxID=119072;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MB4T / JCM11007;
RX MEDLINE=21992816; PubMed=11997336;
RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
RA Tan H., Chen R., Wang J., Yu J., Yang H.;
RT "A complete sequence of T. tengcongensis genome.";
RL Genome Res. 12:689-700(2002).
DR EMBL; AE013023; AAM23804.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 478 AA; 55449 MW; BB4DB804222759A0 CRC64;

Query Match 69.2%; Score 36; DB 16; Length 478;
Best Local Similarity 75.0%; Pred. No. 82;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTSSYD 8
|||||
Db 434 GTSFSTYD 441

RESULT 12
Q8RC71 PRELIMINARY; PRT; 478 AA.
ID Q8RC71;
AC Q8RC71;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DE Hypothetical protein TTE0571.
GN TTE0571.
OS Thermoanaerobacter tengcongensis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC Thermoanaerobacteriales; Thermoanaerobacteriaceae; Thermoanaerobacter.
OX NCBI_TaxID=119072;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MB4T / JCM11007;
RX MEDLINE=21992816; PubMed=11997336;
RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
RA Tan H., Chen R., Wang J., Yu J., Yang H.;
RT "A complete sequence of T. tengcongensis genome.";
RL Genome Res. 12:689-700(2002).
DR EMBL; AE013026; AAM23843.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 478 AA; 55668 MW; F1D14E9BEF4B9382 CRC64;

Query Match 69.2%; Score 36; DB 16; Length 478;
Best Local Similarity 75.0%; Pred. No. 82;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTSSYD 8
|||||
Db 434 GTSFSTYD 441

RESULT 13
Q8RBR9 PRELIMINARY; PRT; 478 AA.
ID Q8RBR9;
AC Q8RBR9;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DE Hypothetical protein TTE0742.
GN TTE0742.
OS Thermoanaerobacter tengcongensis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC Thermoanaerobacteriales; Thermoanaerobacteriaceae; Thermoanaerobacter.
OX NCBI_TaxID=119072;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MB4T / JCM11007;
RX MEDLINE=21992816; PubMed=11997336;
RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
RA Tan H., Chen R., Wang J., Yu J., Yang H.;
RT "A complete sequence of T. tengcongensis genome.";
RL Genome Res. 12:689-700(2002).
DR EMBL; AE013041; AAM24003.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 478 AA; 55727 MW; 239DE70C16B86D7B CRC64;

Query Match 69.2%; Score 36; DB 16; Length 478;
Best Local Similarity 75.0%; Pred. No. 82;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTSSYD 8
|||||
Db 434 GTSFSTYD 441

RESULT 14
Q8RBC4

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ID Q8RBG4 PRELIMINARY; PRT; 478 AA.
AC Q8RBG4
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical protein TTE0855.
GN TTE0855.
OS Thermoanaerobacter tengcongensis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC Thermoanaerobacteriales; Thermoanaerobacteriaceae; Thermoanaerobacter.
OX NCBI_TaxID=119072;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MB4T / JCM11007;
RA MEDLINE=21992816; PubMed=11997336;
RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
RA Tan H., Chen R., Wang J., Yu J., Yang H.;
RT "A complete sequence of T. tengcongensis genome.";
RL Genome Res. 12:689-700(2002).
DR EMBL: AE013052; AM24112.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 478 AA; 55337 MW; FBA33826316E5DC5 CRC64;

Query Match 69.2%; Score 36; DB 16; Length 478;
Best Local Similarity 75.0%; Pred. No. 82;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTFSSYD 8
Db 434 GTSFSAYD 441

RESULT 15
Q8RAT9
ID Q8RAT9 PRELIMINARY; PRT; 478 AA.
AC Q8RAT9;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical protein TTE1107.
GN TTE1107.
OS Thermoanaerobacter tengcongensis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC Thermoanaerobacteriales; Thermoanaerobacteriaceae; Thermoanaerobacter.
OX NCBI_TaxID=119072;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MB4T / JCM11007;
RA MEDLINE=21992816; PubMed=11997336;
RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
RA Tan H., Chen R., Wang J., Yu J., Yang H.;
RT "A complete sequence of T. tengcongensis genome.";
RL Genome Res. 12:689-700(2002).
DR EMBL: AE013074; AM24347.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 478 AA; 55455 MW; 7F865EAD6D651 CRC64;

Query Match 69.2%; Score 36; DB 16; Length 478;
Best Local Similarity 75.0%; Pred. No. 82;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTFSSYD 8
Db 434 GTSFSAYD 441

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Search completed: November 18, 2002, 17:40:34
Job time : 12.4912 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:21:57 : Search time 13.8235 Seconds
(without alignments)
96.394 Million cell updates/sec

Title: US-09-016-061-48
Perfect score: 52
Sequence: 1 GTTFSSYDMS 10

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	52	100.0	10	19	AAW76014
2	52	100.0	10	22	AAW761372
3	45	86.5	10	19	AAW76007
4	45	86.5	10	22	AAW761365
5	45	86.5	117	19	AAW76001
6	45	86.5	117	22	AAW76001
7	45	86.5	117	22	AAW76001
8	42	80.8	117	20	AAW86137
9	42	80.8	123	18	AAW15536
10	42	80.8	128	19	AAW54000
					LM609 grafted anti
					Mutant VH CDR1 pep
					LM609 grafted anti
					LM609 VH CDR1 pep
					Vitaxin antibody h
					A heavy chain vari
					Vitaxin heavy chai
					Protein sequence o
					Anti-TGF beta-1 sc
					Anti-CD4 antibody

11	42	80.8	134	13	AAW24713	Sequence encoded b
12	42	80.8	256	23	ABP45381	Human Blys binding
13	42	80.8	256	23	ABP46108	Human Blys binding
14	42	80.8	466	13	AAW24812	Sequence encoded b
15	41	78.8	97	21	AAW40112	Anti-hIL12 antibod
16	41	78.8	102	22	ABW39276	Peptide #6782 enco
17	41	78.8	102	22	AAW59940	Human brain expres
18	41	78.8	102	22	AAW72535	Human bone marrow
19	41	78.8	102	22	AAW32779	Peptide #6816 enco
20	41	78.8	102	23	ABG42355	Human peptide enco
21	41	78.8	139	18	AAW21652	Humanised reshaped
22	41	78.8	252	23	ABP45601	Human Blys binding
23	41	78.8	470	23	AAU74298	Anti-human AILIM m
24	41	78.8	470	23	AAU74300	Anti-human AILIM m
25	40	76.9	10	19	AAW76015	LM609 grafted anti
26	40	76.9	10	22	AAW61373	Mutant VH CDR1 pep
27	40	76.9	117	19	AAW76003	LM609 antibody hea
28	40	76.9	117	20	AAW06381	Murine monoclonal
29	40	76.9	117	22	AAW63589	A heavy chain vari
30	40	76.9	117	22	AAW61361	Antibody LM609 hea
31	40	76.9	130	20	AAW06379	Murine monoclonal
32	40	76.9	239	14	AAW34511	Fv(TU25). Homo sa
33	40	76.9	247	16	AAW11917	Murine Mab SK48-E2
34	39	75.0	10	19	AAW76016	LM609 grafted anti
35	39	75.0	10	22	AAW61374	Mutant VH CDR1 pep
36	39	75.0	115	22	AAW69601	Huntingtin minimal
37	39	75.0	117	20	AAW86141	Protein sequence o
38	39	75.0	119	16	AAW11919	Humanised Mab SK48
39	39	75.0	123	19	AAW53998	Anti-CD4 antibody
40	39	75.0	239	22	AAW69603	Huntingtin intrabo
41	38	73.1	10	21	AAW78322	Anti-zeta-chain an
42	38	73.1	10	22	AAU07457	Synthetic peptide
43	38	73.1	87	22	AAE06990	Mouse germline hea
44	38	73.1	89	22	AAE06985	Mouse germline hea
45	38	73.1	97	21	AAW40089	Anti-hIL12 antibod

ALIGNMENTS

RESULT 1
AAW76014
ID AAW76014 standard; Protein; 10 AA.
XX
AC AAW76014;
XX
DT 02-NOV-1998 (first entry)
XX
DE LM609 grafted antibody V-H region CDR1 protein fragment #2.
XX
KW Vitaxin; antibody; variable region; heavy chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
XX
OS Mus sp.
XX
PN WO9833919-A2.
XX
PD 06-AUG-1998.
XX
PF 30-JAN-1998; 98WO-US01826.
XX
PR 30-JAN-1997; 97US-0791391.
XX
PA (IXSV-) IXSVS INC.
XX
PI Glaser SM, Huse WD;
XX
DR WPI; 1998-437472/37.
DR N-PSDB; AAW49851.

XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
PS Claim 60; Page 41; 129pp: English.
XX
CC AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
CC antibodies contain non-murine framework regions so are suitable for use
CC in humans. Enhanced types of LM609 have affinity more than 90 times
CC greater than that of parent the parent antibody.
XX
SQ Sequence 10 AA;
Query Match 100.0%; Score 52; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTFSSYDMS 10
Db 1 GTTFSSYDMS 10
|||||
RESULT 2
AAB61372
ID AAB61372 standard; peptide; 10 AA.
XX
AC AAB61372;
XX
XX 03-APR-2001 (first entry)
XX
DE Mutant VH CDR1 peptide #1.
XX
XX LM609; grafted antibody; alphaVbeta3 integrin; angiogenesis;
KW inflammatory; cancer; retina; restenosis; osteoporosis.
XX
XX Unidentified.
OS
XX WO200078815-A1.
PN
XX 28-DEC-2000.
PD
XX 23-JUN-2000; 2000WO-US17454.
PF
XX 24-JUN-1999; 99US-0339922.
PR
XX (MOLE-) APPLIED MOLECULAR EVOLUTION.
PA
XX Huse WD, Wu H;
PI
XX WPI; 2001-050110/06.
DR
XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
PT osteoporosis -
XX
XX Disclosures; Page 40; 132pp: English.
PS
XX The present invention relates to enhanced LM609 grafted antibodies
CC exhibiting selective binding affinity to alphaVbeta3 integrin or
CC their functional fragments. The antibodies or their functional
CC fragments can be used in the diagnosis and treatment of
CC alphaVbet&3-mediated diseases such as angiogenesis, inflammatory

CC diseases (such as psoriasis and chronic articular rheumatism),
CC disorders associated with inappropriate or inopportune invasion of
CC vessels (such as diabetic retinopathy, neovascular glaucoma and
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
CC diseases (such as macular degeneration), restenosis and
CC osteoporosis.
XX
SQ Sequence 10 AA;
Query Match 100.0%; Score 52; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTFSSYDMS 10
Db 1 GTTFSSYDMS 10
|||||
RESULT 3
AAW76007
ID AAW76007 standard; Protein; 10 AA.
XX
AC AAW76007;
XX
XX 02-NOV-1998 (first entry)
DT
XX
DE LM609 grafted antibody V-H region CDR1 protein fragment #1.
XX
XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
XX
OS Mus sp.
XX
XX WO9833919-A2.
PN
XX 06-AUG-1998.
PD
XX 30-JAN-1998; 98WO-US01826.
PF
XX 30-JAN-1997; 97US-0791391.
PR
XX (IXSY-) IXSYS INC.
PA
XX Glaser SM, Huse WD;
PI
XX WPI; 1998-437472/37.
DR
XX N-PSDB; AAV49844.
DR
XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
PS Disclosures; Page 40; 129pp: English.
XX
XX AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
CC antibodies contain non-murine framework regions so are suitable for use
CC in humans. Enhanced types of LM609 have affinity more than 90 times
CC greater than that of parent the parent antibody.
XX
SQ Sequence 10 AA;

Query Match 86.5%; Score 45; DB 19; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.045;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTFSSYDMS 10
 | | | | | | | |
 Db 1 GTTFSSYDMS 10

RESULT 4
 AAB61365
 ID AAB61365 standard; peptide: 10 AA.
 XX
 AC AAB61365;
 XX
 DT 03-APR-2001 (first entry)
 XX
 DE LM609 VH CDR1 peptide.
 XX
 KW LM609; grafted antibody; alphaVbeta₃ integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis.
 XX
 OS Unidentified.
 XX
 PN WO200078815-A1.
 XX
 PD 28-DEC-2000.
 XX
 XX 23-JUN-2000; 2000WO-US17454.
 XX
 XX 24-JUN-1999; 99US-0339922.
 XX
 PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
 XX
 PI Huse WD, Wu H;
 XX
 DR WPI; 2001-050110/06.
 XX
 XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta₃ integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis.
 XX
 PS Claim 4; Page 39; 132pp; English.
 XX
 CC The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphaVbeta₃ integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphaVbeta₃-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.
 XX
 SQ Sequence 10 AA;

Query Match 86.5%; Score 45; DB 22; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.045;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTFSSYDMS 10
 | | | | | | | |
 Db 1 GTTFSSYDMS 10

RESULT 5
 AAW76001
 ID AAW76001 standard; Protein: 117 AA.
 XX

AAW76001;
 02-NOV-1998 (first entry)
 Vitaxin antibody heavy chain variable region protein fragment.
 Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 LM609; inhibitor; integrin-mediated signal transduction; treatment;
 diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 macular degeneration; osteoporosis.
 Mus sp.
 WO9833919-A2.
 06-AUG-1998.
 30-JAN-1998; 98WO-US01826.
 30-JAN-1997; 97US-0791391.
 (IXSY-) IXSYS INC.
 Glaser SM, Huse WD;
 WPI; 1998-437472/37.
 N-PSDB; AAV49820.
 Humanised antibody, Vitaxin, that binds selectively to alphaVbeta₃
 integrin - and related antibodies based on murine monoclonal
 LM609, also related nucleic acid, used to treat, prevent or diagnose
 angiogenesis or restenosis
 Claim 1; Fig 1a; 129pp; English.
 This sequence represents a fragment of the vitaxin antibody variable
 heavy chain region. Vitaxin and the antibody LM609 bind selectively to
 integrin alphaVbeta₃ and can be used to inhibit binding of alphaVbeta₃
 to a ligand and thus block integrin-mediated signal transduction. This is
 useful in the treatment, prevention and diagnosis of alphaVbeta₃-mediated
 disease, specifically angiogenesis and restenosis (but also e.g.
 (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,
 cancer, psoriasis, rheumatoid arthritis, macular degeneration,
 osteoporosis etc.). The antibodies contain non-murine framework regions
 so are suitable for use in humans. Enhanced types of LM609 have affinity
 more than 90 times greater than that of parent the parent antibody.
 Sequence 117 AA;

Query Match 86.5%; Score 45; DB 19; Length 117;
 Best Local Similarity 90.0%; Pred. No. 0.6;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTFSSYDMS 10
 | | | | | | | |
 Db 26 GTTFSSYDMS 35

RESULT 6
 AAG63587
 ID AAG63587 standard; Protein: 117 AA.
 XX
 AC AAG63587;
 XX
 DT 15-OCT-2001 (first entry)
 XX
 DE A heavy chain variable region of LM609 grafted antibody.
 XX
 KW Grafted antibody; LM609; integrin; alphaVbeta₃; inflammatory disorder;
 KW chronic articular rheumatism; psoriasis; diabetic retinopathy;
 KW neovascular glaucoma; capillary proliferation; atherosclerotic plaque;
 KW cancer.

XX Reducing immunogenicity of proteins - by modifying the amino acid
PT sequence of the protein to eliminate potential epitopes for T-cells
PT of a given species
XX
PS Example 5; Fig 25; 77pp; English.
XX
CC The invention relates to a method for the production of non-immunogenic
CC proteins. The method comprises determining at least part of the amino
CC acid sequence of the protein; (b) identifying in the amino acid sequence
CC one or more potential epitopes for T-cells (T-cell epitopes) of the given
CC species; and (c) modifying the amino acid sequence to eliminate at least
CC one of the T-cell epitopes identified in step (b) thereby to eliminate or
CC reduce the immunogenicity of the protein when exposed to the immune
CC system of the given species. A method of analysing a pre-existing protein
CC to predict the basis for immunogenic responses is also provided. The
CC methods can be used particularly for reducing the immunogenicity of
CC immunoglobulins or therapeutic proteins, e.g. Streptokinase (SK). The
CC products can be used for diagnosis and therapy. The present sequence
CC represents the protein sequence of de-immunised humanised A33 Vh.
XX
SQ Sequence 117 AA;
Query Match 80.8%; Score 42; DB 20; Length 117;
Best Local Similarity 80.0%; Pred. No. 2.2;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GTTFSSYDMS 10
Db 26 GTTFSTYDMS 35

RESULT 9
AAW15536
ID AAW15536 standard; Protein; 123 AA.
XX
AC AAW15536;
XX
DT 27-NOV-1997 (first entry)
XX
DE Anti-TGF beta-1 scFv antibody 27C1 VH domain.
XX
KW Transforming growth factor beta-1; TGF-beta-1; human;
KW antibody engineering; scFv; phage display; lung fibrosis;
KW arterial injury; proliferative retinopathy; retinal detachment;
KW adult respiratory distress syndrome; liver cirrhosis;
KW post myocardial infarction; post-angioplasty restenosis;
KW scleroderma; vascular disease; cataract; glaucoma; scarring;
KW glomerulonephritis; osteoporosis; immune disease; inflammation;
KW rheumatoid arthritis; macrophage deficiency disease;
KW macrophage pathogen infection; therapy.
XX
OS Homo sapiens.
XX
XX GB2305921-A.
PN
XX 23-APR-1997.
PD
XX 07-OCT-1996; 96GB-0020920.
XX
XX 19-JAN-1996; 96GB-0001081.
PR
XX 06-OCT-1995; 95GB-0020486.
XX
XX (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
XX Bacon L, Green JA, Jackson RH, Johnson KS, Pope AR;
PI Tempest PR, Thompson JE, Vaughan TJ, Williams AJ;
PI Wilton AJ;
XX
XX WPI; 1997-215360/20.
DR
XX N-PSDB; AAT60382.
XX
XX Agent contg. antigen-binding domain of human antibody to

PT transforming growth factor beta 1 or 2 - and nucleic acid encoding
PT it, used to neutralise effects of TGF, e.g. for control of fibrosis,
PT immune and inflammatory disease
XX
PS Claim 16; Fig 1c(i); 184pp; English.
XX
CC This polypeptide sequence comprises the VH domain of human scFv
CC antibody 31G9, which is specific for transforming growth factor
CC (TGF) beta-1. It is encoded by a gene (AAR60382) obtained from a
CC CDR3 spiking experiment. The antigen-binding domains of human
CC antibodies (see AAW15522-40) to TGF beta-1 and/or beta-2 can be
CC used to counter the adverse effects of TGF beta, such as (i)
CC promotion of fibrosis (in dermal, ocular or keloid scarring, lung
CC fibrosis, arterial injury, proliferative retinopathy, retinal
CC detachment, adult respiratory distress syndrome, liver cirrhosis,
CC post myocardial infarction, post-angioplasty restenosis,
CC scleroderma, vascular disorders, cataract, glaucoma, or esp. neural
CC scarring and glomerulonephritis, also (not claimed) osteoporosis),
CC or (ii) immune and inflammatory diseases (e.g. rheumatoid
CC arthritis, macrophage deficiency diseases or macrophage pathogen
CC infection). Nucleic acids encoding human antibody VH and VL can be
CC used for prodn. of recombinant antigen-binding domains. These are
CC highly specific, have low dissociation constants (pref. less than 5
CC nM) and low IC50s for neutralisation.
XX
SQ Sequence 123 AA;
Query Match 80.8%; Score 42; DB 18; Length 123;
Best Local Similarity 88.9%; Pred. No. 2.3;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GTTFSSYDM 9
Db 26 GLTFSSYDM 34

RESULT 10
AAW54000
ID AAW54000 standard; Protein; 128 AA.
XX
AC AAW54000;
XX
DT 29-JUL-1998 (first entry)
XX
DE Anti-CD4 antibody VH3 monkey clone 3-40.
XX
KW Anti-CD4 antibody; monkey; human; therapy; variable heavy domain;
KW Old World monkey; constant domain; eczema; immuno-modulated disease;
KW rheumatoid arthritis.
XX
OS Primate sp.
XX
XX Key Location/Qualifiers
FT Misc-difference 1..128 /note= "xaa= unspecified amino acid"
XX
XX US5750105-A.
PN
XX 12-MAY-1998.
PD
XX 07-JUN-1995; 95US-0476349.
PF
XX 10-JUL-1992; 92US-0912292.
PR
XX 25-JUL-1991; 91US-0735064.
PR
XX 23-MAR-1992; 92US-0856281.
PR
XX 05-DEC-1995; 95US-0379072.
PR
XX 07-JUN-1995; 95US-0476349.
XX
XX (IDEC-) IDEC PHARM CORP.
XX
XX Hanna N, Newman RA, Raab RW;
PI
XX WPI; 1998-296690/26.
DR

XX Improved method for antibody treatment - uses an antibody comprising
PT an Old World monkey variable region and a human constant domain
XX
XX
XX Example 1; Fig 9c; 84pp; English.
XX
CC This sequence represents the VH3 domain of an anti-CD4 antibody
CC (Ab). This sequence can be used in the method of the invention for
CC treating a subject, where the treatment comprises administration of an
CC Ab. The method comprises the administration of an antibody which has an
CC Old World monkey (e.g. baboon or macaque) variable region which binds to
CC an antigen (Ag) (or Ag binding portion), and a human constant domain. The
CC method is useful for the treatment of eczema and immuno-modulated
CC diseases and especially rheumatoid arthritis. The recombinant antibodies
CC used are sufficiently different from native monkey antibodies to allow
CC human antigens to raise these antibodies, but similar enough to human
CC antibody so there is no immune response to the antibodies in humans.
CC Compared to antibodies used in therapy in prior art, these antibodies do
CC not induce human anti-antibodies on repeated administration. They also
CC have longer half-lives and do not have a lack of effector function with
CC human cells.
XX
SQ Sequence 128 AA;
Query Match 80.8%; Score 42; DB 19; Length 128;
Best Local Similarity 80.0%; Pred. No. 2.4;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTTFSSYDMS 10
Db | | | | | | | | | |
26 GTTFSSYDMN 35
RESULT 11
AAR24713
ID AAR24713 standard; Protein; 134 AA.
XX
AC AAR24713;
XX
DT 28-DEC-1992 (first entry)
XX
DE Sequence encoded by the genomic chimeric heavy chain variable region
DE (VFH) gene.
XX
KW Chimeric monoclonal antibody; anti-fibrin antibody; PCR;
KW antithrombotic agent; myocardial infarction therapy.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT /label= leader
FT Region 23..49
FT /label= Framework Region (FR) 1
FT Region 50..54
FT /label= Complementarity determining region(CDR)1
FT Region 55..68
FT /label= FR-2
FT Region 69..84
FT /label= CDR-2
FT Region 85..114
FT /label= FR-3
FT Region 115..123
FT /label= CDR-3
FT Region 124..134
FT /label= FR-4
XX
PN EP491351-A.
XX
PD 24-JUN-1992.
XX
PF 17-DEC-1991; 91EP-0121591.
XX

PR 18-DEC-1990; 90JP-0413829.
PR 11-NOV-1991; 91JP-0294464.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
XX Iwasa S, Taka H, Watanabe T, Tada H;
PI
XX
DR WPI; 1992-209528/26.
DR N-PSDB; AAQ25666.
XX
XX Chimeric monoclonal antibodies - contain anti-human fibrin
PT antibody light and heavy chain variable and constant for treating
PT thrombotic conditions e.g. myocardial infarction
XX
XX Example; Figure 4; 87pp; English.
XX
CC PCR primers 5'mvH and 3'mvH were used to produce a VH gene-contg.
CC fragment of about 330bp. The fragment was isolated and subcloned in
CC pUC119. The fragment was found to be a functional VH structural
CC gene, referred to as VFH, comprising a VH gene belonging to the
CC subgroup III (VHIII) and the DSP2 and JH4 genes. Northern blot
CC analysis using the whole RNA of FIB1-11 cells confirmed that VFH
CC was the gene expressed in FIB1-11 cells. The sequence is given in
CC AAQ25666.
XX
SQ Sequence 134 AA;
Query Match 80.8%; Score 42; DB 13; Length 134;
Best Local Similarity 80.0%; Pred. No. 2.5;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTTFSSYDMS 10
Db | | | | | | | | | |
45 GTTFSSYDMS 54
RESULT 12
ABP45381
ID ABP45381 standard; Protein; 256 AA.
XX
XX
AC ABP45381;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human BlyS binding scFv SEQ ID 1392.
XX
DE
XX
KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
XX WO200202641-A1.
PN
XX
PD 10-JAN-2002.
XX
XX 15-JUN-2001; 2001WO-US19110.
XX
XX 16-JUN-2000; 2000US-212210P.
PR 17-OCT-2000; 2000US-240816P.
PR 16-MAR-2001; 2001US-276248P.
PR 21-MAR-2001; 2001US-277379P.
PR 25-MAY-2001; 2001US-293499P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
PI
XX WPI; 2002-114799/15.
DR

XX Antibodies against B Lymphocyte Stimulating polypeptides, useful for
 PT the diagnosis and treatment of cancers and immune disorders -
 XX
 XX
 PS Claim 1; Page 2064-2065; 3148pp; English.
 XX
 CC This invention describes novel antibodies that immunospecifically bind to
 CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antirheumatic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys
 CC and so may be used to detect and quantitate the presence of Blys in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of Blys. They may also be
 CC administered to treat diseases associated with aberrant Blys expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method
 CC of the invention.
 XX
 SQ Sequence 256 AA;

Query Match 80.8%; Score 42; DB 23; Length 256;
 Best Local Similarity 80.0%; Pred. No. 4.9;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 GTTFSSYDMS 10
 | | | | | | | |
 Db 26 GTTFSSYDMS 35

RESULT 13
 ABP46108
 ID ABP46108 standard; Protein; 256 AA.
 XX
 AC ABP46108;
 XX
 DT 19-AUG-2002 (first entry)
 XX
 DE Human Blys binding scFv SEQ ID 2119.
 XX
 KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;
 KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.
 XX
 OS Homo sapiens.
 XX
 PN WO200202641-A1.
 XX
 PD 10-JAN-2002.
 XX
 PF 15-JUN-2001; 2001WO-US19110.
 XX
 PR 16-JUN-2000; 2000US-212210P.
 PR 17-OCT-2000; 2000US-240816P.
 PR 16-MAR-2001; 2001US-276248P.
 PR 21-MAR-2001; 2001US-277379P.
 PR 25-MAY-2001; 2001US-293499P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX
 PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 XX WPI; 2002-114799/15.
 DR
 XX

PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for
 PT the diagnosis and treatment of cancers and immune disorders -
 XX
 XX
 PS Claim 1; Page 2924-2925; 3148pp; English.
 XX
 CC This invention describes novel antibodies that immunospecifically bind to
 CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antirheumatic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys
 CC and so may be used to detect and quantitate the presence of Blys in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of Blys. They may also be
 CC administered to treat diseases associated with aberrant Blys expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method
 CC of the invention.
 XX
 SQ Sequence 256 AA;

Query Match 80.8%; Score 42; DB 23; Length 256;
 Best Local Similarity 80.0%; Pred. No. 4.9;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 GTTFSSYDMS 10
 | | | | | | | |
 Db 26 GTTFSSYDMS 35

RESULT 14
 AAR24812
 ID AAR24812 standard; Protein; 466 AA.
 XX
 AC AAR24812;
 XX
 DT 28-DEC-1992 (first entry)
 XX
 DE Sequence encoded by the chimeric H chain cDNA contained in pTB1373.
 XX
 KW Chimeric monoclonal antibody; anti-fibrin antibody; primer;
 KW antithrombotic agent; myocardial infarction therapy.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Peptide 13..19
 FT /label= Leader
 FT Region 20..134
 FT /label= VH
 FT Region 135..232
 FT /label= CH1
 FT Region 233..247
 FT /label= hinge
 FT Region 248..357
 FT /label= CH2
 FT Region 358..464
 FT /label= CH3
 FT Misc-difference 465
 FT /note= "translated stop codon"
 XX
 PN EP491351-A.
 XX
 PD 24-JUN-1992.
 XX
 PF 17-DEC-1991; 91EP-0121591.
 XX
 PR 18-DEC-1990; 90JP-0413829.
 PR 11-NOV-1991; 91JP-0294464.

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XX (TAKE ) TAKEDA CHEM IND LTD.
PA
XX
XX Iwasa S, Taka H, Watanabe T, Tada H;
PI
XX
XX WPI; 1992-209528/26.
DR
XX N-FSDB; AAQ25692.
DR
XX
XX Chimeric monoclonal antibodies - contain anti-human fibrin
PT antibody light and heavy chain variable and constant for treating
PT thrombotic conditions e.g. myocardial infarction
XX
XX Example; Figure 11; 87pp; English.
PS
XX
XX Plasmid pTB1373 contains the whole length of a mouse-human
CC chimeric anti-human fibrin heavy chain cDNA open reading
CC frame. It was prepd. using Poly(A)+ RNA from the anti-fibrin
CC chimeric Ab-producing transformant FIB1-H01/X63 as a template
CC to clone human C-kappa cDNA, using the oligo-dT (Pharmacia) primer as
CC a primer for first strand cDNA synthesis and the 5'C2H and 3'EH
CC primers for the PCR. A human gamma-1 chain CH2-CH3 domain encoding
CC cDNA was amplified. Similarly a human gamma-1 chain CH1 domain
CC encoding cDNA and an anti-fibrin antibody VH cDNA and a leader
CC peptide cDNA were amplified using the primers 3'EH, 3'C2H and 3'CLH
CC respectively as a primer for first strand cDNA synthesis and the
CC primer combination of 5'CLH and 3'C2H, of 5'EH and 3'CLH and of
CC 5'GH and 3'EH respectively as primers for PCR. The amplified gene
CC products were isolated and used to produce plasmids. After
CC confirmation of the cDNA sequence of each plasmid, the cDNA
CC encoding LH, VH, CH1 and CH2CH3 were joined together to give
CC plasmid pTB1373 contg. the whole length chimeric H chain
CC (LH, VH, CH1, CH2CH3), also abbreviated as IgH-FIB,
XX
XX Sequence 466 AA;
SQ
Query Match 80.8%; Score 42; DB 13; Length 466;
Best Local Similarity 80.0%; Pred. NO. 9.3;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTTFSSYDMS 10
Db 45 GTFSSYDMS 54
RESULT 15
AAB40112
ID AAB40112 standard; Protein; 97 AA.
XX
XX AAB40112;
XX
XX 05-FEB-2001 (first entry)
XX
XX Anti-HLL12 antibody H chain V region amino acid sequence SEQ ID 638.
XX
XX Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;
XX complementarity determining region; CDR; antirheumatic; antiarthritic;
XX antisclerotic; neuroprotective; antipsoriatic; antiasthmatic; cardiant;
XX antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
XX multiple sclerosis; rheumatoid arthritis.
XX
XX Homo sapiens.
XX
XX WO2000056772-A1.
XX
XX 28-SEP-2000.
XX
XX 24-MAR-2000; 2000WO-US07946.
XX
XX 25-MAR-1999; 99US-0126603.
XX
XX (BADI ) BASF AG.
XX (GEM ) GENETICS INST INC.
XX

```

```

PI Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;
PI Kaymakalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A;
PI Veldman GM, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR;
PI Derbyshire EJ, Carmen S, Smith S, Holtet TL, Du Fou SL;
XX
XX WPI; 2000-638250/61.
DR
XX
XX New human antibody specific for human interleukin-12 (IL-12) used to
PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
PT disease and multiple sclerosis -
XX
XX Claim 75; Page 121; 377pp; English.
PS
XX
XX This invention relates to a new human antibody specific for human
CC interleukin-12 (IL-12). The invention also includes antigen binding
CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human
CC anti-IL-12 antibody heavy and light chain complementarity determining
CC region (CDR) amino acid sequences, and also includes variable region
CC amino acid sequences. Other variable region amino acid sequences are
CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771
CC represent anti-IL-12 CDR3 related amino acid sequences. AAB39772-B40063
CC represent other CDR sequences. Light chain CDR3 consensus sequences are
CC given in AAB40064-B40067. Primers used in the identification and
CC construction of the antibodies of the invention are given in
CC AAC61062-C61071. The antibody of the invention is a neutralising
CC antibody and has antirheumatic; antiarthritic; antisclerotic;
CC antiinflammatory; neuroprotective; antipsoriatic; antiasthmatic;
CC cardiant; antiparasitic; antibacterial and immunosuppressive activity.
CC The antibodies or antigen-binding fragments are useful in the treatment
CC of disorders associated with detrimental release of human IL-12,
CC especially Crohn's disease, multiple sclerosis and rheumatoid arthritis.
CC They can also be used in the manufacture of a pharmaceutical composition
CC to treat human IL-12 disorders.
XX
XX Sequence 97 AA;
SQ
Query Match 78.8%; Score 41; DB 21; Length 97;
Best Local Similarity 88.9%; Pred. NO. 2.7;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTTFSSYDM 9
Db 26 GTFSSYDM 34
Search completed: November 18, 2002, 17:31:33
Job time : 14.8235 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:54:45 ; Search time 1.96078 Seconds
(without alignments)
76.811 Million cell updates/sec

Title: US-09-016-061-48
Perfect score: 52
Sequence: 1 GTTFSSVDS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 97044 seqs, 15060890 residues

Total number of hits satisfying chosen parameters: 97044

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications,AA:*

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3: /cgn2_6/ptodata/1/pubaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubaa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubaa/PC1US_PUBCOMB.pep.*
8: /cgn2_6/ptodata/1/pubaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubaa/US09_NEW_PUB.pep.*
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11: /cgn2_6/ptodata/1/pubaa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/1/pubaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/1/pubaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	45	86.5	117	8	US-08-790-540A-2
2	45	86.5	117	8	US-08-791-391A-2
3	42	80.8	128	10	US-09-850-165-110
4	41	78.8	102	10	US-09-864-761-43848
5	41	78.8	470	10	US-09-859-053-32
6	41	78.8	470	10	US-09-859-053-36
7	40	76.9	117	8	US-08-790-540A-6
8	40	76.9	117	8	US-08-791-391A-6
9	39	75.0	123	10	US-09-850-165-112
10	38	73.1	87	10	US-09-840-459-53
11	38	73.1	89	10	US-09-840-459-48
12	38	73.1	98	10	US-09-840-459-38
13	38	73.1	98	10	US-09-840-459-39
14	38	73.1	98	10	US-09-840-459-44
15	38	73.1	98	10	US-09-840-459-45
16	38	73.1	98	12	US-10-066-895-4
17	38	73.1	118	9	US-09-423-800-46
18	38	73.1	118	9	US-09-423-800-56
19	38	73.1	137	9	US-09-423-800-76

20	38	73.1	137	9	US-09-423-800-77	Sequence 77, Appl
21	38	73.1	140	10	US-09-286-240-4	Sequence 4, Appl
22	38	73.1	144	10	US-09-881-823-12	Sequence 12, Appl
23	37	71.2	88	10	US-09-840-459-51	Sequence 51, Appl
24	37	71.2	89	10	US-09-840-459-49	Sequence 49, Appl
25	37	71.2	98	10	US-09-823-698A-18	Sequence 18, Appl
26	37	71.2	98	10	US-09-840-459-40	Sequence 40, Appl
27	37	71.2	98	12	US-10-025-687-19	Sequence 19, Appl
28	37	71.2	113	10	US-09-056-1608-11	Sequence 11, Appl
29	37	71.2	116	10	US-09-840-459-80	Sequence 80, Appl
30	37	71.2	118	9	US-09-144-886-64	Sequence 64, Appl
31	37	71.2	118	9	US-09-144-886-65	Sequence 65, Appl
32	37	71.2	118	9	US-09-144-886-66	Sequence 66, Appl
33	37	71.2	118	9	US-09-144-886-67	Sequence 67, Appl
34	37	71.2	119	10	US-09-811-123-3	Sequence 3, Appl
35	37	71.2	120	10	US-09-840-459-85	Sequence 85, Appl
36	37	71.2	120	12	US-10-025-687-4	Sequence 4, Appl
37	37	71.2	121	10	US-09-840-459-92	Sequence 92, Appl
38	37	71.2	123	10	US-09-840-459-82	Sequence 82, Appl
39	37	71.2	124	10	US-09-840-459-81	Sequence 81, Appl
40	37	71.2	124	10	US-09-840-459-89	Sequence 89, Appl
41	37	71.2	125	10	US-09-840-459-76	Sequence 76, Appl
42	37	71.2	125	10	US-09-850-165-107	Sequence 107, Appl
43	37	71.2	127	10	US-09-811-737-1	Sequence 1, Appl
44	37	71.2	127	10	US-09-840-459-87	Sequence 87, Appl
45	37	71.2	128	10	US-09-840-459-77	Sequence 77, Appl

ALIGNMENTS

RESULT 1
US-08-790-540A-2
; Sequence 2, Application US/08790540A
; Patent No. US20010011125A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,540A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-790-540A-2

Query Match 86.5%; Score 45; DB 8; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.076;

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Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTFSSYDMS 10
   | | | | | | | |
Db 26 GTTFSSYDMS 35

RESULT 2
US-08-791-391A-2
; Sequence 2, Application US/08791391A
; Patent No. US20010016645A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/791,391A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-391A-2

Query Match 86.5%; Score 45; DB 8; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.076;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTFSSYDMS 10
   | | | | | | | |
Db 26 GTTFSSYDMS 35

RESULT 3
US-09-850-165-110
; Sequence 110, Application US/09850165
; Patent No. US20020150580A1
; GENERAL INFORMATION:
; APPLICANT: NEWMAN, ROLAND A.
; APPLICANT: HANNA, NABIL
; APPLICANT: RAAB, RONALD W.
; TITLE OF INVENTION: RECOMBINANT ANTIBODIES FOR HUMAN THERAPY
; FILE REFERENCE: 037003-0280614
; CURRENT APPLICATION NUMBER: US/09/850,165
; CURRENT FILING DATE: 2001-05-08
; PRIOR APPLICATION NUMBER: 09/082,472
; PRIOR FILING DATE: 1998-05-21
; PRIOR APPLICATION NUMBER: 08/476,237
; PRIOR FILING DATE: 1995-06-07
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; PRIOR APPLICATION NUMBER: 08/397,072
; PRIOR FILING DATE: 1995-04-17
; PRIOR APPLICATION NUMBER: 07/912,292
; PRIOR FILING DATE: 1992-07-10
; PRIOR APPLICATION NUMBER: 07/856,281
; PRIOR FILING DATE: 1992-03-23
; PRIOR APPLICATION NUMBER: 07/735,064
; PRIOR FILING DATE: 1991-07-25
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 110
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Monkey
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (12)
; OTHER INFORMATION: Ile or Val
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (23)
; OTHER INFORMATION: Ser, Val or Ala
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (49)
; OTHER INFORMATION: Any amino acid, preferably Gly, Ser or Ala
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (79)
; OTHER INFORMATION: Val, Ala or Leu
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (87)
; OTHER INFORMATION: Lys, Glu or Arg
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (88)
; OTHER INFORMATION: Thr, Pro or Ala
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; NAME/KEY: MOD_RES
; LOCATION: (93)
; OTHER INFORMATION: Leu or Val
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; NAME/KEY: MOD_RES
; LOCATION: (95)
; OTHER INFORMATION: Phe or Tyr
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (97)
; OTHER INFORMATION: Thr or Ala
US-09-850-165-110

Query Match 80.8%; Score 42; DB 10; Length 128;
Best Local Similarity 80.0%; Pred. No. 0.3;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTFSSYDMS 10
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Db 26 GTTFSSYDMS 35

RESULT 4
US-09-864-761-43848
; Sequence 43848, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
```


;; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
;; FILE REFERENCE: Aecomica-X-1
;; CURRENT APPLICATION NUMBER: US/09/864,761
;; CURRENT FILING DATE: 2001-05-23
;; PRIOR APPLICATION NUMBER: US 60/180,312
;; PRIOR FILING DATE: 2000-02-04
;; PRIOR APPLICATION NUMBER: US 60/207,456
;; PRIOR FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: US 09/632,366
;; PRIOR FILING DATE: 2000-08-03
;; PRIOR APPLICATION NUMBER: GB 24263.6
;; PRIOR FILING DATE: 2000-10-04
;; PRIOR APPLICATION NUMBER: US 60/236,359
;; PRIOR FILING DATE: 2000-09-27
;; PRIOR APPLICATION NUMBER: PCT/US01/00666
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00667
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00664
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00669
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00665
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00668
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00663
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00662
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00661
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00670
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: US 60/234,687
;; PRIOR FILING DATE: 2000-09-21
;; PRIOR APPLICATION NUMBER: US 09/608,408
;; PRIOR FILING DATE: 2000-06-30
;; PRIOR APPLICATION NUMBER: US 09/774,203
;; PRIOR FILING DATE: 2001-01-29
;; NUMBER OF SEQ ID NOS: 49117
;; SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
;; SEQ ID NO 43848
;; LENGTH: 102
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: MAP TO AB019440.1
;; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.84
;; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.89
;; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
;; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
;; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.95
;; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1
;; OTHER INFORMATION: EST_HUMAN HIT: AW405458.1, EVALUE 3.00e-43
;; OTHER INFORMATION: SWISSPROT HIT: P01766, EVALUE 2.00e-39
US-09-864-761-43848

Query Match 78.8%; Score 41; DB 10; Length 102;
Best Local Similarity 88.9%; Pred. No. 0.36;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTFSSYDM 9
Db 17 GTTFSSYDM 25

RESULT 5
US-09-859-053-32
; Sequence 32, Application US/09859053
; Patent No. US20020102658A1
; GENERAL INFORMATION:
; APPLICANT: Tsuji, Takashi

;; APPLICANT: Tezuka, Katsunari
;; APPLICANT: Hori, No. US20020102658A1uaki
;; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
;; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
;; TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
;; FILE REFERENCE: 06501-079001
;; CURRENT APPLICATION NUMBER: US/09/859,053
;; CURRENT FILING DATE: 2001-05-16
;; PRIOR APPLICATION NUMBER: JP 2001-99508
;; PRIOR FILING DATE: 2001-03-30
;; PRIOR APPLICATION NUMBER: JP 2000-147116
;; PRIOR FILING DATE: 2000-05-18
;; NUMBER OF SEQ ID NOS: 43
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 32
;; LENGTH: 470
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-859-053-32

Query Match 78.8%; Score 41; DB 10; Length 470;
Best Local Similarity 88.9%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTFSSYDM 9
Db 45 GTTFSSYDM 53

RESULT 6
US-09-859-053-36
; Sequence 36, Application US/09859053
; Patent No. US20020102658A1
; GENERAL INFORMATION:
; APPLICANT: Tsuji, Takashi
; APPLICANT: Tezuka, Katsunari
; APPLICANT: Hori, No. US20020102658A1uaki
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
; TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
; FILE REFERENCE: 06501-079001
; CURRENT APPLICATION NUMBER: US/09/859,053
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: JP 2001-99508
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-147116
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-859-053-36

Query Match 78.8%; Score 41; DB 10; Length 470;
Best Local Similarity 88.9%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTFSSYDM 9
Db 45 GTTFSSYDM 53

RESULT 7
US-08-790-540A-6
; Sequence 6, Application US/08790540A
; Patent No. US2001001125A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 24

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,540A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-790-540A-6

Query Match 76.9%; Score 40; DB 8; Length 117;
Best Local Similarity 80.0%; Pred. No. 0.64; Indels 0;
Matches 8; Conservative 0; Mismatches 2; Gaps 0;

Qy 1 GTTFSSYDMS 10
| | | | | | | |
Db 26 GFAFSSYDMS 35

RESULT 8
US-08-791-391A-6
; Sequence 6, Application US/08791391A
; Patent No. US20010016645A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,391A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949

; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-791-391A-6
Query Match 76.9%; Score 40; DB 8; Length 117;
Best Local Similarity 80.0%; Pred. No. 0.64; Indels 0;
Matches 8; Conservative 0; Mismatches 2; Gaps 0;
Qy 1 GTTFSSYDMS 10
| | | | | | | |
Db 26 GFAFSSYDMS 35
RESULT 9
US-09-850-165-112
; Sequence 112, Application US/09850165
; Patent No. US20020150580A1
; GENERAL INFORMATION:
; APPLICANT: NEWMAN, ROLAND A.
; APPLICANT: HANNA, NABIL
; APPLICANT: RAAB, RONALD W.
; TITLE OF INVENTION: RECOMBINANT ANTIBODIES FOR HUMAN THERAPY
; FILE REFERENCE: 037003-0280614
; CURRENT APPLICATION NUMBER: US/09/850,165
; CURRENT FILING DATE: 2001-05-08
; PRIOR APPLICATION NUMBER: 09/082,472
; PRIOR FILING DATE: 1998-05-21
; PRIOR APPLICATION NUMBER: 08/476,237
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/397,072
; PRIOR FILING DATE: 1995-04-17
; PRIOR APPLICATION NUMBER: 07/912,292
; PRIOR FILING DATE: 1992-07-10
; PRIOR APPLICATION NUMBER: 07/856,281
; PRIOR FILING DATE: 1992-03-23
; PRIOR APPLICATION NUMBER: 07/735,064
; PRIOR FILING DATE: 1991-07-25
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 112
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Monkey
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (12)
; OTHER INFORMATION: Ile or Val
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (23)
; OTHER INFORMATION: Ser, Val or Ala
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (74)
; OTHER INFORMATION: Asn or Asp
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (75)
; OTHER INFORMATION: Ala or Ser
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (78)
; OTHER INFORMATION: Met, Ser or Thr

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FEATURE:
NAME/KEY: MOD_RES
LOCATION: (79)
OTHER INFORMATION: Val, Ala or Leu
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (80)
OTHER INFORMATION: Phe or Tyr
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (84)
OTHER INFORMATION: Ser, Asp or Asn
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (87)
OTHER INFORMATION: Lys, Glu or Arg
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (93)
OTHER INFORMATION: Thr, Pro or Ala
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (95)
OTHER INFORMATION: Phe or Tyr
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (97)
OTHER INFORMATION: Thr or Ala
US-09-850-165-112
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Query Match 75.0%; Score 39; DB 10; Length 123;
Best Local Similarity 70.0%; Pred. No. 1;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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QY 1 GTTFSSYDMS 10
| | | | |
DB 26 GTTFSTYDMT 35
```

```
RESULT 10
US-09-840-459-53
; Sequence 53, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 53
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Mus musculus
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US-09-840-459-53
Query Match 73.1%; Score 38; DB 10; Length 87;
Best Local Similarity 80.0%; Pred. No. 1.1;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
| | | | |
DB 15 GTTFSSYDMS 24
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RESULT 11
US-09-840-459-48
; Sequence 48, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 48
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-840-459-48
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Query Match 73.1%; Score 38; DB 10; Length 89;
Best Local Similarity 80.0%; Pred. No. 1.1;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
| | | | |
DB 17 GTTFSSYDMS 26

RESULT 12
US-09-840-459-38
; Sequence 38, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
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; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 38
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-840-459-38

Query Match 73.1%; Score 38; DB 10; Length 98;
Best Local Similarity 80.0%; Pred. No. 1.3;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
| | | | | | | |
Db 26 GTTFSSYDMS 35

RESULT 13
US-09-840-459-39
; Sequence 39, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 39
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-840-459-39

Query Match 73.1%; Score 38; DB 10; Length 98;
Best Local Similarity 80.0%; Pred. No. 1.3;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
| | | | | | | |
Db 26 GTTFSSYDMS 35

RESULT 14
US-09-840-459-44
; Sequence 44, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND

; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 44
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-840-459-44

Query Match 73.1%; Score 38; DB 10; Length 98;
Best Local Similarity 80.0%; Pred. No. 1.3;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
| | | | | | | |
Db 26 GTTFSSYDMS 35

RESULT 15
US-09-840-459-45
; Sequence 45, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 45
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-840-459-45

Query Match 73.1%; Score 38; DB 10; Length 98;
Best Local Similarity 80.0%; Pred. No. 1.3;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
| | | | | | | |
Db 26 GTTFSSYDMS 35

Search completed: November 18, 2002, 18:45:12
Job time : 1.96078 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:01 ; Search time 4.2402 Seconds
(without alignments)
69.390 Million cell updates/sec

Title: US-09-016-061-48

Perfect score: 52

Sequence: 1 GTTFSSYDMS 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep.*

3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep.*

4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep.*

5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep.*

6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	42	80.8	128	1	US-08-478-039-73
2	42	80.8	128	1	US-08-478-039-102
3	42	80.8	128	1	US-08-476-349A-73
4	42	80.8	128	1	US-08-476-349A-102
5	40	76.9	239	2	US-07-956-399-4
6	40	76.9	247	5	PCT-US94-07659-2
7	39	75.0	119	5	PCT-US94-07659-6
8	39	75.0	123	1	US-08-478-039-71
9	39	75.0	123	1	US-08-478-039-104
10	39	75.0	123	1	US-08-476-349A-71
11	39	75.0	123	1	US-08-476-349A-104
12	38	73.1	98	2	US-08-665-202-31
13	38	73.1	116	3	US-08-545-809A-101
14	38	73.1	116	4	US-08-983-607-36
15	38	73.1	122	1	US-08-276-852-80
16	38	73.1	122	1	US-08-899-575-80
17	38	73.1	122	1	US-08-899-575-80
18	38	73.1	122	5	PCT-US95-08743-80
19	38	73.1	123	2	US-08-665-202-30
20	38	73.1	239	2	US-08-553-497A-18
21	37	71.2	35	2	US-08-765-179B-1
22	37	71.2	98	2	US-08-428-197-48
23	37	71.2	98	5	PCT-US93-10535-48
24	37	71.2	102	2	US-08-273-146-65
25	37	71.2	110	1	US-08-211-202-117
26	37	71.2	113	3	US-08-974-899-6
27	37	71.2	116	2	US-08-428-197-2

28	37	71.2	116	5	PCT-US93-10555-2
29	37	71.2	117	3	US-08-545-809A-109
30	37	71.2	117	4	US-08-983-607-46
31	37	71.2	117	4	US-08-752-693A-3
32	37	71.2	117	4	US-08-752-693A-4
33	37	71.2	117	4	US-09-157-370-1
34	37	71.2	118	2	US-08-652-816A-12
35	37	71.2	118	4	US-08-487-761-15
36	37	71.2	118	5	PCT-US93-08435-10
37	37	71.2	120	4	US-09-025-769B-38
38	37	71.2	120	4	US-09-025-769B-63
39	37	71.2	121	1	US-08-339-582-2
40	37	71.2	122	2	US-07-934-373C-21
41	37	71.2	122	3	US-08-437-642B-21
42	37	71.2	122	4	US-08-146-206C-21
43	37	71.2	122	5	PCT-US93-07832-21
44	37	71.2	122	5	PCT-US93-08435-12
45	37	71.2	122	5	PCT-US93-08435-14

ALIGNMENTS

RESULT 1

US-08-478-039-73
; Sequence 73, Application US/08478039
; Patent No. 5681722
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raeb, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,039
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-160
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant

TOPOLOGY: not relevant
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Monkey
POSITION IN GENOME:
CHROMOSOME/SEGMENT: VH3 clone 3-40
US-08-478-039-73

Query Match 80.8%; Score 42; DB 1; Length 128;
Best Local Similarity 80.0%; Pred. No. 0.9;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
DB 26 GTTFSSYDMN 35

RESULT 2

US-08-478-039-102
; Sequence 102, Application US/08478039
; Patent No. 5681722
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404

COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,039
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/379,072
FILING DATE: 25-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912,292
FILING DATE: 10-JUL-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JUL-1991

ATTORNEY/AGENT INFORMATION:
NAME: Teskin Esq., Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-160
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021

INFORMATION FOR SEQ ID NO: 102:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant

MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Monkey
POSITION IN GENOME:
CHROMOSOME/SEGMENT: #40

US-08-478-039-102

Query Match 80.8%; Score 42; DB 1; Length 128;
Best Local Similarity 80.0%; Pred. No. 0.9;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
DB 26 GTTFSSYDMN 35

RESULT 3

US-08-476-349A-73
; Sequence 73, Application US/08476349A
; Patent No. 5750105
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404

COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,349A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/379,072
FILING DATE: 25-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912,292
FILING DATE: 10-JUL-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JUL-1991

ATTORNEY/AGENT INFORMATION:
NAME: Teskin Esq., Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-161
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021

INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant

MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Monkey
POSITION IN GENOME:
CHROMOSOME/SEGMENT: VH3 clone 3-40
US-08-476-349A-73

Query Match 80.8%; Score 42; DB 1; Length 128;
Best Local Similarity 80.0%; Pred. No. 0.9;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
| | | | |
Db 26 GTTFSSYDMN 35

RESULT 4

US-08-476-349A-102
; Sequence 102, Application US/08476349A
; Patent No. 5750105
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476.349A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-161
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-8620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 102:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Monkey
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: #40
US-08-476-349A-102

Query Match 80.8%; Score 42; DB 1; Length 128;
Best Local Similarity 80.0%; Pred. No. 0.9;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
| | | | |
Db 26 GTTFSSYDMN 35

RESULT 5

US-07-956-399-4
; Sequence 4, Application US/07956399
; Patent No. 5876717
; GENERAL INFORMATION:
; APPLICANT: SHIMAMURA, TOSHIRO
; APPLICANT: TAKI, SHINSUKE
; APPLICANT: HAMURO, JUNJI
; TITLE OF INVENTION: POLYPEPTIDES CAPABLE OF BINDING TO HEAVY
; CHAINS OF IL-2 RECEPTORS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MATER & NEUSTADT,
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/956,399
; FILING DATE: 19921005
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5876717man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 10-586-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-956-399-4

Query Match 76.9%; Score 40; DB 2; Length 239;
Best Local Similarity 80.0%; Pred. No. 4.2;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
| | | | |
Db 148 GFAFSSYDMS 157

RESULT 6
PCT-US94-07659-2
; Sequence 2, Application PC/TUS9407659
; GENERAL INFORMATION:
; APPLICANT: Young, Peter
; APPLICANT: Gross, Mitchell
; APPLICANT: Jonak, Zdenka L.
; APPLICANT: Theisen, Timothy
; APPLICANT: Hurler, Mark
; APPLICANT: Jackson, Jeffrey R.
; TITLE OF INVENTION: Recombinant and Humanized IL-1 beta
; TITLE OF INVENTION: Antibodies for Treatment of IL-1 Mediated Inflammatory
; TITLE OF INVENTION: Disorders in Man
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation - Corp.
; ADDRESSEE: Intellectual Property
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA

; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07659
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/090,534
; FILING DATE: 09-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50171-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 270-5024
; TELEFAX: (610) 270-5090
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 247 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-07659-2

Query Match 76.9%; Score 40; DB 5; Length 247;
Best Local Similarity 80.0%; Pred. No. 4.3; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 2;

QY 1 GTTFSSYDMS 10
| | | | | | | |
DB 45 GFASFSSYDMS 54

RESULT 7
PCT-US94-07659-6
; Sequence 6, Application PC/TUS9407659
; GENERAL INFORMATION:
; APPLICANT: Young, Peter
; APPLICANT: Gross, Mitchell
; APPLICANT: Jonak, Zdenka L.
; APPLICANT: Theisen, Timothy
; APPLICANT: Hurle, Mark
; APPLICANT: Jackson, Jeffrey R.
; TITLE OF INVENTION: Recombinant and Humanized IL-1 beta
; TITLE OF INVENTION: Antibodies for Treatment of IL-1 Mediated Inflammatory
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Smithkline Beecham Corporation - Corp.
; ADDRESSEE: Intellectual Property
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07659
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/090,534
; FILING DATE: 09-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.

; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50171-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 270-5024
; TELEFAX: (610) 270-5090
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-07659-6

Query Match 75.0%; Score 39; DB 5; Length 119;
Best Local Similarity 80.0%; Pred. No. 2.9;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
| | | | | | | |
DB 26 GFIFSSYDMS 35

RESULT 8
US-08-478-039-71
; Sequence 71, Application US/08478039
; Patent No. 5681722
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabill
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,039
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-160
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 123 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant

MOLECULE TYPE: peptide
ORIGINAL SOURCE: Monkey
ORGANISM: Monkey
POSITION IN GENOME: VH3 clone 3-34
CHROMOSOME/SEGMENT: VH3 clone 3-34

US-08-478-039-71

Query Match 75.0%; Score 39; DB 1; Length 123;
Best Local Similarity 70.0%; Pred. No. 3;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
Db 26 GTFESTYDMT 35

RESULT 9
US-08-478-039-104
Sequence 104, Application US/08478039
Patent No. 5681722
GENERAL INFORMATION:
APPLICANT: Newman, Roland A.
APPLICANT: Hanna, Nabil
APPLICANT: Raab, Ronald W.
TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince St.
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,039
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/379,072
FILING DATE: 25-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912,292
FILING DATE: 10-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Teskin Esq., Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-160
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
ORIGINAL SOURCE: Monkey
ORGANISM: Monkey
POSITION IN GENOME: #34
CHROMOSOME/SEGMENT: #34

US-08-478-039-104

Query Match 75.0%; Score 39; DB 1; Length 123;
Best Local Similarity 70.0%; Pred. No. 3;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
Db 26 GTFESTYDMT 35

RESULT 10
US-08-476-349A-71
Sequence 71, Application US/08476349A
Patent No. 5750105
GENERAL INFORMATION:
APPLICANT: Newman, Roland A.
APPLICANT: Hanna, Nabil
APPLICANT: Raab, Ronald W.
TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince St.
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,349A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/379,072
FILING DATE: 25-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912,292
FILING DATE: 10-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Teskin Esq., Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-161
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
ORIGINAL SOURCE: Monkey
ORGANISM: Monkey
POSITION IN GENOME: VH3 clone 3-34
CHROMOSOME/SEGMENT: VH3 clone 3-34

US-08-476-349A-71

Query Match 75.0%; Score 39; DB 1; Length 123;
Best Local Similarity 70.0%; Pred. No. 3;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10

```

Db      26 GTTFSTYDMT 35

RESULT 11
US-08-476-349A-104
; Sequence 104, Application US/08476349A
; Patent No. 5750105
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,349A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-161
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 123 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Monkey
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: #34
US-08-476-349A-104

Query Match 75.0%; Score 39; DB 1; Length 123;
Best Local Similarity 70.0%; Pred. No. 3;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GTTFSSYDMS 10
Db      26 GTTFSTYDMT 35

RESULT 12
US-08-665-202-31
; Sequence 31, Application US/08665202
; Patent No. 5977322
; GENERAL INFORMATION:
; APPLICANT: Marks, James D.
; APPLICANT: Schier, Robert
; TITLE OF INVENTION: No. 5977322e1 High Affinity Human Antibodies to
; Tumor Antigens
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,202
; FILING DATE: 13-JUN-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,238
; FILING DATE: 14-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,250
; FILING DATE: 15-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 02307E-061410
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-665-202-31

Query Match 73.1%; Score 38; DB 2; Length 98;
Best Local Similarity 70.0%; Pred. No. 3.6;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GTTFSSYDMS 10
Db      26 GTTFSSYEMN 35

RESULT 13
US-08-545-809A-101
; Sequence 101, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; APPLICANT: Matsuda, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:

```

; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,809A
; FILING DATE: 27-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 06501/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 101:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-545-809A-101

Query Match 73.1%; Score 38; DB 3; Length 116;
Best Local Similarity 77.8%; Pred. No. 4.3;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTFSSYDM 9
| | | | |
Db 45 GTTFSSYDM 53

RESULT 14
US-08-983-607-36
; Sequence 36, Application US/08983607
; Patent No. 614070
; GENERAL INFORMATION:
; APPLICANT: Alan Garen
; APPLICANT: Xiaohong Cai
; TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-
; TITLE OF INVENTION: bodies
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Department of Molecular Biophysics
; ADDRESSEE: and Biochemistry, Yale University
; STREET: 266 Whitney Avenue
; CITY: New Haven
; STATE: Connecticut
; COUNTRY: United States of America
; ZIP: 06520-8114
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" 1.44 Mb diskette
; COMPUTER: IBM PC
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Word Processing
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/983,607
; FILING DATE: April 27, 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/IB96/01032
; FILING DATE: June 28, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mary M. Krinsky
; REGISTRATION NUMBER: 32423
; REFERENCE/DOCKET NUMBER: OCR-679
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 203-773-9544
; TELEFAX: 203-773-1183

; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 residues
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
; DESCRIPTION: polypeptide
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens (melanoma patient immu-
; ORGANISM: nized with autologous tumor cells)
; INDIVIDUAL ISOLATE: peripheral blood lymphocytes
; IMMEDIATE SOURCE:
; LIBRARY: DM414 scFv antibodies obtained from
; LIBRARY: FUSES fusion phage construct
; CLONE: V474
; FEATURE:
; NAME/KEY: heavy chain
US-08-983-607-36

Query Match 73.1%; Score 38; DB 4; Length 116;
Best Local Similarity 80.0%; Pred. No. 4.3;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTFSSYDMS 10
| | | | |
Db 26 GTTFSSYDMS 35

RESULT 15
US-08-276-852-80
; Sequence 80, Application US/08276852
; Patent No. 5652138
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
; STREET: Mail Drop tpc8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276,852
; FILING DATE: 18-JUL-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCR1452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:

;
; LENGTH: 122 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-276-852-80

Query Match 73.1%; Score 38; DB 1; Length 122;
Best Local Similarity 70.0%; Pred. No. 4.6;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTFSSYDMS 10
| | | | | | | |
Db 23 GTTFSSYEMN 32

Search completed: November 18, 2002, 17:43:33
Job time : 5.2402 secs

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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:01 ; Search time 4.90196 seconds
(without alignments)
196.114 Million cell updates/sec

Title: US-09-016-061-50
Perfect score: 58
Sequence: 1 GFTWSSYDMS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_73: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	48	82.8	94	2 S14580	Ig heavy chain V r
2	44	75.9	97	2 S26890	Ig heavy chain V r
3	43	74.1	113	2 S26468	Ig heavy chain V r
4	43	74.1	117	1 HVMS34	Ig heavy chain pre
5	43	74.1	121	2 D27888	Ig heavy chain V r
6	43	74.1	124	2 C27888	Ig heavy chain V r
7	41	70.7	40	2 S33406	Ig heavy chain V r
8	41	70.7	83	2 C25913	Ig heavy chain V r
9	41	70.7	98	2 S26891	Ig heavy chain V r
10	41	70.7	108	2 PL0248	Ig heavy chain V r
11	41	70.7	108	2 PH1006	Ig heavy chain V r
12	41	70.7	117	1 HVMS84	Ig heavy chain pre
13	41	70.7	117	2 PL0249	Ig heavy chain V r
14	41	70.7	117	2 PL0252	Ig heavy chain V r
15	41	70.7	118	2 S38491	Ig heavy chain - h
16	41	70.7	119	2 F27888	Ig heavy chain V r
17	41	70.7	122	2 E27888	Ig heavy chain V r
18	41	70.7	138	2 S09258	Ig heavy chain V r
19	41	70.7	325	2 T25122	hypothetical prote
20	40	69.0	92	2 S56009	Ig heavy chain var
21	40	69.0	92	2 S56008	Ig heavy chain var
22	40	69.0	97	1 HVMS91	Ig heavy chain V r
23	40	69.0	97	2 PH0872	Ig heavy chain V r
24	40	69.0	98	2 S26889	Ig heavy chain V r
25	40	69.0	100	2 D48223	Ig heavy chain V r
26	40	69.0	102	2 S14581	Ig heavy chain V r
27	40	69.0	108	2 PH1648	Ig heavy chain V r
28	40	69.0	108	2 PH1011	Ig heavy chain V r
29	40	69.0	109	2 PH1649	Ig heavy chain V r

30 40 69.0 111 2 PH1659 Ig heavy chain V r
31 40 69.0 111 2 S40090 Ig heavy chain - m
32 40 69.0 111 2 PH1007 Ig heavy chain V r
33 40 69.0 112 2 S26327 Ig heavy chain V r
34 40 69.0 112 2 PH1647 Ig heavy chain V r
35 40 69.0 113 2 S25571 Ig heavy chain V r
36 40 69.0 113 1 H3HU26 Ig heavy chain pre
37 40 69.0 117 2 A45953 Ig heavy chain pre
38 40 69.0 117 2 B34964 Ig heavy chain pre
39 40 69.0 117 2 S34012 Ig heavy chain V r
40 40 69.0 118 2 S31121 Ig heavy chain - h
41 40 69.0 119 2 C36005 Ig heavy chain V r
42 40 69.0 119 2 D36005 Ig heavy chain V r
43 40 69.0 119 2 S31107 Ig heavy chain - h
44 40 69.0 119 2 S31108 Ig heavy chain - h
45 40 69.0 120 2 S48798 Ig heavy chain V r

ALIGNMENTS

RESULT 1

S14580
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C:Accession: S14580
R:Chen, Q.; Stenzel-Poore, M.; Rittenberg, M.B.
submitted to the EMBL Data Library, March 1991
A:Description: Natural polyclonal antibodies differ from Ag-induced antibodies in V
A:Reference number: S14484
A:Accession: S14580
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-94 <CHE>
A:Cross-references: EMBL:X58652; NID:g51293; PIDN:CAA41509.1; PID:g51294
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:7-90/Domain: immunoglobulin homology <IMM>

Query Match 82.8%; Score 48; DB 2; Length 94;
Best Local Similarity 90.0%; Pred. No. 0.18;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
|||:|||||
Db 18 GFTFSSYDMS 27

RESULT 2

S26890
Ig heavy chain V region (DP-48) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S26890
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups o
A:Reference number: S26885; MUID:93021117; PMID:1404388
A:Accession: S26890
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-97 <TOM>
A:Cross-references: EMBL:X12348; NID:g32916; PIDN:CAA78218.1; PID:g32917
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:15-97/Domain: immunoglobulin homology <IMM>

Query Match 75.9%; Score 44; DB 2; Length 97;
Best Local Similarity 88.9%; Pred. No. 0.91;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTWSSYDM 9

Db 26 GFTSSYDM 34
||||:|||||

RESULT 3

S26468 Ig heavy chain V region - mouse

C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C:Accession: S26468

R:Kavaler, J. submitted to the EMBL Data Library, April 1991

A:Reference number: S26459

A:Accession: S26468

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-113 <KAV>

A:Cross-references: EMBL:X59107; NID:g51944; PIDN:CAA41833.1; PID:g51945

C:Superfamily: immunoglobulin V region; Immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:11-94/Domain: immunoglobulin homology <IMM>

Query Match 74.1%; Score 43; DB 2; Length 113;

Best Local Similarity 80.0%; Pred. No. 1.6;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GFTSSYDMS 10

Db 22 GFAFSSYDMS 31

RESULT 4

HVMS34

Ig heavy chain precursor V region (345) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 31-Mar-1997

C:Accession: J70502

R:Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.

J. Exp. Med. 169, 2007-2019, 1989

A:Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary

A:Reference number: J70501; MUID:89279149; PMID:2499654

A:Accession: J70502

A>Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-117 <LEV>

A:Experimental source: strain BALB/cJ

A:Note: This sequence belongs to the VH7183 subfamily

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-117/Product: Ig heavy chain V region (345) #status predicted <MAT>

F:34-117/Domain: immunoglobulin homology <IMM>

F:41-115/Disulfide bonds: #status predicted

Query Match 74.1%; Score 43; DB 1; Length 117;

Best Local Similarity 80.0%; Pred. No. 1.7;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GFTSSYDMS 10

Db 45 GFAFSSYDMS 54

RESULT 5

D27888

Ig heavy chain V region (H37-60) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996

C:Accession: D27888

R:Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.

EMBO J. 5, 1577-1587, 1986

A:Title: Structural and functional implications of a restricted antibody response to a

A:Reference number: A91043; MUID:86300658; PMID:2427335

A:Accession: D27888
A:Molecule type: DNA
A:Residues: 1-121 <CAT>

A:Experimental source: strain Balb/c

A:Note: This sequence was determined from the germline gene

C:Species: Mus musculus (house mouse)

C:Comment: This chain was isolated from a hybridoma protein that binds influenza viru

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 74.1%; Score 43; DB 2; Length 121;

Best Local Similarity 80.0%; Pred. No. 1.7;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GFTSSYDMS 10

Db 26 GFAFSSYDMS 35

RESULT 6

C27888

Ig heavy chain V region (H37-62) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996

C:Accession: C27888

R:Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.

EMBO J. 5, 1577-1587, 1986

A:Title: Structural and functional implications of a restricted antibody response to

A:Reference number: A91043; MUID:86300658; PMID:2427335

A:Accession: C27888

A:Molecule type: DNA

A:Residues: 1-124 <CAT>

A:Experimental source: strain Balb/c

A:Note: This sequence was determined from the germline gene

C:Species: Mus musculus (house mouse)

C:Comment: This chain was isolated from a hybridoma protein that binds influenza viru

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 74.1%; Score 43; DB 2; Length 124;

Best Local Similarity 80.0%; Pred. No. 1.8;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GFTSSYDMS 10

Db 26 GFAFSSYDMS 35

RESULT 7

S33406

Ig heavy chain V region - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 19-Mar-1997 #sequence_revision 24-Jul-1997 #text_change 17-Jul-1998

C:Accession: S33406

R:Kettleborough, C.A.; Saldanha, J.; Ansell, K.H.; Bendig, M.M.

Eur. J. Immunol. 23, 206-211, 1993

A:Title: Optimization of primers for cloning libraries of mouse immunoglobulin genes

A:Reference number: S33391; MUID:93122092; PMID:8419173

A:Accession: S33406

A:Molecule type: mRNA

A:Residues: 1-40 <KET>

A:Cross-references: EMBL:X73009

A:Experimental source: strain BALB/c

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-40/Domain: immunoglobulin homology (fragment) <IMM>

Query Match

Best Local Similarity 70.7%; Score 41; DB 2; Length 40;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GFTSSYDMS 10

Db 11:|||||

Db 26 GFTWSSYDMS 35

RESULT 8

C25913

Ig heavy chain V region (BF114) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 16-Aug-1996

C:Accession: C25913

R:Lawler, A. M.; Lin, P. S.; Gearhart, P. J.

Proc. Natl. Acad. Sci. U.S.A. 84, 2454-2458, 1987

A:Title: Adult B-cell repertoire is biased toward two heavy-chain variable-region genes

A:Reference number: A94148; MUID:87175692; PMID:3104915

A:Accession: C25913

A:Molecule type: DNA

A:Residues: 1-83 <LAW>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 70.7%; Score 41; DB 2; Length 83;

Best Local Similarity 80.0%; Pred. No. 2.6;

Matches 8; Conservative 1; Mismatches 0; Gaps 0;

QY 1 GFTWSSYDMS 10

|||||

Db 11 GFTFSSYDMS 20

RESULT 9

S26891

Ig heavy chain V region (DP-58) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C:Accession: S26891

R:Tomlinson, I. M.; Walter, G.; Marks, J. D.; Llewellyn, M. B.; Winter, G.

J. Mol. Biol. 227, 776-798, 1992

A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V

A:Reference number: S26885; MUID:93021117; PMID:1404388

A:Accession: S26891

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-98 <TON>

A:Cross-references: EMBL:212358; NID:g32935; PIDN:CAA78228.1; PID:g32936

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 70.7%; Score 41; DB 2; Length 98;

Best Local Similarity 70.0%; Pred. No. 3.1;

Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10

|||||

Db 26 GFTFSSYDMS 35

RESULT 10

PL0248

Ig heavy chain V region (anti-DNA, DP12VH) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996

C:Accession: PL0248

R:Shlomchik, M.; Mascello, M.; Shan, H.; Radic, M. Z.; Pisetsky, D.; Marshak-Rothstein, A.

J. Exp. Med. 171, 265-297, 1990

A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic

A:Reference number: PL0231; MUID:90111618; PMID:2104919

A:Accession: PL0248

A:Molecule type: mRNA

A:Residues: 1-108 <SHL>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-24/Region: framework 1

F:15-92/Domain: immunoglobulin homology <IMM>

Query Match 70.7%; Score 41; DB 1; Length 117;

Best Local Similarity 80.0%; Pred. No. 3.7;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10

|||||

F:25-29/Region: complementarity-determining 1
F:30-43/Region: framework 2
F:44-60/Region: complementarity-determining 2
F:61-92/Region: framework 3
F:93-99/Region: complementarity-determining 3
F:100-108/Region: framework 4

Query Match 70.7%; Score 41; DB 2; Length 108;

Best Local Similarity 80.0%; Pred. No. 3.4;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10

|||||

Db 20 GFTFSSYDMS 29

RESULT 11

PH1006

Ig heavy chain V region (clone 202.33) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C:Accession: PH1006

R:Tillman, D. M.; Jou, N. T.; Hill, R. J.; Marion, T. N.

J. Exp. Med. 176, 761-779, 1992

A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective

A:Reference number: PH0971; MUID:92381444; PMID:1512540

A:Accession: PH1006

A>Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-108 <TIL>

A:Experimental source: B cell, strain [NZB x NZW]F1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:10-93/Domain: immunoglobulin homology <IMM>

Query Match 70.7%; Score 41; DB 2; Length 108;

Best Local Similarity 80.0%; Pred. No. 3.4;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10

|||||

Db 21 GFTFSSYDMS 30

RESULT 12

HVMS84

Ig heavy chain precursor V region (5-84) - mouse

C:Species: Mus musculus (house mouse)

C>Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 31-Mar-1997

C:Accession: JT0505

R:Levy, N. S.; Malipiero, U. V.; Lebecque, S. G.; Gearhart, P. J.

J. Exp. Med. 169, 2007-2019, 1989

A:Title: Early onset of somatic mutation in immunoglobulin VH genes during the primar

A:Reference number: JT0501; MUID:89279149; PMID:2499654

A:Accession: JT0505

A>Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-117 <LEV>

A:Experimental source: strain BALB/cJ

A>Note: This sequence belongs to the VH7183 subfamily

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-117/Product: Ig heavy chain V region (5-84) #status predicted <MAT>

F:34-117/Domain: immunoglobulin homology <IMM>

F:41-115/Disulfide bonds: #status predicted

Db 45 GFTSSSYTMS 54

RESULT 13

PL0249

Ig heavy chain V region (anti-DNA, 3E12VH) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996

C:Accession: PL0249

R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A

J. Exp. Med. 171, 265-297, 1990

A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic

A:Reference number: PL0231; MUID:90111618; PMID:2104919

A:Accession: PL0249

A:Molecule type: mRNA

A:Residues: 1-117 <SHL>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-30/Region: framework 1

F:15-98/Domain: immunoglobulin homology <IMM>

F:31-35/Region: complementarity-determining 1

F:36-49/Region: framework 2

F:50-66/Region: complementarity-determining 2

F:67-98/Region: framework 3

F:99-108/Region: complementarity-determining 3

F:109-117/Region: framework 4

Query Match 70.7%; Score 41; DB 2; Length 117;

Best Local Similarity 80.0%; Pred. No. 3.7;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GFTSSSYDMS 10

Db 26 GFTSSSYTMS 35

RESULT 14

PL0252

Ig heavy chain V region (anti-DNA, clones 2E3VH, 6B8VH, and 3G9VH) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996

C:Accession: PL0252; PL0251

R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A

J. Exp. Med. 171, 265-297, 1990

A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic

A:Reference number: PL0231; MUID:90111618; PMID:2104919

A:Accession: PL0252

A:Molecule type: mRNA

A:Residues: 1-117 <SHL>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-30/Region: framework 1

F:15-98/Domain: immunoglobulin homology <IMM>

F:31-35/Region: complementarity-determining 1

F:36-49/Region: framework 2

F:50-66/Region: complementarity-determining 2

F:67-98/Region: framework 3

F:99-108/Region: complementarity-determining 3

F:109-117/Region: framework 4

Query Match 70.7%; Score 41; DB 2; Length 117;

Best Local Similarity 80.0%; Pred. No. 3.7;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GFTSSSYDMS 10

Db 26 GFTSSSYTMS 35

RESULT 15

S38491

Ig heavy chain - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C:Accession: S38491

R:Marks, J.D.; Ouwehand, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe

submitted to the EMBL Data Library, June 1993

A:Description: Human antibody fragments specific for human blood group antigens from

A:Reference number: S38488

A:Accession: S38491

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-118 <MAR>

A:Cross-references: EMBL:Z33032; NID:g414029; PIDN:CAA80567.1; PID:g414030

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-97/Domain: immunoglobulin homology <IMM>

Query Match 70.7%; Score 41; DB 2; Length 118;

Best Local Similarity 88.9%; Pred. No. 3.7;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GFTSSSYDM 9

Db 26 GFTSSSYDM 34

Search completed: November 18, 2002, 17:47:00

Job time : 5.90196 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:00 ; Search time 2.45098 Seconds
(without alignments)
169.223 Million cell updates/sec

Title: US-09-016-061-50
Perfect score: 58
Sequence: 1 GFTWSSYDMS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43	74.1	117	1 HV55_MOUSE	P18526 mus musculus
2	41	70.7	117	1 HV54_MOUSE	P18525 mus musculus
3	40	69.0	97	1 HV56_MOUSE	P18527 mus musculus
4	40	69.0	117	1 HV3C_HUMAN	P01764 homo sapien
5	39	67.2	117	1 HV53_MOUSE	P18524 mus musculus
6	38	65.5	117	1 HV59_MOUSE	P18530 mus musculus
7	38	65.5	304	1 K2S3_HUMAN	Q14952 homo sapien
8	38	65.5	450	1 NMT1_MOUSE	P46548 caenorhabdi
9	37	63.8	116	1 HV1A_RABIT	P01826 oryctolagus
10	37	63.8	117	1 HV2B_RABIT	P01828 oryctolagus
11	37	63.8	311	1 PLC_STAAR	P45723 staphylococ
12	37	63.8	491	1 GAT1_STRPN	Q97p15 streptococ
13	36	62.1	115	1 HV3D_HUMAN	P01765 homo sapien
14	36	62.1	367	1 DIAC_RAT	Q01460 rattus norv
15	36	62.1	385	1 DIAC_HUMAN	Q01459 homo sapien
16	36	62.1	423	1 IDH_BACSU	P39126 bacillus su
17	36	62.1	496	1 NMT1_MOUSE	P30419 homo sapien
18	36	62.1	496	1 NMT1_MOUSE	Q70310 mus musculus
19	36	62.1	497	1 NMT1_BOVIN	P31717 bos taurus
20	36	62.1	506	1 C248_DROME	Q97p1 drosophila
21	36	62.1	508	1 AMYP_MOUSE	P00688 mus musculus
22	36	62.1	508	1 AMYP_RAT	P00689 rattus norv
23	36	62.1	511	1 AMYS_MOUSE	P00687 mus musculus
24	36	62.1	517	1 YB3C_SCHPO	O14342 schizosacch
25	36	62.1	565	1 SVX_METTH	O27874 methanobact
26	36	62.1	707	1 TRFL_MOUSE	P08071 mus musculus
27	36	62.1	781	1 GCS1_CAEEL	Q19426 caenorhabdi
28	35	60.3	117	1 HV52_MOUSE	P06327 mus musculus
29	35	60.3	396	1 CBG_RAT	P31211 rattus norv
30	35	60.3	434	1 SLS4_BRAOL	P17841 brassica ol
31	35	60.3	435	1 SLS2_BRAOA	P22553 brassica ol
32	35	60.3	558	1 AWAL_PLACH	P18445 plasmodium
33	34	58.6	105	1 ARSR_BACSU	P45949 bacillus su

34 34 58.6 114 1 HV00_MOUSE P01741 mus musculus
35 34 58.6 114 1 HV01_CANFA P01784 canis famli
36 34 58.6 118 1 ABBE_TRIAB P81116 trimeresuru
37 34 58.6 120 1 HV3E_HUMAN P01766 homo sapien
38 34 58.6 121 1 HV3J_HUMAN P01771 homo sapien
39 34 58.6 127 1 P044_RAT P38718 rattus norv
40 34 58.6 193 1 YLBO_BACSU O34549 bacillus su
41 34 58.6 213 1 COBO_PSEDE P29930 pseudomonas
42 34 58.6 264 1 STE4_SCHPO P36622 schizosacch
43 34 58.6 304 1 YQOB_CAEEL Q09300 caenorhabdi
44 34 58.6 455 1 K3L2_HUMAN P43630 homo sapien
45 34 58.6 491 1 NMT_CRYNE P34809 cryptococcu

ALIGNMENTS

RESULT 1
HV55_MOUSE
ID HV55_MOUSE STANDARD; PRT; 117 AA.
AC P18526;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 345 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Mallipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RT the primary immune response";
RL J. Exp. Med. 169:2007-2019(1989).
CC -I- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; JT0502; HVMS34.
DR HSSP; P01810; 2FBJ.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
KW SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 345.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12902 MW; 49380E4627ACA99A CRC64;
Query Match 74.1%; Score 43; DB 1; Length 117;
Best Local Similarity 80.0%; Pred. No. 0.84;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 GFTWSSYDMS 10
II :|||||
Db 45 GFAFSSYDMS 54
RESULT 2
HV54_MOUSE
ID HV54_MOUSE STANDARD; PRT; 117 AA.
AC P18525;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 5-84 precursor.

```

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RT the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; JT0505; HVMS84.
DR HSSP; P01810; 2FBT.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin V region; Signal.
KW SIGNAL
FT CHAIN 1 19
FT DOMAIN 20 117 IG HEAVY CHAIN V REGION 5-84.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12872 MW; 234055CB6A469861 CRC64;

Query Match
Best Local Similarity 70.7%; Score 41; DB 1; Length 117;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
DB 45 GFTSSYDMS 54

RESULT 3
HV56_MOUSE
ID HV56_MOUSE STANDARD; PRT; 97 AA.
AC P18527;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 914.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RT the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; JT0504; HVMS91.
DR HSSP; P01810; 2FBT.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin V region.
FT NON_TER 97 97
SQ SEQUENCE 97 AA; 10661 MW; C23CB33FF5DA893 CRC64;

Query Match
Best Local Similarity 69.0%; Score 40; DB 1; Length 97;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
DB 26 GFTSSYDMS 35

RESULT 4
HV3C_HUMAN
ID HV3C_HUMAN STANDARD; PRT; 117 AA.
AC P01764;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-III region VH26 precursor.
CS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81101090; PubMed=6450418;
RA Matthysens G., Rabbitts T.H.;
RT "Structure and multiplicity of genes for the human immunoglobulin
RT heavy chain variable region.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).
CC -----
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CC -----
DR EMBL; J00236; AAA53516.1; -.
DR EMBL; M35415; AAA58735.1; -.
DR PIR; A02047; H3HU26.
DR HSSP; P01772; 2FB4.
DR Genew; HGNC:5545; IGHV@.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V-III REGION VH26.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12582 MW; E826733F1A3CB0F1 CRC64;

Query Match
Best Local Similarity 69.0%; Score 40; DB 1; Length 117;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
DB 45 GFTSSYDMS 54

RESULT 5
HV53_MOUSE
ID HV53_MOUSE STANDARD; PRT; 117 AA.
AC P18524;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region RF precursor.
CS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN=BALB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR: J0503; HVMSRF.
DR HSSP: P01810; 2FBJ.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig: 1.
DR SMART: SM00406; IgV: 1.
KW Immunoglobulin V region; Hybridoma; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION RF.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12866 MW; 2CE3295F390F725B CRC64;

Query Match 67.28; Score 39; DB 1; Length 117;
Best Local Similarity 80.08; Pred. No. 4.1;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
DB 45 GFTFSYMS 54
III:III:II

RESULT 6
HV59_MOUSE
ID HV59_MOUSE STANDARD; PRT; 117 AA.
AC P18530;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 7-39 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR: J0503; HVMS39.
DR HSSP: P01810; 2FBJ.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig: 1.
DR SMART: SM00406; IgV: 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 7-39.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12972 MW; D5CA4167D0F1774F CRC64;
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Query Match 65.5%; Score 38; DB 1; Length 117;
Best Local Similarity 70.0%; Pred. No. 6;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
DB 45 GFTFSYMS 54
III:III:II

RESULT 7
K2S3_HUMAN
ID K2S3_HUMAN STANDARD; PRT; 304 AA.
AC Q14952; O00644;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Killer cell immunoglobulin-like receptor 2DS3 precursor (MHC class I
NK cell receptor) (Natural killer associated transcript 7) (NKAT-7).
GN KIR2DS3 OR NKAT7
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96270004; PubMed=8662091;
RA Doehring C., Samaridis J., Colonna M.;
RT "Alternatively spliced forms of human killer inhibitory receptors.";
RL Immunogenetics 44:227-230(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphoid;
RA Biassoni R.;
CC -!- FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR HLA-C ALLELES.
CC -!- DOES NOT INHIBIT THE ACTIVITY OF NK CELLS.
CC -!- SUBCELLULAR LOCATION: type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -!- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC
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CC
CC EMBL: L76670; AAB36598.1; -.
CC EMBL: X97231; CAA65870.1; -.
CC HSSP: P43626; 1NKR.
CC Genew: HGNC:6335; KIR2DS3.
CC MIM: 604954; -.
CC InterPro: IPR003599; Ig.
CC InterPro: IPR003006; Ig_MHC.
CC InterPro: IPR003600; Ig_Like.
CC Pfam: PF00047; Ig: 2.
CC SMART: SM00409; Ig: 1.
CC SMART: SM00410; Ig_Like; 1.
KW Receptor; Immunoglobulin domain; Glycoprotein; Signal; Transmembrane;
KW Repeat; Multigene family.
FT SIGNAL 1 21
FT CHAIN 22 304 BY SIMILARITY.
FT KILLER CELL IMMUNOGLOBULIN-LIKE RECEPTOR
FT 2DS3.
FT DOMAIN 22 245 EXTRACELLULAR (POTENTIAL) . .
FT TRANSMEM 246 284 POTENTIAL.
FT DOMAIN 285 304 CYTOPLASMIC (POTENTIAL) .
FT DOMAIN 42 107 IG-LIKE C2-TYPE DOMAIN 1.
FT DOMAIN 142 205 IG-LIKE C2-TYPE DOMAIN 2.
FT DISULFID 49 100 BY SIMILARITY.
FT DISULFID 149 198 BY SIMILARITY.
FT CARBOHYD 67 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 178 178 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 304 AA; 33717 MW; 80693F79844F9E7E CRC64;

Query Match 65.5%; Score 38; DB 1; Length 304;
Best Local Similarity 85.7%; Pred. No. 15;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TWSSYDM 9
Db 151 SWSSYDM 157

RESULT 8
NMT_CAEEL
ID NMT_CAEEL STANDARD; PRT; 450 AA.
AC P46548;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Probable glycolipid N-tetradecanoyltransferase (EC 2.3.1.97)
DE (Peptide N-myristoyltransferase) (Myristoyl-CoA:protein N-
GN T17E9.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Du Z.;
RL Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Adds a myristoyl group to the N-terminal glycine residue
CC of certain cellular proteins (By similarity).
CC -1- CATALYTIC ACTIVITY: Tetradecanoyl-CoA + glycolipid-peptide = CoA + N-
CC tetradecanoylglycolipid-peptide.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- SIMILARITY: BELONGS TO THE NMT FAMILY.
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DR EMBL; U11280; AAA19436.1; -
DR HSSP; P30418; INMT.
DR WormPep; T17E9.2; CE01406.
DR InterPro; IPR000903; Nmt.
DR Pfam; PF01233; NMT; 1.
DR Pfam; PF02799; NMT_C; 1.
DR PROSITE; PS00975; NMT_1; 1.
DR PROSITE; PS00976; NMT_2; 1.
KW Hypothetical protein; Transferase; Acyltransferase.
SQ SEQUENCE 450 AA; 50889 MW; 5A639808F7DDA38E CRC64;

Query Match 65.5%; Score 38; DB 1; Length 450;
Best Local Similarity 60.0%; Pred. No. 23;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GFTWSSYDMS 10
Db 108 GFRWSNVDS 117

RESULT 9
HV1A_RABIT
ID HV1A_RABIT STANDARD; PRT; 116 AA.
AC P01826;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)

us-09-016-061-50.rsp

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DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-A1 region BS-5.
OS Oryctolagus cuniculus (Rabbit).
OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE OF 1-69.
RX MEDLINE=7320191; PubMed=4146279;
RA Jaton J.-C., Braun D.G.;
RT "Amino acid sequence of the N-terminal sixty-nine residues of heavy
RL chain derived from a homogeneous rabbit antibody.";
RN [2]
RP SEQUENCE OF 64-116.
RX MEDLINE=75183340; PubMed=4142749;
RA Jaton J.-C.;
RT "Completion of the analysis of the primary structure of the variable
RT domain of a homogeneous rabbit antibody to type III pneumococcal
RL polysaccharide.";
RL Biochem. J. 143:723-732(1974).
CC -1- MISCELLANEOUS: THIS GAMMA CHAIN WAS OBTAINED FROM ANTIBODY TO TYPE
CC III PNEUMOCOCCI AND WAS ISOLATED FROM THE SERUM OF A SINGLE
CC RABBIT.
DR PIR; A02102; GARB15.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region.
FT MOD_RES 1 PYRROLIDONE CARBOXYLIC ACID.
FT NON_TER 116
SQ SEQUENCE 116 AA; 12349 MW; 95C6FAC93C788C42 CRC64;

Query Match 63.8%; Score 37; DB 1; Length 116;
Best Local Similarity 77.8%; Pred. No. 8;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GFTWSSYDM 9
Db 25 GFSLSYDM 33

RESULT 10
HV2B_RABIT
ID HV2B_RABIT STANDARD; PRT; 117 AA.
AC P01828;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-A2 region K-25.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE.
RX MEDLINE=76039436; PubMed=241319;
RA Jaton J.-C.;
RT "Comparison of the amino acid sequences of the variable domains of
RT two homogeneous rabbit antibodies to type III pneumococcal
RT polysaccharide.";
RL Biochem. J. 147:235-247(1975).
CC -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM ANTIBODY TO TYPE III
CC PNEUMOCOCCI AND WAS ISOLATED FROM THE SERUM OF A SINGLE RABBIT.
DR PIR; A02104; GARB2K.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region.

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FT MOD-RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT DISULFID 21 91
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12580 MW; 28DD87FDB7AE9B8 CRC64;

Query Match 63.8%; Score 37; DB 1; Length 117;
 Best Local Similarity 70.0%; Pred. No. 8.9;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
 ||:| ||||
 Db 25 GFSLSGYDMS 34

RESULT 11

PLC_STAUAU STANDARD; PRT; 311 AA.
 AC P45723;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 1-phosphatidylinositol phosphodiesterase precursor (EC 3.1.4.10)
 DE (Phosphatidylinositol-specific phospholipase C) (PI-PLC).
 GN PLC.
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Newman;
 RX MEDLINE=94041628; PubMed=8225585;
 RA Daugherty S., Low M.G.;
 RT "Cloning, expression, and mutagenesis of
 RT phosphatidylinositol-specific phospholipase C from Staphylococcus
 RT aureus: a potential staphylococcal virulence factor.";
 RL Infect. Immun. 61:5078-5089(1993).
 CC -!- FUNCTION: CLEAVES GLYCOPHOSPHATIDYLINOSITOL (GPI) AND
 CC PHOSPHATIDYLINOSITOL (PI) ANCHORS BUT NOT PI PHOSPHATES. POTENTIAL
 CC VIRULENCE FACTOR.
 CC -!- CATALYTIC ACTIVITY: 1-phosphatidyl-D-myo-inositol = D-myo-
 CC inositol 1,2-cyclic phosphate + diacylglycerol.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: TO OTHER BACTERIAL PI-PLC.
 CC -!- SIMILARITY: DOMAIN X IS CONSERVED IN DIFFERENT FORMS OF PLC AND IS
 CC ESSENTIAL FOR CATALYTIC ACTIVITY.
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DR EMBL; L19298; AAA16442.1; -;
 DR HSSP; P14262; 2PTD.
 DR InterPro; IPR000909; PI_PLC_Xdom.
 DR Pfam; PF00388; PI-PLC-X; 1.
 DR SMART; SM00148; PLCXC; 1.
 DR PROSITE; PS50007; PIPIC_X_DOMAIN; 1.
 KW Hydrolase; Lipid degradation; Signal; Virulence.
 FT SIGNAL 1 26
 FT CHAIN 27 311 1-PHOSPHATIDYLINOSITOL PHOSPHODIESTERASE.
 FT DOMAIN 27 176 DOMAIN X.
 FT ACT_SITE 40 40 GENERAL BASE (BY SIMILARITY).
 FT ACT_SITE 90 90 GENERAL ACID (BY SIMILARITY).
 SQ SEQUENCE 311 AA; 35235 MW; CC5A1F830776741F CRC64;

Query Match 63.8%; Score 37; DB 1; Length 311;
 Best Local Similarity 62.5%; Pred. No. 23;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTWSSYD 8

Db 293 GYTWPCYD 300
 ||:| ||

RESULT 12

GATL_STRPN STANDARD; PRT; 491 AA.
 AC Q97E15;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Galactose-1-phosphate uridylyltransferase 1 (EC 2.7.7.10) (Gal-1-P
 DE uridylyltransferase 1).
 GN GATL OR SP1829.
 OS Streptococcus pneumoniae.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1313;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TIGR4;
 RX MEDLINE=21357209; PubMed=11463916;
 RA Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
 RA Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,
 RA Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
 RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
 RA Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,
 RA McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.,
 RA Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
 RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
 RT "Complete genome sequence of a virulent isolate of Streptococcus
 RT pneumoniae.";
 RL Science 293:498-506(2001).
 CC -!- CATALYTIC ACTIVITY: UDP + alpha-D-galactose 1-phosphate =
 CC diphosphate + UDP-galactose.
 CC -!- PATHWAY: Galactose metabolism; second step.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
 CC -!- SIMILARITY: BELONGS TO THE GALACTOSE-1-PHOSPHATE
 CC URIDYLYLTRANSFERASE FAMILY 2.
 CC -----
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DR EMBL; AE007475; AAK75902.1; -;
 DR TIGR; SP1829; -;
 DR InterPro; IPR000880; GalP_UDP_transf.
 DR Pfam; PF01087; GalP_UDP_transf; 1.
 DR Pfam; PF02744; GalP_UDP_tr_C; 1.
 DR TIGRFAMS; TIGR01239; galT_2; 1.
 DR PROSITE; PS01163; GAL_P_UDP_TRANSF_II; FALSE_NEG.
 KW Transferase; Nucleotidyltransferase; Galactose metabolism;
 KW Complete proteome.
 SQ SEQUENCE 491 AA; 56381 MW; A11F78D61E4D4B09 CRC64;

Query Match 63.8%; Score 37; DB 1; Length 491;
 Best Local Similarity 85.7%; Pred. No. 37;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 WSSYDMS 10
 ||||:|
 Db 95 WSSYDIS 101

RESULT 13

HV3D_HUMAN
 ID HV3D_HUMAN STANDARD; PRT; 115 AA.
 AC P01765;
 DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DE 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V-III region TIL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=78005528; PubMed=409716;
 RT Wang A.-C., Wang I.Y., Fudenberg H.H.;
 RT "Immunoglobulin structure and genetics. Identity between variable
 RT regions of a mu and a gamma2 chain.";
 RL J. Biol. Chem. 252:7192-7199(1977).
 CC -!- MISCELLANEOUS: THE SEQUENCES OF THE V REGIONS OF THE HEAVY CHAINS
 CC OF IGM AND IGG2 ISOLATED FROM A SINGLE PATIENT WITH BICLONAL
 CC GAMMOPATHY ARE IDENTICAL. THEIR LIGHT CHAINS ARE APPARENTLY ALSO
 CC IDENTICAL.
 CC
 DR PIR: A02048; H3HUTL.
 DR HSSP: P01772; 2FB4.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; Ig_v; 1.
 KW Immunoglobulin V region.
 FT NON_TER 115 115
 SQ SEQUENCE 115 AA; 12356 MW; 4DCC67D179F62326 CRC64;

 Query Match 62.1%; Score 36; DB 1; Length 115;
 Best Local Similarity 70.0%; Pred. No. 13;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

 QY 1 GFTWSSYDMS 10
 |||:|:|
 DB 26 GFTFTYVMS 35

 RESULT 14
 DIAC_RAT
 ID DIAC_RAT STANDARD; PRT; 367 AA.
 AC Q01460;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Di-N-acetylchitinobiose precursor (EC 3.2.1.-).
 GN CTBS OR CTB.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 24-32.
 RC TISSUE=Liver;
 RX MEDLINE=92406917; PubMed=1527079;
 RA Fisher K.J., Aronson N.N. Jr.;
 RT "Cloning and expression of the cDNA sequence encoding the lysosomal
 RT glycosidase di-N-acetylchitinobiose.";
 RL J. Biol. Chem. 267:19607-19616(1992).
 CC -!- FUNCTION: INVOLVED IN THE DEGRADATION OF ASPARAGINE-LINKED
 CC GLYCOPROTEINS. HYDROLYZE OF N-ACETYL-BETA-D-GLUCOSAMINE
 CC (1-4)-N-ACETYLGLUCOSAMINE CHITOBIOSE CORE FROM THE REDUCING END
 CC OF THE BOND, IT REQUIRES PRIOR CLEAVAGE BY GLYCOSYLASPARAGINASE.
 CC -!- SUBCELLULAR LOCATION: Lysosomal.
 CC -!- SIMILARITY: BELONGS TO FAMILY 18 OF GLYCOSYL HYDROLASES.
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 CC -----*-----

DR EMBL; M95768; AAA40924.1; -.
 DR PIR; S27882; S27882.
 DR PIR; C44102; C44102.
 DR InterPro: IPR001579; Chitinase_18/2.
 DR InterPro: IPR001223; Glyco_hydro_18.
 DR Pfam: PF00704; Glyco_hydro_18; 1.
 DR ProDom: PD000471; Glyco_hydro_18; 1.
 DR ProSITE: PS01095; CHITINASE_18; 1.
 KW Hydrolase; Glycosidase; Signal; Lysosome; Glycoprotein.
 FT SIGNAL 1 23
 FT CHAIN 24 367 DI-N-ACETYLCHITOBIOSE.
 FT ACT_SITE 128 128 PROTON DONOR (BY SIMILARITY).
 FT CARBOHYD 100 100 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 178 178 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 213 213 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 247 247 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 284 284 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 367 AA; 41531 MW; 29AB8BE4FC157C16 CRC64;

 Query Match 62.1%; Score 36; DB 1; Length 367;
 Best Local Similarity 75.0%; Pred. No. 41;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

 QY 3 TWSSYDMS 10
 |||:|:|
 DB 54 TWKSYDWS 61

 RESULT 15
 DIAC_HUMAN
 ID DIAC_HUMAN STANDARD; PRT; 385 AA.
 AC Q01459;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Di-N-acetylchitinobiose precursor (EC 3.2.1.-).
 GN CTBS OR CTB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=92406917; PubMed=1527079;
 RA Fisher K.J., Aronson N.N. Jr.;
 RT "Cloning and expression of the cDNA sequence encoding the lysosomal
 RT glycosidase di-N-acetylchitinobiose.";
 RL J. Biol. Chem. 267:19607-19616(1992).
 CC -!- FUNCTION: INVOLVED IN THE DEGRADATION OF ASPARAGINE-LINKED
 CC GLYCOPROTEINS. HYDROLYZE OF N-ACETYL-BETA-D-GLUCOSAMINE
 CC (1-4)-N-ACETYLGLUCOSAMINE CHITOBIOSE CORE FROM THE REDUCING END
 CC OF THE BOND, IT REQUIRES PRIOR CLEAVAGE BY GLYCOSYLASPARAGINASE.
 CC -!- SUBCELLULAR LOCATION: Lysosomal.
 CC -!- SIMILARITY: BELONGS TO FAMILY 18 OF GLYCOSYL HYDROLASES.
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 CC -----*-----
 DR EMBL; M95767; AAA35684.1; -.
 DR EMBL; AF085706; AAC35852.1; -.
 DR EMBL; AF085700; AAC35852.1; JOINED.
 DR EMBL; AF085701; AAC35852.1; JOINED.

DR EMBL; AF085702; AAC35852.1; JOINED.
DR EMBL; AF085703; AAC35852.1; JOINED.
DR EMBL; AF085704; AAC35852.1; JOINED.
DR EMBL; AF085705; AAC35852.1; JOINED.
DR PIR; A44102; A44102.
DR PIR; S27959; S27959.
DR Genew; HGNC:2496; CTBS.
DR MIN; 600873; -.
DR InterPro; IPR001579; Chitinase_18/2.
DR InterPro; IPR001223; Glyco_hydro_18.
DR Pfam; PF00704; Glyco_hydro_18; 1.
DR ProDom; PD000471; Glyco_hydro_18; 1.
DR PROSITE; PS01095; CHITINASE_18; 1.
KW Hydrolase; Glycosidase; Signal; Lysosome; Glycoprotein.
FT SIGNAL 1 38
FT CHAIN 39 385
FT ACT_SITE 143 143
FT CARBOHYD 193 193
FT CARBOHYD 228 228
FT CARBOHYD 262 262
FT CARBOHYD 299 299
SQ SEQUENCE 385 AA; 43759 MW; 0A9D14C8B52EE CRC64;

Query Match 62.1%; Score 36; DB 1; Length 385;
Best Local Similarity 75.0%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TWSSYDMS 10
Db 69 TWKSYDWS 76

Search completed: November 18, 2002, 17:33:19
Job time : 3.45098 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:01 ; Search time 10.4412 Seconds
(without alignments)
197.341 Million cell updates/sec

Title: US-09-016-061-50
Perfect score: 58
Sequence: 1 GFTWSSYDMS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: sp_archea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriap.*
- 17: sp_archeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	41	70.7	119	11	Q920E7 mus musculus
2	41	70.7	325	5	O02322 caenorhabdi
3	41	70.7	486	11	Q91207 mus musculus
4	40	69.0	104	17	Q8TUF5
5	40	69.0	437	11	Q9RIA4
6	40	69.0	487	11	Q99KA4
7	39	67.2	99	16	Q8VK94 mycobacteri
8	39	67.2	118	4	Q9UL91
9	39	67.2	471	4	Q8TC77
10	39	67.2	511	16	Q9PM91
11	38	65.5	95	4	Q9ULB6
12	38	65.5	147	4	Q9Y509
13	38	65.5	228	5	O02109
14	38	65.5	327	10	Q9SZ60
15	38	65.5	335	10	O64692
16	38	65.5	356	10	O04710

17	38	65.5	375	5	Q23244
18	38	65.5	412	16	Q92VB2
19	38	65.5	452	5	Q95ZN7
20	38	65.5	571	12	Q8QQV4
21	38	65.5	581	17	Q8TV69
22	38	65.5	703	12	Q8QQV5
23	38	65.5	1857	17	Q8TM75
24	38	65.5	2408	5	Q22184
25	37	63.8	113	4	Q9UL90
26	37	63.8	140	10	Q9ARP0
27	37	63.8	230	10	Q94LI3
28	37	63.8	256	10	Q9S7P0
29	37	63.8	272	5	Q9GS05
30	37	63.8	286	3	O60065
31	37	63.8	309	5	Q9N7W6
32	37	63.8	356	16	Q986F3
33	37	63.8	476	5	Q9V935
34	37	63.8	491	16	Q97P15
35	37	63.8	493	5	Q8T8T5
36	37	63.8	510	10	Q9ST51
37	37	63.8	537	3	Q96TU3
38	37	63.8	537	3	O42801
39	37	63.8	613	4	Q8WUK1
40	37	63.8	702	10	Q9LNL6
41	37	63.8	889	5	Q9NEE9
42	37	63.8	1156	5	O61137
43	36	62.1	116	4	Q9UL93
44	36	62.1	134	17	Q97UQ4
45	36	62.1	134	17	Q973W3

ALIGNMENTS

RESULT 1

Q920E7 PRELIMINARY; PRT; 119 AA.
ID Q920E7
AC Q920E7;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Pterin-mimicking anti-idiotope heavy chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Atkin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.;
RT "Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed
in Mammalian Cells."
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307937; AAL09421.1; -;
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig; 1.
FT NON_TER 1
FT NON_TER 119
SQ SEQUENCE 119 AA; 13025 MW; F6E904044381CA7C CRC64;

Query Match 70.7%; Score 41; DB 11; Length 119;
Best Local Similarity 80.0%; Pred. No. 7.2;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
||| ||| ||
Db 26 GFTFSSYGMS 35

RESULT 2

O02322 PRELIMINARY; PRT; 325 AA.
ID O02322
AC O02322;


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DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE T2265.1 protein.
GN T2265.1
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Smye R.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; Z81127; CAB03386.1; -.
DR InterPro; IPR004129; GDPD.
DR Pfam; PF03009; GDPD; 1.
SQ SEQUENCE 325 AA; 36754 MW; EE9D338E16F8AC9F CRC64;

Query Match 70.7%; Score 41; DB 5; Length 325;
Best Local Similarity 60.0%; Pred. No. 21;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
|||||
DB 218 GFTWRSELS 227

RESULT 3
ID Q91207 PRELIMINARY; PRT; 486 AA.
AC Q91207;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical 52.7 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC010324; AAH10324.1; -.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein; Immunoglobulin domain.
SQ SEQUENCE 486 AA; 52682 MW; 4FEF835125DA870B CRC64;

Query Match 70.7%; Score 41; DB 11; Length 486;
Best Local Similarity 70.0%; Pred. No. 33;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
|||||
DB 45 GFSFTSYDMS 54

RESULT 4
ID Q8TUF5 PRELIMINARY; PRT; 104 AA.
AC Q8TUF5;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)

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DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Archaeal transcription factor S.
GN MA0112.
OS Methanosarcina acetivorans.
OC Archaea; Euryarchaeota; Methanococci; Methanosarcinales;
OC Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2214;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C2A / ATCC 35395 / DSM 2834;
RX MEDLINE=21929760; PubMed=11932238;
RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,
RA FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,
RA Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R.,
RA Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,
RA Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A.,
RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
RA Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,
RA Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,
RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
RA Metcalf W.W., Birren B.;
RT "The genome of Methanosarcina acetivorans reveals extensive metabolic
RT and physiological diversity.";
RL Genome Res. 12:532-542(2002).
DR EMBL; AE010668; AAM03566.1; -.
KW Complete proteome.
SQ SEQUENCE 104 AA; 11883 MW; 627BAB427F735F6D CRC64;

Query Match 69.0%; Score 40; DB 17; Length 104;
Best Local Similarity 75.0%; Pred. No. 9.4;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTWSSYD 8
|||||
DB 97 GFTWREYD 104

RESULT 5
ID Q9R1A4 PRELIMINARY; PRT; 437 AA.
AC Q9R1A4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Gammaal heavy chain of Mab7 (Fragment).
GN IGH-4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT antibody (Mab 7, its light and heavy chains) and construction of a
RT single chain antibody (scFv).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF152372; AAD40243.1; -.
DR HSSP; P01842; 7FAB.
DR MGD; MGI:96446; Igh-4.
DR InterPro; IPR003600; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_Like; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR NON_TER 1
FT NON_TER 437
SQ SEQUENCE 437 AA; 48142 MW; 5C3A7BB3EE7D697C CRC64;

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```
Query Match          69.0%; Score 40; DB 11; Length 437;
Best Local Similarity 80.0%; Pred. No. 44;
Matches      8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy  1 GFTWSSYDMS 10
    |||:|||||
Db  25 GFTFSSYAMS 34

RESULT 6
Q99KA4      PRELIMINARY;      PRT;      487 AA.
AC  Q99KA4;
DT  01-JUN-2001 (TrEMBLrel. 17, Created)
DT  01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT  01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE  Hypothetical 52.6 kDa protein.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Strausberg R.;
RL  Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR  EMBL; BC004786; AAH04786.1; -.
DR  HSP; P01810; 2FBJ.
DR  InterPro; IPR003599; Ig.
DR  InterPro; IPR003597; Ig.cl.
DR  InterPro; IPR003600; Ig.like.
DR  InterPro; IPR003006; Ig_MHC.
DR  InterPro; IPR003596; Ig_V.
DR  Pfam; PF00047; Ig; 4.
DR  SMART; SM00409; IG; 3.
DR  SMART; SM00407; IGcl; 3.
DR  SMART; SM00406; IGV; 1.
DR  SMART; SM00410; IG_Like; 1.
DR  PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW  Hypothetical protein.
SQ  SEQUENCE 487 AA; 52554 MW; 70C8E96DB333077B CRC64;

Query Match          69.0%; Score 40; DB 11; Length 487;
Best Local Similarity 80.0%; Pred. No. 49;
Matches      8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy  1 GFTWSSYDMS 10
    |||:|||||
Db  45 GFTFSSYAMS 54

RESULT 7
Q8VK94      PRELIMINARY;      PRT;      99 AA.
AC  Q8VK94;
DT  01-MAR-2002 (TrEMBLrel. 20, Created)
DT  01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT  01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE  Hypothetical protein Mt1040.1.
GN  Mt1040.1.
OS  Mycobacterium tuberculosis.
OC  Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC  Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX  NCBI_TaxID=1773;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  STRAIN=CDC 1551 / OSHKOSH;
RA  Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA  Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
RA  Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
RA  Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA  Bishai W.;
RT  "Whole genome comparison of Mycobacterium tuberculosis clinical and
    laboratory strains.";
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RL  Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AS006987; AAK45291.1; -.
DR  TIGR; MT1040; -.
KW  Hypothetical protein.
SQ  SEQUENCE 99 AA; 11069 MW; BA2546A358B75BDB CRC64;

Query Match          67.2%; Score 39; DB 16; Length 99;
Best Local Similarity 66.7%; Pred. No. 13;
Matches      6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy  1 GFTWSSYDM 9
    ||:|||||
Db  32 GFSWSAYRM 40

RESULT 8
Q9UL91      PRELIMINARY;      PRT;      118 AA.
AC  Q9UL91;
DT  01-MAY-2000 (TrEMBLrel. 13, Created)
DT  01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT  01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE  Myosin-reactive immunoglobulin heavy chain variable region
    (Fragment).
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  MEDLINE-98277139; PubMed-9614934;
RA  Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA  Young D.C.;
RT  "Myosin-reactive autoantibodies in rheumatic carditis and normal
    fetus.";
RL  Clin. Immunol. Immunopathol. 87:184-192(1998).
DR  EMBL; AF035023; AAD56259.1; -.
DR  HSP; P01772; 2FB4.
DR  InterPro; IPR003006; Ig_MHC.
DR  InterPro; IPR003596; Ig_V.
DR  Pfam; PF00047; Ig; 1.
DR  SMART; SM00406; IGV; 1.
DR  NON_TER 1
FT  NON_TER 118
SQ  SEQUENCE 118 AA; 12843 MW; D0633949F2AC149D CRC64;

Query Match          67.2%; Score 39; DB 4; Length 118;
Best Local Similarity 70.0%; Pred. No. 16;
Matches      7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy  1 GFTWSSYDMS 10
    |||:|||||
Db  26 GFTFSSYSMN 35

RESULT 9
Q8TC77      PRELIMINARY;      PRT;      471 AA.
AC  Q8TC77;
DT  01-JUN-2002 (TrEMBLrel. 21, Created)
DT  01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT  01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE  Hypothetical 51.8 kDa protein.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  TISSUE=SPLEEN;
RA  Strausberg R.;
RL  Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR  EMBL; BC024289; AAH24289.1; -.

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KW Hypothetical protein.
SQ SEQUENCE 471 AA, 51791 MW, 388F7F4CF588660E CRC64;

Query Match      67.2%; Score 39; DB 4; Length 471;
Best Local Similarity 70.0%; Pred. No. 71;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
   |||:|||||
Db 45 GFTSSYSMN 54

RESULT 10
Q9PM91
ID Q9PM91 PRELIMINARY; PRT; 511 AA.
AC Q9PM91;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative peptide ABC-transport system periplasmic peptide-binding
DE protein.
DE CJI584C.
GN CJI584C.
OS Campylobacter jejuni.
OC Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
OC Campylobacter.
OX NCBI_TaxID=197;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NTC 11168;
RX MEDLINE=20150912; PubMed=10688204;
RA Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
RA Basham D., Chillingworth T., Davies R.M., Feltham T., Holt R.D.,
RA Jags K., Karyshev A.V., Moule S., Pallen M.J., Penn C.W.,
RA Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
RA Whitehead S., Barrett B.G.;
RT "The genome sequence of the food-borne pathogen Campylobacter jejuni
RT reveals hypervariable sequences."
RL Nature 403:665-668(2000).
DR EMBL; AL139079; CAB73572.1; -.
DR InterPro; IPR002052; N6.Mtase.
DR InterPro; IPR000914; SBP_bac_5.
DR Pfam; PF00496; SBP_bac_5; 1.
DR PROSITE; PS00092; N6_MTASE; UNKNOWN_1.
DR Complete proteome.
KW SEQUENCE 511 AA; 58856 MW; 7139374B316CBBEB CRC64;

Query Match      67.2%; Score 39; DB 16; Length 511;
Best Local Similarity 60.0%; Pred. No. 78;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
   |||:|||||
Db 501 GFTWVIEWS 510

RESULT 11
Q9ULB6
ID Q9ULB6 PRELIMINARY; PRT; 95 AA.
AC Q9ULB6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Immunoglobulin heavy chain (Fragment).
DE VH.
GN VH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tange Y., Kayano H.;
RT "Human VH gene sequence."
RT Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.

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DR EMBL; AB035268; BAA87067.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 95
SQ SEQUENCE 95 AA; 10527 MW; 90A8C6D16D22574A CRC64;

Query Match      65.5%; Score 38; DB 4; Length 95;
Best Local Similarity 80.0%; Pred. No. 19;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
   |||:|||||
Db 25 GFTSSYWS 34

RESULT 12
Q9Y509
ID Q9Y509 PRELIMINARY; PRT; 147 AA.
AC Q9Y509;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE VH3 protein (Fragment).
DE VH3.
GN VH3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96071149; PubMed=7475288;
RA Cao J., Vescio R.A., Rettig M.B., Hong C.H., Kim A., Lee J.C.,
RA Lichtenstein A.K., Berenson J.R.;
RT "A CD10-positive subset of malignant cells is identified in multiple
RT myeloma using PCR with patient-specific immunoglobulin gene primers."
RL Leukemia 9:1948-1953(1995).
DR EMBL; S80860; AAD14339.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 147
SQ SEQUENCE 147 AA; 15768 MW; 8489FCAAA7BC925C CRC64;

Query Match      65.5%; Score 38; DB 4; Length 147;
Best Local Similarity 70.0%; Pred. No. 31;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
   |||:|||||
Db 26 GFTSTYGMS 35

RESULT 13
O02109
ID O02109 PRELIMINARY; PRT; 228 AA.
AC O02109;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE W08F4.3 protein.
DE W08F4.3.
GN W08F4.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN=BRISTOL N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favell A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Ropota A., Saunders D., Showkneen R.,
RA Smalton N., Smith A., Sonhammer E., Staden R., Sulston J.,
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Nature 368:32-38(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Madsen C., Graves T.;
RT "The sequence of C. elegans cosmid W08F4.";
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston R.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF000266; RAC71167.1; -. 2EC0801189EB1985 CRC64;
SQ SEQUENCE 228 AA; 25615 MW; 2EC0801189EB1985 CRC64;

Query Match 65.5%; Score 38; DB 5; Length 228;
Best Local Similarity 60.0%; Pred. No. 49;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
DB 24 GLRWKSYDIS 33

RESULT 14
ID Q9SZ60 PRELIMINARY; PRT; 327 AA.
AC Q9SZ60;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Hypothetical 35.8 kDa protein.
GN F16213.20 OR AT4G11950.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Bevan M., Hilbert H., Braun M., Holzer E., Brandt A., Duesterhoeft A.,
RA Bancroft I., Mewes H.W., Mayer K.F.X., Schueller C.;
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Hilbert H., Braun M., Holzer E., Brandt A., Duesterhoeft A.,
RA Mewes H.W., Lemcke K., Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL049638; CAB40936.1; -.
DR EMBL: AL161533; CAB78238.1; -.
KW Hypothetical protein.

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SQ SEQUENCE 327 AA; 35845 MW; B2BB47DF4A83E635 CRC64;

Query Match 65.5%; Score 38; DB 10; Length 327;
Best Local Similarity 85.7%; Pred. No. 73;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTWSSY 7
DB 107 GFNWSSY 113

RESULT 15
ID O64692 PRELIMINARY; PRT; 335 AA.
AC O64692;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative GA4 protein.
GN T31E10.11 OR GA2OX3.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Rounsley S.D., Kaul S., Lin X., Ketchum K.A., Crosby M.L.,
RA Brandon R.C., Sykes S.M., Mason T.M., Kerlavage A.R., Adams M.D.,
RA Somerville C.R., Venter J.C.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99218343; PubMed=10200325;
RA Thomas S.G., Phillips A.L., Hedden P.;
RT "Molecular cloning and functional expression of gibberellin 2-
RT oxidases, multifunctional enzymes involved in gibberellin
RT deactivation.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:4698-4703(1999).
DR EMBL: AC004077; AAM14908.1; -.
DR EMBL: AJ132437; CAB41009.1; -.
DR InterPro: IPR005123; 2OG-FeII_Oxy.
DR Pfam: PF03171; 2OG-FeII_Oxy; 1.
SQ SEQUENCE 335 AA; 38216 MW; 181F6EAAEEIC331 CRC64;

Query Match 65.5%; Score 38; DB 10; Length 335;
Best Local Similarity 66.7%; Pred. No. 75;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FTWSSYDMS 10
DB 302 FTWSQYKLS 310

Search completed: November 18, 2002, 17:40:35
Job time : 11.4912 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:21:57 ; Search time 13.8235 Seconds
(without alignments)
96.394 Million cell updates/sec

Title: US-09-016-061-50
Perfect score: 58
Sequence: 1 GFTWSSYDMS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	58	100.0	10	AAW76015	LM609 grafted anti
2	58	100.0	10	AAW76015	Mutant VH CDRI pep
3	48	82.8	10	AAW76007	LM609 grafted anti
4	48	82.8	10	AAW76007	LM609 VH CDRI pep
5	48	82.8	117	AAW76001	vitaxin antibody h
6	48	82.8	117	AAW76001	A heavy chain vari
7	48	82.8	117	AAW76001	vitaxin heavy chai
8	45	77.6	117	AAW86137	Protein sequence o
9	45	77.6	128	AAW54000	Anti-CD4 antibody
10	45	77.6	134	AAW24713	Sequence encoded b

11	45	77.6	256	23	ABP45381	Human BLYS binding
12	45	77.6	256	23	ABP46108	Human BLYS binding
13	45	77.6	466	13	AAW24812	Sequence encoded b
14	44	75.9	97	21	AAW40112	Anti-hIL12 antibod
15	44	75.9	102	22	ABW39276	Peptide #6782 enco
16	44	75.9	102	22	AAW59940	Human brain expres
17	44	75.9	102	22	AAW72535	Human bone marrow
18	44	75.9	102	22	AAW32779	Peptide #6816 enco
19	44	75.9	102	22	ABG42355	Human peptide enco
20	44	75.9	139	18	AAW21652	Humanised reshaped
21	44	75.9	252	23	ABP45601	Human BLYS binding
22	44	75.9	470	23	AAU74298	Anti-human AILIM m
23	44	75.9	470	23	AAU74300	Anti-human AILIM m
24	43	74.1	117	19	AAW76003	LM609 antibody hea
25	43	74.1	117	20	AAW06381	Murine monoclonal
26	43	74.1	117	22	AAW63589	A heavy chain vari
27	43	74.1	117	22	AAW61361	Antibody LM609 hea
28	43	74.1	130	20	AAW06379	Murine monoclonal
29	43	74.1	239	14	AAW34511	Fv(TU25). Homo sa
30	43	74.1	247	16	AAW11917	Murine MAb SK48-E2
31	42	72.4	10	19	AAW76016	LM609 grafted anti
32	42	72.4	10	22	AAW61374	Mutant VH CDRI pep
33	42	72.4	96	23	ABG60417	Selective targetin
34	42	72.4	115	22	AAW69601	Huntingtin minimal
35	42	72.4	117	20	AAW86141	Protein sequence o
36	42	72.4	119	16	AAW11919	Humanised MAb SK48
37	42	72.4	123	19	AAW53998	Anti-CD4 antibody
38	42	72.4	239	22	AAW69603	Huntingtin intrabo
39	41	70.7	10	22	AAU07457	Synthetic peptide
40	41	70.7	87	22	AAE06990	Mouse germline hea
41	41	70.7	89	22	AAE06985	Mouse germline hea
42	41	70.7	97	21	AAW40089	Anti-hIL12 antibod
43	41	70.7	98	19	AAW59614	Anti-RSV F protein
44	41	70.7	98	21	AAW40113	Anti-hIL12 antibod
45	41	70.7	98	22	AAE06975	Mouse germline hea

ALIGNMENTS

RESULT 1
AAW76015
ID AAW76015 standard; Protein; 10 AA.
XX
AC AAW76015;
XX
DT 02-NOV-1998 (first entry)
XX
DE LM609 grafted antibody V-H region CDRI protein fragment #3.
XX
KW Vitaxin; antibody; variable region; heavy chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
XX
OS Mus sp.
XX
PN WO9833919-A2.
XX
PD 06-AUG-1998.
XX
PF 30-JAN-1998; 98WO-US01826.
XX
PR 30-JAN-1997; 97US-0791391.
XX
PA (IXSY-) IXSYS INC.
XX
PI Glaser SM, Huse WD;
XX
DR WPI; 1998-437472/37.
DR N-PSDB; AAW49852.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
PS Claim 60; Page 41; 129pp; English.
XX
CC AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
CC antibodies contain non-murine framework regions so are suitable for use
CC in humans. Enhanced types of LM609 have affinity more than 90 times
CC greater than that of parent the parent antibody.
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 58; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
|||||
Db 1 GFTWSSYDMS 10

RESULT 2
AAB61373
ID AAB61373 standard; peptide; 10 AA.
XX
AC AAB61373;
XX
DT 03-APR-2001 (first entry)
XX
DE Mutant VH CDR1 peptide #2.
XX
KW LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
KW inflammatory; cancer; retina; restenosis; osteoporosis.
XX
OS Unidentified.
XX
XX WO200078815-A1.
XX
PD 28-DEC-2000.
XX
XX 23-JUN-2000; 2000WO-US17454.
XX
XX 24-JUN-1999; 99US-0339922.
XX
PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX
XX Huse WD, Wu H;
PI
PI WPI; 2001-050110/06.
XX
XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
PT osteoporosis -
XX
XX Disclosure; Page 41; 132pp; English.
XX
XX The present invention relates to enhanced LM609 grafted antibodies
CC exhibiting selective binding affinity to alphavbeta_3 integrin or
CC their functional fragments. The antibodies or their functional
CC fragments can be used in the diagnosis and treatment of
CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory

CC diseases (such as psoriasis and chronic articular rheumatism),
CC disorders associated with inappropriate or inopportune invasion of
CC vessels (such as diabetic retinopathy, neovascular glaucoma and
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
CC diseases (such as macular degeneration), restenosis and
CC osteoporosis.
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 58; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
|||||
Db 1 GFTWSSYDMS 10

RESULT 3
AAW76007
ID AAW76007 standard; Protein; 10 AA.
XX
AC AAW76007;
XX
DT 02-NOV-1998 (first entry)
XX
DE LM609 grafted antibody V-H region CDR1 protein fragment #1.
XX
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
XX
OS Mus sp.
XX
PN WO9833919-A2.
XX
PD 06-AUG-1998.
XX
PF 30-JAN-1998; 98WO-US01826.
XX
PR 30-JAN-1997; 97US-0791391.
XX
PA (IXSY-) IXSYS INC.
XX
PI Glaser SM, Huse WD;
XX
XX WPI; 1998-437472/37.
DR N-PSDB; AAV49844.
XX
XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
PS Disclosure; Page 40; 129pp; English.
XX
XX AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
CC antibodies contain non-murine framework regions so are suitable for use
CC in humans. Enhanced types of LM609 have affinity more than 90 times
CC greater than that of parent the parent antibody.
XX
SQ Sequence 10 AA;

AC	AAW76001;
XX	
XX	02-NOV-1998 (first entry)
XX	
DE	Vitaxin antibody heavy chain variable region protein fragment.
XX	
KW	Vitaxin; antibody; variable region; heavy chain; light chain; integrin; LM609; inhibitor; integrin-mediated signal transduction; treatment; diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy; neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine; macular degeneration; osteoporosis.
KW	
XX	
OS	Mus sp.
XX	
XX	WO9833919-A2.
XX	
XX	06-AUG-1998.
PD	
XX	
PF	30-JAN-1998; 98WO-US01826.
XX	
XX	30-JAN-1997; 97US-0791391.
PR	
XX	
XX	(IXSY-) IXSYS INC.
PA	
XX	
PI	Glaser SM, Huse WD;
XX	
XX	WPI: 1998-437472/37.
DR	
DR	N-PSDB; AAV49820.
XX	
XX	
PT	Humanised antibody, Vitaxin, that binds selectively to alphavbeta3 integrin - and related grafted antibodies based on murine monoclonal LM609, also related nucleic acid, used to treat, prevent or diagnose angiogenesis or restenosis
PT	
XX	
PS	Claim 1; Fig 1a; 129pp; English.
XX	
CC	This sequence represents a fragment of the vitaxin antibody variable heavy chain region. Vitaxin and the antibody LM609 bind selectively to integrin alphavbeta3 and can be used to inhibit binding of alphavbeta3 to a ligand and thus block integrin-mediated signal transduction. This is useful in the treatment, prevention and diagnosis of alphavbeta3-mediated disease, specifically angiogenesis and restenosis (but also e.g. (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis etc.). The antibodies contain non-murine framework regions so are suitable for use in humans. Enhanced types of LM609 have affinity more than 90 times greater than that of parent the parent antibody.
CC	
XX	Sequence 117 AA;
XX	
Qy	Query Match 82.8%; Score 48; DB 19; Length 117;
XX	Best Local Similarity 90.0%; Pred. No. 0.97;
XX	Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps
DB	
XX	
Qy	1 GFTWSSYDMS 10
XX	
DB	26 GFTSSYDMS 35
XX	
RESULT 6	
AAG63587	
ID	AAG63587 standard; Protein; 117 AA.
XX	
AC	AAG63587;
XX	
DT	15-OCT-2001 (first entry)
XX	
DE	A heavy chain variable region of LM609 grafted antibody.
XX	
KW	Grafted antibody; LM609; integrin; alphavbeta3; inflammatory disorder; chronic articular rheumatism; psoriasis; diabetic retinopathy; neovascular glaucoma; capillary proliferation; atherosclerotic plaque; cancer.
KW	

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XX OS Synthetic.
XX Mus sp.
XX PN US2001011125-A1.
XX PD 02-AUG-2001.
XX XX
XX PF 30-JAN-1997; 97US-0790540.
XX PR 30-JAN-1997; 97US-0790540.
XX PA (HUSE/) HUSE W D.
XX PI Huse WD;
XX WPI; 2001-496171/54.
XX N-PSDB; AAH74623.
XX
XX New LM609 grafted antibody exhibiting selective binding affinity to
XX alphavbeta3, comprising at least one LM609 grafted heavy and light
XX chain polypeptide, useful for diagnosing and treating e.g. inflammatory
XX disorders or cancer.
XX Claim 1; Fig 1A; 25pp; English.
XX
XX The present sequence represents the heavy chain variable region of the
XX grafted monoclonal antibody LM609. LM609 is a murine antibody which
XX specifically recognises the integrin alphavbeta3, and inhibits its
XX functional activity. The LM609 grafted antibody has the
XX complementarity determining regions (CDRs) substituted into a non-murine
XX framework. Nucleic acids encoding LM609 grafted heavy and light chain
XX polypeptides and fragments are useful in diagnostic and therapeutic
XX purposes, such as in the production of LM609 grafted antibodies and
XX fragments having binding specificity and inhibitory activity against
XX the integrin alphavbeta3. The antibody can be used for the diagnosis
XX or treatment of alphavbeta3-mediated diseases (e.g. inflammatory
XX disorders, chronic articular rheumatism, psoriasis, disorders
XX associated with inappropriate or inopportune invasion of vessels such
XX as diabetic retinopathy, neovascular glaucoma and capillary
XX proliferation in atherosclerotic plaques, or cancers), and to inhibit
XX binding activity of alphavbeta3 that are necessary for progression of
XX an alphavbeta3-mediated disease.
XX
XX Sequence 117 AA;
XX
XX Query Match 82.8%; Score 48; DB 22; Length 117;
XX Best Local Similarity 90.0%; Pred. No. 0.97;
XX Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GFTWSSYDMS 10
XX III:IIIIII
XX Db 26 GFTFSSYDMS 35
XX
XX RESULT 7
XX AAB61359
XX ID AAB61359 standard; protein; 117 AA.
XX XX
XX AC AAB61359;
XX XX
XX DT 03-APR-2001 (first entry)
XX XX
XX DE Vitaxin heavy chain variable region protein.
XX XX
XX KW LM609; grafted antibody; alphaVbeta3 integrin; angiogenesis;
XX KW inflammatory; cancer; retina; restenosis; osteoporosis.
XX XX
XX OS Unidentified.
XX XX
XX PN WO200078815-A1.
XX PD 28-DEC-2000.

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XX XX 23-JUN-2000; 2000WO-US17454.
XX XX
XX PR 24-JUN-1999; 99US-0339922.
XX XX
XX PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX XX
XX PI Huse WD, Wu H;
XX XX
XX DR WPI; 2001-050110/06.
XX XX
XX PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity
XX to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
XX PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
XX PT osteoporosis.
XX XX
XX PS Disclosure; Fig 1; 132pp; English.
XX XX
XX CC The present invention relates to enhanced LM609 grafted antibodies
XX exhibiting selective binding affinity to alphavbeta3 integrin or
XX CC their functional fragments. The antibodies or their functional
XX CC fragments can be used in the diagnosis and treatment of
XX CC alphavbeta3-mediated diseases such as angiogenesis, inflammatory
XX CC diseases (such as psoriasis and chronic articular rheumatism),
XX CC disorders associated with inappropriate or inopportune invasion of
XX CC vessels (such as diabetic retinopathy, neovascular glaucoma and
XX CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
XX CC diseases (such as macular degeneration), restenosis and
XX CC osteoporosis.
XX XX
XX SQ Sequence 117 AA;
XX
XX Query Match 82.8%; Score 48; DB 22; Length 117;
XX Best Local Similarity 90.0%; Pred. No. 0.97;
XX Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GFTWSSYDMS 10
XX III:IIIIII
XX Db 26 GFTFSSYDMS 35
XX
XX RESULT 8
XX AAW86137
XX ID AAW86137 standard; Protein; 117 AA.
XX XX
XX AC AAW86137;
XX XX
XX DT 03-MAR-1999 (first entry)
XX XX
XX DE Protein sequence of de-immunised humanised A33 Vh.
XX XX
XX KW Non-immunogenic; epitope; T-cell; immunogenicity; immune system; SK;
XX KW immunogl bulin; therapeutic; streptokinase; humanised; de-immunised.
XX XX
XX OS Homo sapiens.
XX XX
XX PN WO9852976-A1.
XX XX
XX PD 26-NOV-1998.
XX XX
XX PF 21-MAY-1998; 98WO-GB01473.
XX XX
XX PR 14-APR-1998; 98GB-0007751.
XX PR 21-MAY-1997; 97GB-0010480.
XX PR 31-JUL-1997; 97GB-0016197.
XX PR 28-NOV-1997; 97GB-0025270.
XX PR 02-DEC-1997; 97US-0067235.
XX XX
XX PA (BIOV-) BIOVATION LTD.
XX XX
XX PI Carr FJ;
XX XX
XX DR WPI; 1999-045301/04.

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XX PT Reducing immunogenicity of proteins - by modifying the amino acid
XX PT sequence of the protein to eliminate potential epitopes for T-cells
XX PT of a given species
XX PS
XX PS Example 5; Fig 25; 77pp; English.
XX CC The invention relates to a method for the production of non-immunogenic
XX CC proteins. The method comprises determining at least part of the amino
XX CC acid sequence of the protein; (b) identifying in the amino acid sequence
XX CC one or more potential epitopes for T-cells (T-cell epitopes) of the given
XX CC species; and (c) modifying the amino acid sequence to eliminate at least
XX CC one of the T-cell epitopes identified in step (b) thereby to eliminate or
XX CC reduce the immunogenicity of the protein when exposed to the immune
XX CC system of the given species. A method of analysing a pre-existing protein
XX CC to predict the basis for immunogenic responses is also provided. The
XX CC methods can be used particularly for reducing the immunogenicity of
XX CC immunoglobulins or therapeutic proteins, e.g. Streptokinase (SK). The
XX CC products can be used for diagnosis and therapy. The present sequence
XX CC represents the protein sequence of de-immunised humanised A33 Vh.
XX SQ Sequence 117 AA;
Query Match 77.6%; Score 45; DB 20; Length 117;
Best Local Similarity 80.0%; Pred. No. 3.1;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GFTWSSYDMS 10
Db 26 GFTFSTYDMS 35
|||||
RESULT 9
AAW54000
ID AAW54000 standard; Protein; 128 AA.
AC AAW54000;
XX
XX 29-JUL-1998 (first entry)
DT
DE Anti-CD4 antibody VH3 monkey clone 3-40.
XX
XX Anti-CD4 antibody; monkey; human; therapy; variable heavy domain;
KW Old World monkey; constant domain; eczema; immuno-modulated disease;
KW rheumatoid arthritis.
XX
XX Primate sp.
OS
FH Key Location/Qualifiers
FT Misc-difference 1..128
FT /note= "Xaa= unspecified amino acid"
XX
XX US5750105-A.
XX
XX 12-MAY-1998.
XX
XX 07-JUN-1995; 95US-0476349.
XX
XX 10-JUL-1992; 92US-0912292.
XX
XX 25-JUL-1991; 91US-0735064.
XX
XX 23-MAR-1992; 92US-0856281.
XX
XX 05-DEC-1995; 95US-0379072.
XX
XX 07-JUN-1995; 95US-0476349.
XX
XX (IDEC-) IDEC PHARM CORP.
XX
XX Hanna N, Newman RA, Raab RW;
XX
XX WPI; 1998-296690/26.
XX
XX Improved method for antibody treatment - uses an antibody comprising
XX PT an Old World monkey variable region and a human constant domain
XX

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PS Example 1; Fig 9c; 84pp; English.
XX
XX This sequence represents the VH3 domain of an anti-CD4 antibody
XX (Ab). This sequence can be used in the method of the invention for
XX treating a subject, where the treatment comprises administration of an
XX Ab. The method comprises the administration of an antibody which has an
XX Old World monkey (e.g. baboon or macaque) variable region which binds to
XX an antigen (Ag) (or Ag binding portion), and a human constant domain. The
XX method is useful for the treatment of eczema and immuno-modulated
XX diseases and especially rheumatoid arthritis. The recombinant antibodies
XX used are sufficiently different from native monkey antibodies to allow
XX human antigens to raise these antibodies, but similar enough to human
XX antibody so there is no immune response to the antibodies in humans.
XX Compared to antibodies used in therapy in prior art, these antibodies do
XX not induce human anti-antibodies on repeated administration. They also
XX have longer half-lives and do not have a lack of effector function with
XX human cells.
XX SQ Sequence 128 AA;
Query Match 77.6%; Score 45; DB 19; Length 128;
Best Local Similarity 80.0%; Pred. No. 3.4;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GFTWSSYDMS 10
Db 26 GFTFSSYDMN 35
|||||
RESULT 10
AAR24713
ID AAR24713 standard; Protein; 134 AA.
XX
XX AAR24713;
XX
XX 28-DEC-1992 (first entry)
DT
DE Sequence encoded by the genomic chimeric heavy chain variable region
DE (VFH) gene.
XX
XX Chimeric monoclonal antibody; anti-fibrin antibody; PCR;
KW antithrombotic agent; myocardial infarction therapy.
XX
XX Mus musculus.
OS
FH Key Location/Qualifiers
FT Peptide 1..19
FT /label= leader
FT Region 23..49
FT /label= Framework Region (FR) 1
FT Region 50..54
FT /label= Complementarity determining region(CDR)1
FT Region 55..68
FT /label= FR-2
FT Region 69..84
FT /label= CDR-2
FT Region 85..114
FT /label= FR-3
FT Region 115..123
FT /label= CDR-3
FT Region 124..134
FT /label= FR-4
XX
XX EP491351-A.
XX
XX 24-JUN-1992.
XX
XX 17-DEC-1991; 91EP-0121591.
XX
XX 18-DEC-1990; 90JP-0413929.
XX 11-NOV-1991; 91JP-0294464.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
XX PA

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XX PI Iwasa S, Taka H, Watanabe T, Tada H;
 XX WPI; 1992-209528/26.
 DR N-PSDB; AAQ25666.
 XX Chimeric monoclonal antibodies - contain anti-human fibrin
 PT antibody light and heavy chain variable and constant for treating
 PT thrombotic conditions e.g. myocardial infarction
 XX Example; Figure 4; 87pp; English.
 XX PCR primers 5'mVH and 3'mVH were used to produce a VH gene-contg.
 CC fragment of about 330bp. The fragment was isolated and subcloned in
 CC pUC119. The fragment was found to be a functional VH structural
 CC gene, referred to as VFH, comprising a VH gene belonging to the
 CC subgroup III (VHIII) and the D Σ P2 and JH4 genes. Northern blot
 CC analysis using the whole RNA of FIBL-11 cells confirmed that VFH
 CC is the gene expressed in FIBL-11 cells. The sequence is given in
 CC AAQ25666.
 XX SQ Sequence 134 AA;
 Query Match 77.6%; Score 45; DB 13; Length 134;
 Best Local Similarity 80.0%; Pred. No. 3.6;
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GFTWSSYDMS 10
 III:I:IIII
 DB 45 GFTFSNYDMS 54
 RESULT 11
 ABP45381
 ID ABP45381 standard; Protein; 256 AA.
 AC ABP45381;
 DT 19-AUG-2002 (first entry)
 DE Human Blys binding scFv SEQ ID 1392.
 XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;
 KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.
 XX OS Homo sapiens.
 XX WO200202641-A1.
 PN 10-JAN-2002.
 PD 15-JUN-2001; 2001WO-US19110.
 PF 16-JUN-2000; 2000US-212210P.
 PR 17-OCT-2000; 2000US-240816P.
 PR 16-MAR-2001; 2001US-276248P.
 PR 21-MAR-2001; 2001US-277379P.
 PR 25-MAY-2001; 2001US-293499P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 PI WPI; 2002-114799/15.
 XX Antibodies against B Lymphocyte Stimulating polypeptides, useful for
 PT the diagnosis and treatment of cancers and immune disorders -
 XX Claim 1; Page 2924-2925; 3148pp; English.

PS Claim 1; Page 2064-2065; 3148pp; English.
 XX This invention describes novel antibodies that immunospecifically bind to
 CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antirheumatic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys
 CC and so may be used to detect and quantitate the presence of Blys in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of Blys. They may also be
 CC administered to treat diseases associated with aberrant Blys expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method
 CC of the invention.
 XX SQ Sequence 256 AA;
 Query Match 77.6%; Score 45; DB 23; Length 256;
 Best Local Similarity 80.0%; Pred. No. 7.3;
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GFTWSSYDMS 10
 III:I:IIII
 DB 26 GFTFSNYDMS 35
 RESULT 12
 ABP46108
 ID ABP46108 standard; Protein; 256 AA.
 XX AC ABP46108;
 DT 19-AUG-2002 (first entry)
 DE Human Blys binding scFv SEQ ID 2119.
 XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;
 KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.
 XX OS Homo sapiens.
 XX WO200202641-A1.
 PN 10-JAN-2002.
 PD 15-JUN-2001; 2001WO-US19110.
 PF 16-JUN-2000; 2000US-212210P.
 PR 17-OCT-2000; 2000US-240816P.
 PR 16-MAR-2001; 2001US-276248P.
 PR 21-MAR-2001; 2001US-277379P.
 PR 25-MAY-2001; 2001US-293499P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 PI WPI; 2002-114799/15.
 XX Antibodies against B Lymphocyte Stimulating polypeptides, useful for
 PT the diagnosis and treatment of cancers and immune disorders -
 XX Claim 1; Page 2924-2925; 3148pp; English.

XX This invention describes novel antibodies that immunospecifically bind to
CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method
CC of the invention.
XX
SQ Sequence 256 AA;

Query Match 77.6%; Score 45; DB 23; Length 256;
Best Local Similarity 80.0%; Pred. No. 7.3;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 GFTWSSYDMS 10
Db 26 GFTFSYDMSN 35
||||:|||||

RESULT 13
AAR24812
ID AAR24812 standard; Protein; 466 AA.
XX
AC AAR24812;
XX
XX
DT 28-DEC-1992 (first entry)
XX
DE Sequence encoded by the chimeric H chain cDNA contained in pTB1373.
XX
KW Chimeric monoclonal antibody; anti-fibrin antibody; primer;
KW antithrombotic agent; myocardial infarction therapy.
XX
OS Synthetic.

XX Key Location/Qualifiers
FH Peptide 13..19
FT /label= Leader
FT Region 20..134
FT /label= VH
FT Region 135..232
FT /label= CH1
FT Region 233..247
FT /label= hinge
FT Region 248..357
FT /label= CH2
FT Region 358..464
FT /label= CH3
FT Misc-difference 465
FT /note= "translated stop codon"

XX
PN EP491351-A.
XX
PD 24-JUN-1992.
XX
XX 17-DEC-1991; 91EP-0121591.
XX
PR 18-DEC-1990; 90JP-0413829.
PR 11-NOV-1991; 91JP-0294464.
XX
XX (TAKE) TAKEDA CHEM IND LTD.
XX
XX Iwasa S, Taka H, Watanabe T, Tada H;

XX WPI: 1992-209528/26.
DR N-PSDB; AAQ25692.
XX
PT Chimeric monoclonal antibodies - contain anti-human fibrin
PT antibody light and heavy chain variable and constant for treating
PT thrombotic conditions e.g. myocardial infarction
XX
XX Example; Figure 11; 87pp; English.
XX
XX Plasmid pTB1373 contains the whole length of a mouse-human
CC chimeric anti-human fibrin heavy chain cDNA open reading
CC frame. It was prepd. using Poly(A)+ RNA from the anti-fibrin
CC chimeric Ab-producing transformant FIB1-H01/X63 as a template
CC to clone human C-kappa cDNA, using the oligo-dT (Pharmacia) primer as
CC a primer for first strand cDNA synthesis and the 5'C2H and 3'EH
CC primers for the PCR. A human gamma-1 chain CH2-CH3 domain encoding
CC cDNA was amplified. Similarly a human gamma-1 chain CH1 domain
CC encoding cDNA and an anti-fibrin antibody VH cDNA and a leader
CC peptide cDNA were amplified using the primers 3'EH, 3'C2H and 3'ClH
CC respectively as a primer for first strand cDNA synthesis and the
CC primer combination of 5'ClH and 3'C2H, of 5'LIH and 3'CIH and of
CC 5'SH and 3'LIH respectively as primers for PCR. The amplified gene
CC products were isolated and used to produce plasmids. After
CC confirmation of the cDNA sequence of each plasmid, the cDNA
CC encoding LH, VH, CH1 and CH2CH3 were joined together to give
CC plasmid pTB1373 contg. the whole length chimeric H chain
CC (LH, VH, CH1, CH2CH3), also abbreviated as IgH-FIB,
XX
SQ Sequence 466 AA;

Query Match 77.6%; Score 45; DB 13; Length 466;
Best Local Similarity 80.0%; Pred. No. 14;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 GFTWSSYDMS 10
Db 45 GFTFSNYDMS 54
||||:|||||

RESULT 14
AAB40112
ID AAB40112 standard; Protein; 97 AA.
XX
AC AAB40112;
XX
DT 05-FEB-2001 (first entry)
XX
DE Anti-hIL12 antibody H chain V region amino acid sequence SEQ ID 638.
XX
KW Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;
KW complementarity determining region; CDR: antirheumatic; antiarthritis;
KW antisclerotic; neuroprotective; antipsoriatic; antiasthmatic; cardiant;
KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
KW multiple sclerosis; rheumatoid arthritis.
XX
OS Homo sapiens.
XX
XX WO200056772-A1.
PN
PD 28-SEP-2000.
XX
XX 24-MAR-2000; 2000WO-US07946.
XX
XX 25-MAR-1999; 99US-0126603.
XX
XX (BADI) BASF AG.
PA (GEMY) GENETICS INST INC.
XX
XX Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;
PI Kaymakalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A;
PI Veidman GW, Venturini A, Warne NW, Wlodom A, Elvin JG, Duncan AR;
PI Derbyshire EJ, Carmen S, Smith S, Holtet TL, Du Fou SL;

```

XX WPI; 2000-638250/61.
XX New human antibody specific for human interleukin-12 (IL-12) used to
XX treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
XX disease and multiple sclerosis -
XX Claim 75; Page 121; 377pp; English.
XX This invention relates to a new human antibody specific for human
XX interleukin-12 (IL-12). The invention also includes antigen binding
XX portions that bind to IL-12. Sequences AAB39485-B39516 represent human
XX anti-IL-12 antibody heavy and light chain complementarity determining
XX region (CDR) amino acid sequences, and also includes variable region
XX amino acid sequences. Other variable region amino acid sequences are
XX given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771
XX represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063
XX represent other CDR sequences. Light chain CDR3 consensus sequences are
XX given in AAB40064-B40067. Primers used in the identification and
XX construction of the antibodies of the invention are given in
XX AAC61062-C61071. The antibody of the invention is a neutralising
XX antibody and has antirheumatic; antiarthritic; antisclerotic;
XX antiinflammatory; neuroprotective; antipsoriatic; antiasthmatic;
XX cardiant; antiparasitic; antibacterial and immunosuppressive activity.
XX The antibodies or antigen-binding fragments are useful in the treatment
XX of disorders associated with detrimental release of human IL-12,
XX especially Crohn's disease, multiple sclerosis and rheumatoid arthritis.
XX They can also be used in the manufacture of a pharmaceutical composition
XX to treat human IL-12 disorders.
XX SQ Sequence 97 AA;
Query Match 75.9%; Score 44; DB 21; Length 97;
Best Local Similarity 88.9%; Pred. No. 3.7;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTWSSYDM 9
Db 26 GFTFSSYDM 34
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RESULT 15
ABB39276
ID ABB39276 standard; Peptide: 102 AA.
AC ABB39276;
XX
XX 04-FEB-2002 (first entry)
DT
DE Peptide #6782 encoded by human foetal liver single exon probe.
XX
XX Human; foetal liver; gene expression; single exon nucleic acid probe.
XX
XX Homo sapiens.
XX
XX WO200157277-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US00669.
XX
XX 04-FEB-2000; 2000US-0180312.
XX
XX 26-MAY-2000; 2000US-0207456.
XX
XX 30-JUN-2000; 2000US-0608408.
XX
XX 03-AUG-2000; 2000US-0632366.
XX
XX 21-SEP-2000; 2000US-0234687.
XX
XX 27-SEP-2000; 2000US-0236359.
XX
XX 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-); MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX

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```

DR WPI; 2001-483447/52.
XX Human genome-derived single exon nucleic acid probes useful for
XX analyzing gene expression in human fetal liver -
XX Claim 27; SEQ ID NO 31911; 639pp + sequence listing; English.
XX The invention relates to a single exon nucleic acid probe for
XX measuring human gene expression in a sample derived from human foetal
XX liver. The single exon nucleic acid probes may be used for predicting,
XX measuring and displaying gene expression in samples derived from human
XX foetal liver. The present sequence is a peptide encoded by a single exon
XX nucleic acid probe of the invention.
XX Note: The sequence data for this patent did not form part of the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 102 AA;
Query Match 75.9%; Score 44; DB 22; Length 102;
Best Local Similarity 88.9%; Pred. No. 3.9;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTWSSYDM 9
Db 17 GFTFSSYDM 25
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Search completed: November 19, 2002, 17:31:34
Job time : 14.8235 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:54:45 ; Search time 1.96078 Seconds
(without alignments)
76.811 Million cell updates/sec

Title: US-09-016-061-50
Perfect score: 58
Sequence: 1 GFTWSSYDMS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 97044 seqs, 15060890 residues

Total number of hits satisfying chosen parameters: 97044

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published-Applications_AA:*
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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB pep.*
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7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB pep.*
11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB pep.*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB pep.*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB pep.*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	48	82.8	117	8	US-08-790-540A-2
2	48	82.8	117	8	US-08-791-391A-2
3	45	77.6	128	10	US-09-850-165-110
4	44	75.9	102	10	US-09-864-761-43848
5	44	75.9	470	10	US-09-859-053-32
6	44	75.9	470	10	US-09-859-053-36
7	43	74.1	117	8	US-08-790-540A-6
8	43	74.1	117	8	US-08-791-391A-6
9	42	72.4	123	10	US-09-850-165-112
10	41	70.7	87	10	US-09-840-459-53
11	41	70.7	89	10	US-09-840-459-48
12	41	70.7	98	10	US-09-840-459-38
13	41	70.7	98	10	US-09-840-459-39
14	41	70.7	98	10	US-09-840-459-44
15	41	70.7	98	10	US-09-840-459-45
16	41	70.7	98	12	US-10-066-895-4
17	41	70.7	118	9	US-09-423-800-46
18	41	70.7	118	9	US-09-423-800-56
19	41	70.7	137	9	US-09-423-800-76

20	41	70.7	137	9	US-09-423-800-77
21	41	70.7	140	10	US-09-286-240-4
22	41	70.7	144	10	US-09-881-823-12
23	40	69.0	88	10	US-09-840-459-51
24	40	69.0	89	10	US-09-840-459-49
25	40	69.0	98	10	US-09-822-698A-18
26	40	69.0	98	10	US-09-840-459-40
27	40	69.0	98	12	US-10-025-687-19
28	40	69.0	113	10	US-09-056-160B-11
29	40	69.0	116	10	US-09-840-459-80
30	40	69.0	118	9	US-09-144-886-64
31	40	69.0	118	9	US-09-144-886-65
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33	40	69.0	118	9	US-09-144-886-67
34	40	69.0	119	10	US-09-811-123-3
35	40	69.0	120	10	US-09-840-459-85
36	40	69.0	120	12	US-10-025-687-4
37	40	69.0	121	10	US-09-840-459-92
38	40	69.0	123	10	US-09-840-459-82
39	40	69.0	124	10	US-09-840-459-81
40	40	69.0	124	10	US-09-840-459-89
41	40	69.0	125	10	US-09-840-459-76
42	40	69.0	125	10	US-09-850-165-107
43	40	69.0	127	10	US-09-811-737-1
44	40	69.0	127	10	US-09-840-459-87
45	40	69.0	128	10	US-09-840-459-77

ALIGNMENTS

RESULT 1
US-08-790-540A-2
; Sequence 2, Application US/08790540A
; Patent No. US20010011125A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,540A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acid
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-790-540A-2
Query Match 82.8%; Score 48; DB 8; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.13;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTWSSYDMS 10
| | | : | | | | | | | |
Db 26 GFTFSSYDMS 35

RESULT 2
US-08-791-391A-2
; Sequence 2, Application US/08791391A
; Patent No. US20010016645A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08791.391A
; APPLICATION NUMBER: US/08791.391A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-391A-2

Query Match 82.8%; Score 48; DB 8; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.13;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTWSSYDMS 10
| | | : | | | | | | | |
Db 26 GFTFSSYDMS 35

RESULT 3
US-09-850-165-110
; Sequence 110, Application US/09850165
; Patent No. US20020150580A1
; GENERAL INFORMATION:
; APPLICANT: NEWMAN, ROLAND A.
; APPLICANT: HANNA, NABIL
; APPLICANT: RAAB, RONALD W.
; TITLE OF INVENTION: RECOMBINANT ANTIBODIES FOR HUMAN THERAPY
; FILE REFERENCE: 037003-0280614
; CURRENT APPLICATION NUMBER: US/09/850.165
; CURRENT FILING DATE: 2001-05-08
; PRIOR APPLICATION NUMBER: 09/082,472
; PRIOR FILING DATE: 1998-05-21
; PRIOR APPLICATION NUMBER: 08/476,237
; PRIOR FILING DATE: 1995-06-07

; PRIOR APPLICATION NUMBER: 08/397,072
; PRIOR FILING DATE: 1995-04-17
; PRIOR APPLICATION NUMBER: 07/912,292
; PRIOR FILING DATE: 1992-07-10
; PRIOR APPLICATION NUMBER: 07/856,281
; PRIOR FILING DATE: 1992-03-23
; PRIOR APPLICATION NUMBER: 07/735,064
; PRIOR FILING DATE: 1991-07-25
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 110
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Monkey
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (12)
; OTHER INFORMATION: Ile or Val
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (23)
; OTHER INFORMATION: Ser, Val or Ala
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (49)
; OTHER INFORMATION: Any amino acid, preferably Gly, Ser or Ala
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (79)
; OTHER INFORMATION: Val, Ala or Leu
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (87)
; OTHER INFORMATION: Lys, Glu or Arg
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (88)
; OTHER INFORMATION: Thr, Pro or Ala
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (93)
; OTHER INFORMATION: Leu or Val
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (95)
; OTHER INFORMATION: Phe or Tyr
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (97)
; OTHER INFORMATION: Thr or Ala
US-09-850-165-110

Query Match 77.6%; Score 45; DB 10; Length 128;
Best Local Similarity 80.0%; Pred. No. 0.44;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTWSSYDMS 10
| | | : | | | | | | | |
Db 26 GFTFSSYDMS 35

RESULT 4
US-09-864-761-43848
; Sequence 43848, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO

; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Acomica-x-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
; SEQ ID NO 43848
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AB019440.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.84
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.89
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.95
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1
; OTHER INFORMATION: EST_HUMAN HIT: AW405458.1, EVALUE 3.00e-43
; OTHER INFORMATION: SWISSPROT HIT: P01766, EVALUE 2.00e-39
US-09-864-761-43848

Query Match 75.9%; Score 44; DB 10; Length 102;
Best Local Similarity 88.9%; Pred. No. 0.51;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTWSSYDM 9
Db 17 GFTFSSYDM 25
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RESULT 5
US-09-859-053-32
; Sequence 32, Application US/09859053
; Patent No. US/0020102658A1
; GENERAL INFORMATION:
; APPLICANT: Tsuji, Takashi

; APPLICANT: Tezuka, Katsunari
; APPLICANT: Hori, No. US20020102658A1uaki
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
; TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
; FILE REFERENCE: 06501-079001
; CURRENT APPLICATION NUMBER: US/09/859,053
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: JP 2001-99508
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-147116
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-859-053-32

Query Match 75.9%; Score 44; DB 10; Length 470;
Best Local Similarity 88.9%; Pred. No. 2.2;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTWSSYDM 9
Db 45 GFTFSSYDM 53
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RESULT 6
US-09-859-053-36
; Sequence 36, Application US/09859053
; Patent No. US20020102658A1
; GENERAL INFORMATION:
; APPLICANT: Tsuji, Takashi
; APPLICANT: Tezuka, Katsunari
; APPLICANT: Hori, No. US20020102658A1uaki
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
; TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
; FILE REFERENCE: 06501-079001
; CURRENT APPLICATION NUMBER: US/09/859,053
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: JP 2001-99508
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-147116
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-859-053-36

Query Match 75.9%; Score 44; DB 10; Length 470;
Best Local Similarity 88.9%; Pred. No. 2.2;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTWSSYDM 9
Db 45 GFTFSSYDM 53
|||:|||||

RESULT 7
US-08-790-540A-6
; Sequence 6, Application US/08790540A
; Patent No. US2001001125A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 24

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,540A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-790-540A-6

Query Match 74.1%; Score 43; DB 8; Length 117;
Best Local Similarity 80.0%; Pred. No. 0.86;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GFTWSSYDMS 10
|| :|||||
Db 26 GFAFSSYDMS 35

RESULT 8
US-08-791-391A-6
; Sequence 6, Application US/08791391A
; Patent No. US20010016645A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,391A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949

; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-791-391A-6

Query Match 74.1%; Score 43; DB 8; Length 117;
Best Local Similarity 80.0%; Pred. No. 0.86;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GFTWSSYDMS 10
|| :|||||
Db 26 GFAFSSYDMS 35

RESULT 9
US-09-850-165-112
; Sequence 112, Application US/09850165
; Patent No. US20020150580A1
; GENERAL INFORMATION:
; APPLICANT: NEWMAN, ROLAND A.
; APPLICANT: RAAB, RONALD W.
; TITLE OF INVENTION: RECOMBINANT ANTIBODIES FOR HUMAN THERAPY
; FILE REFERENCE: 037003-0280614
; CURRENT APPLICATION NUMBER: US/09/850,165
; CURRENT FILING DATE: 2001-05-08
; PRIOR APPLICATION NUMBER: 09/082,472
; PRIOR FILING DATE: 1998-05-21
; PRIOR APPLICATION NUMBER: 08/476,237
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/397,072
; PRIOR FILING DATE: 1995-04-17
; PRIOR APPLICATION NUMBER: 07/912,292
; PRIOR FILING DATE: 1992-07-10
; PRIOR APPLICATION NUMBER: 07/856,281
; PRIOR FILING DATE: 1992-03-23
; PRIOR APPLICATION NUMBER: 07/735,064
; PRIOR FILING DATE: 1991-07-25
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 112
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Monkey
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (12)
; OTHER INFORMATION: Ile or Val
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (23)
; OTHER INFORMATION: Ser, Val or Ala
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (49)
; OTHER INFORMATION: Any amino acid, preferably Gly, Ser or Ala
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (74)
; OTHER INFORMATION: Asn or Asp
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (75)
; OTHER INFORMATION: Ala or Ser
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (78)
; OTHER INFORMATION: Met, Ser or Thr


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; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (79)
; OTHER INFORMATION: Val, Ala or Leu
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (80)
; OTHER INFORMATION: Phe or Tyr
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (84)
; OTHER INFORMATION: Ser, Asp or Asn
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (87)
; OTHER INFORMATION: Lys, Glu or Arg
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (88)
; OTHER INFORMATION: Thr, Pro or Ala
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (93)
; OTHER INFORMATION: Leu or Val
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (95)
; OTHER INFORMATION: Phe or Tyr
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (97)
; OTHER INFORMATION: Thr or Ala
;
US-09-850-165-112
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Query Match 72.4%; Score 42; DB 10; Length 123;
Best Local Similarity 70.0%; Pred. No. 1.3;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GFTWSSYDMS 10
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DB 26 GFTFTYDMD 35
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RESULT 10
US-09-840-459-53
; Sequence 53, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 53
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Mus musculus
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US-09-840-459-53

Query Match 70.7%; Score 41; DB 10; Length 87;
Best Local Similarity 80.0%; Pred. No. 1.4;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 1 GFTWSSYDMS 10
   |||:||||:
DB 15 GFTFSSYTMS 24
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RESULT 11
US-09-840-459-48
; Sequence 48, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 48
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-840-459-48
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Query Match 70.7%; Score 41; DB 10; Length 89;
Best Local Similarity 80.0%; Pred. No. 1.4;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 1 GFTWSSYDMS 10
   |||:||||:
DB 17 GFTFSSYDMS 26
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RESULT 12
US-09-840-459-38
; Sequence 38, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
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; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 38
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-840-459-38

Query Match 70.7%; Score 41; DB 10; Length 98;
Best Local Similarity 80.0%; Pred. No. 1.6;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
 | | | : | | | | |
DB 26 GFTFSSYTMS 35

RESULT 13

US-09-840-459-39
; Sequence 39, Application US/09840459
; Patent No. US20020150576A1

; GENERAL INFORMATION:

; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.

; APPLICANT: O'Keefe, Theresa

; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-012

; CURRENT APPLICATION NUMBER: US/09/840,459

; CURRENT FILING DATE: 2001-02-02

; PRIOR APPLICATION NUMBER: PCT/US01/03537

; PRIOR FILING DATE: 2001-02-02

; PRIOR APPLICATION NUMBER: 09/497,625

; PRIOR FILING DATE: 2000-02-03

; PRIOR APPLICATION NUMBER: 09/359,193

; PRIOR FILING DATE: 1999-07-22

; PRIOR APPLICATION NUMBER: 09/121,781

; PRIOR FILING DATE: 1998-07-23

; NUMBER OF SEQ ID NOS: 107

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 39

; LENGTH: 98

; TYPE: PRT

; ORGANISM: Mus musculus

US-09-840-459-39

Query Match 70.7%; Score 41; DB 10; Length 98;
Best Local Similarity 80.0%; Pred. No. 1.6;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
 | | | : | | | | |
DB 26 GFTFSSYTMS 35

RESULT 14

US-09-840-459-44
; Sequence 44, Application US/09840459
; Patent No. US20020150576A1

; GENERAL INFORMATION:

; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.

; APPLICANT: O'Keefe, Theresa

; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND

Search completed: November 18, 2002, 18:45:13
Job time : 2.96078 secs

; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 44
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-840-459-44

Query Match 70.7%; Score 41; DB 10; Length 98;
Best Local Similarity 80.0%; Pred. No. 1.6;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
 | | | : | | | | |
DB 26 GFTFSSYTMS 35

RESULT 15

US-09-840-459-45

; Sequence 45, Application US/09840459

; Patent No. US20020150576A1

; GENERAL INFORMATION:

; APPLICANT: LaRosa, Gregory J.

; APPLICANT: Horvath, Christopher

; APPLICANT: Newman, Walter

; APPLICANT: Jones, S. Tarran

; APPLICANT: O'Brien, Siobhan H.

; APPLICANT: O'Keefe, Theresa

; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND

; FILE REFERENCE: 1855.1052-012

; CURRENT APPLICATION NUMBER: US/09/840,459

; CURRENT FILING DATE: 2001-02-02

; PRIOR APPLICATION NUMBER: PCT/US01/03537

; PRIOR FILING DATE: 2001-02-02

; PRIOR APPLICATION NUMBER: 09/497,625

; PRIOR FILING DATE: 2000-02-03

; PRIOR APPLICATION NUMBER: 09/359,193

; PRIOR FILING DATE: 1999-07-22

; PRIOR APPLICATION NUMBER: 09/121,781

; PRIOR FILING DATE: 1998-07-23

; NUMBER OF SEQ ID NOS: 107

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 45

; LENGTH: 98

; TYPE: PRT

; ORGANISM: Mus musculus

US-09-840-459-45

Query Match 70.7%; Score 41; DB 10; Length 98;
Best Local Similarity 80.0%; Pred. No. 1.6;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
 | | | : | | | | |
DB 26 GFTFSSYTMS 35

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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:01 ; Search time 4.2402 Seconds
(without alignments)
69.390 Million cell updates/sec

Title: US-09-016-061-50

Perfect score: 58

Sequence: 1 GFTWSSYDMS 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	77.6	128	1	US-08-478-039-73
2	45	77.6	128	1	Sequence 73, Appl
3	45	77.6	128	1	Sequence 102, App
4	45	77.6	128	1	Sequence 73, Appl
5	43	74.1	239	2	US-08-476-349A-102
6	43	74.1	247	5	US-07-936-399-4
7	42	72.4	119	5	Sequence 4, Appl
8	42	72.4	123	1	Sequence 2, Appl
9	42	72.4	123	1	Sequence 6, Appl
10	42	72.4	123	1	Sequence 71, Appl
11	42	72.4	123	1	Sequence 104, App
12	41	70.7	98	2	Sequence 71, Appl
13	41	70.7	116	3	Sequence 104, App
14	41	70.7	116	4	Sequence 31, Appl
15	41	70.7	122	1	Sequence 101, App
16	41	70.7	122	1	Sequence 36, Appl
17	41	70.7	122	1	Sequence 80, Appl
18	41	70.7	122	5	Sequence 80, Appl
19	41	70.7	123	2	Sequence 80, Appl
20	41	70.7	239	2	Sequence 30, Appl
21	40	69.0	35	2	Sequence 18, Appl
22	40	69.0	98	2	Sequence 1, Appl
23	40	69.0	98	5	Sequence 48, Appl
24	40	69.0	102	2	Sequence 48, Appl
25	40	69.0	110	3	Sequence 65, Appl
26	40	69.0	113	3	Sequence 117, App
27	40	69.0	116	2	Sequence 6, Appl
					Sequence 2, Appl

28 40 69.0 116 5 PCT-US93-10555-2 Sequence 2, Appl
29 40 69.0 117 3 US-08-545-809A-109 Sequence 109, App
30 40 69.0 117 4 US-08-983-607-46 Sequence 46, Appl
31 40 69.0 117 4 US-08-752-693A-3 Sequence 3, Appl
32 40 69.0 117 4 US-08-752-693A-4 Sequence 4, Appl
33 40 69.0 117 4 US-09-157-370-1 Sequence 1, Appl
34 40 69.0 118 2 US-08-652-816A-12 Sequence 12, Appl
35 40 69.0 118 4 US-08-487-761-15 Sequence 15, Appl
36 40 69.0 118 5 PCT-US93-08435-10 Sequence 10, Appl
37 40 69.0 120 4 US-09-025-769B-38 Sequence 38, Appl
38 40 69.0 120 4 US-09-025-769B-63 Sequence 63, Appl
39 40 69.0 121 1 US-08-339-582-2 Sequence 2, Appl
40 40 69.0 122 2 US-07-934-373C-21 Sequence 21, Appl
41 40 69.0 122 3 US-08-437-642B-21 Sequence 21, Appl
42 40 69.0 122 4 US-08-146-206C-21 Sequence 21, Appl
43 40 69.0 122 5 PCT-US93-07832-21 Sequence 21, Appl
44 40 69.0 122 5 PCT-US93-08435-12 Sequence 12, Appl
45 40 69.0 122 5 PCT-US93-08435-14 Sequence 14, Appl

ALIGNMENTS

RESULT 1

US-08-478-039-73
; Sequence 73, Application US/08478039
; Patent No. 5681722
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/478,039
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-160
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant

; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Monkey
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: VH3 clone 3-40
US-08-478-039-73

Query Match 77.6%; Score 45; DB 1; Length 128;
Best Local Similarity 80.0%; Pred. No. 2.1;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
Db 26 GFTSSYDMN 35
|||||

RESULT 2

US-08-478-039-102
; Sequence 102, Application US/08478039
; Patent No. 5681722
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,039
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-160
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021

; INFORMATION FOR SEQ ID NO: 102:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Monkey
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: #40

US-08-478-039-102

Query Match 77.6%; Score 45; DB 1; Length 128;
Best Local Similarity 80.0%; Pred. No. 2.1;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
Db 26 GFTSSYDMN 35
|||||

RESULT 3

US-08-476-349A-73
; Sequence 73, Application US/08476349A
; Patent No. 5750105
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,349A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-161
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021

; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Monkey
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: VH3 clone 3-40

US-08-476-349A-73
Query Match 77.6%; Score 45; DB 1; Length 128;
Best Local Similarity 80.0%; Pred. No. 2.1;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GETWSSYDMS 10
Db 26 GFTFSSYDMN 35

RESULT 4

US-08-476-349A-102
; Sequence 102, Application US/08476349A
; Patent No. 5750105
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476.349A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin Esq., Robln L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-161
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 102:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Monkey
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: #40
US-08-476-349A-102

Query Match 77.6%; Score 45; DB 1; Length 128;
Best Local Similarity 80.0%; Pred. No. 2.1;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GETWSSYDMS 10
Db 26 GFTFSSYDMN 35

RESULT 5

US-07-956-399-4
; Sequence 4, Application US/07956399
; Patent No. 5876717
; GENERAL INFORMATION:
; APPLICANT: SHIMAMURA, TOSHIRO
; APPLICANT: TAKI, SHINSUKE
; APPLICANT: HAMURO, JUNJI
; TITLE OF INVENTION: POLYPEPTIDES CAPABLE OF BINDING TO HEAVY
; CHAINS OF IL-2 RECEPTORS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/956,399
; FILING DATE: 19921005
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, NO. 5876717man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 10-586-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-956-399-4

Query Match 74.1%; Score 43; DB 2; Length 239;
Best Local Similarity 80.0%; Pred. No. 8.1;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GETWSSYDMS 10
Db 148 GFAFSSYDMS 157

RESULT 6

PCT-US94-07659-2
; Sequence 2, Application PC/TUS9407659
; GENERAL INFORMATION:
; APPLICANT: Young, Peter
; APPLICANT: Gross, Mitchell
; APPLICANT: Jonak, Zdenka L.
; APPLICANT: Theisen, Timothy
; APPLICANT: Hurle, Mark
; APPLICANT: Jackson, Jeffrey R.
; TITLE OF INVENTION: Recombinant and Humanized IL-1 beta
; Antibodies for Treatment of IL-1 Mediated Inflammatory
; Disorders in Man
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation - Corp.
; ADDRESSEE: Intellectual Property
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA

; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07659
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/090,534
; FILING DATE: 09-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50171-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 270-5024
; TELEFAX: (610) 270-5090
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 247 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US94-07659-2

Query Match 74.1%; Score 43; DB 5; Length 247;
Best Local Similarity 80.0%; Pred. No. 8.4;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GFTWSSYDMS 10
|| :|||||
Db 45 GFATSSYDMS 54

RESULT 7
PCT-US94-07659-6
; Sequence 6, Application PC/TUS9407659
; GENERAL INFORMATION:
; APPLICANT: Young, Peter
; APPLICANT: Gross, Mitchell
; APPLICANT: Jonak, Zdenka L.
; APPLICANT: Thelsen, Timothy
; APPLICANT: Hurle, Mark
; APPLICANT: Jackson, Jeffrey R.
; TITLE OF INVENTION: Recombinant and Humanized Il-1 beta
; TITLE OF INVENTION: Antibodies for Treatment of Il-1 Mediated Inflammatory
; TITLE OF INVENTION: Disorders in Man
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Smithkline Beecham Corporation - Corp.
; ADDRESSEE: Intellectual Property
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07659
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/090,534
; FILING DATE: 09-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.

; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50171-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 270-5024
; TELEFAX: (610) 270-5090
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US94-07659-6
Query Match 72.4%; Score 42; DB 5; Length 119;
Best Local Similarity 80.0%; Pred. No. 5.8;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GFTWSSYDMS 10
|| :|||||
Db 26 GFIFSSYDMS 35
RESULT 8
US-08-478-039-71
; Sequence 71, Application US/08478039
; Patent No. 5681722
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,039
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-160
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 123 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant

;; MOLECULE TYPE: peptide
;; ORIGINAL SOURCE:
;; ORGANISM: Monkey
;; POSITION IN GENOME:
;; CHROMOSOME/SEGMENT: VH3 clone 3-34
US-08-478-039-71

Query Match 72.4%; Score 42; DB 1; Length 123;
Best Local Similarity 70.0%; Pred. No. 6;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
Db 26 GFTFSTYDWT 35
||||:||||:

RESULT 9
US-08-478-039-104
; Sequence 104, Application US/08478039
; Patent No. 5681722
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,039
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-160
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 123 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Monkey
; POSITION IN GENOME: #34
; CHROMOSOME/SEGMENT: US-08-478-039-104

Query Match 72.4%; Score 42; DB 1; Length 123;
Best Local Similarity 70.0%; Pred. No. 6;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
Db 26 GFTFSTYDWT 35
||||:||||:

RESULT 10
US-08-476-349A-71
; Sequence 71, Application US/08476349A
; Patent No. 5750105
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,349A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-161
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 123 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Monkey
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: VH3 clone 3-34
; US-08-476-349A-71

Query Match 72.4%; Score 42; DB 1; Length 123;
Best Local Similarity 70.0%; Pred. No. 6;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10

```
Db      26 GFTFSTDYMT 35

RESULT 11
US-08-476-349A-104
; Sequence 104, Application US/08476349A
; Patent No. 5750105
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,349A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-161
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 123 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Monkey
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: #34
US-08-476-349A-104

Query Match      72.4%; Score 42; DB 1; Length 123;
Best Local Similarity 70.0%; Pred. No. 6;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 GFTWSSYDMS 10
Db      26 GFTFSTDYMT 35

RESULT 12
US-08-665-202-31

Query Match      70.7%; Score 41; DB 2; Length 98;
Best Local Similarity 70.0%; Pred. No. 6.8;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 GFTWSSYDMS 10
Db      26 GFTFSSYEMN 35

RESULT 13
US-08-545-809A-101
; Sequence 101, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; APPLICANT: Matsuda, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
```


; MEDIWA TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545.809A
; FILING DATE: 27-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 06501/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-8906
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 101:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-545-809A-101

Query Match 70.7%; Score 41; DB 3; Length 116;
Best Local Similarity 77.8%; Pred. No. 8.1;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTWSSYDM 9
Db 45 GFTFSNYDM 53
||||:||||

RESULT 14
US-08-983-607-36
; Sequence 36, Application US/08983607
; Patent No. 6140470
; GENERAL INFORMATION:
; APPLICANT: Alan Garen
; APPLICANT: Xiaohong Cai
; TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-
; bodies
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Department of Molecular Biophysics
; ADDRESSEE: and Biochemistry, Yale University
; STREET: 266 Whitney Avenue
; CITY: New Haven
; STATE: Connecticut
; COUNTRY: United States of America
; ZIP: 06520-8114
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" 1.44 Mb diskette
; COMPUTER: IBM PC
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Word Processing
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/983.607
; FILING DATE: April 27, 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/IB96/01032
; FILING DATE: June 28, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mary M. Krinsky
; REGISTRATION NUMBER: 32423
; REFERENCE/DOCKET NUMBER: OCR-679
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 203-773-9544
; TELEFAX: 203-773-1183

; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 residues
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: polypeptide
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens (melanoma patient immu-
; ORGANISM: nized with autologous tumor cells)
; INDIVIDUAL ISOLATE: peripheral blood lymphocytes
; IMMEDIATE SOURCE:
; LIBRARY: DM414 scfv antibodies obtained from
; LIBRARY: fUSE5 fusion phage construct
; CLONE: V474
; FEATURE:
; NAME/KEY: heavy chain
; US-08-983-607-36
Query Match 70.7%; Score 41; DB 4; Length 116;
Best Local Similarity 80.0%; Pred. No. 8.1;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GFTWSSYDM 10
Db 26 GFTFSYTM 35
||||:||||

RESULT 15
US-08-276-852-80
; Sequence 80, Application US/08276852
; Patent No. 5652138
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276.852
; FILING DATE: 18-JUL-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCRI452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 122 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-276-852-80

Query Match 70.7%; Score 41; DB 1; Length 122;
Best Local Similarity 70.0%; Pred. No. 8.5;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTWSSYDMS 10
|||:||||:
Db 23 GFTFSSYEMN 32

Search completed: November 18, 2002, 17:43:33
Job time : 4.2402 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:01 ; Search time 4.90196 Seconds
(without alignments)
196.114 Million cell updates/sec

Title: US-09-016-061-52
Perfect score: 53
Sequence: 1 GFTFLSYDMS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: pir1.*
- 2: pir2.*
- 3: pir3.*
- 4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	88.7	94	2 S14580	Ig heavy chain V r
2	43	81.1	97	2 S26890	Ig heavy chain V r
3	42	79.2	113	2 S26468	Ig heavy chain V r
4	42	79.2	117	1 HWS34	Ig heavy chain pre
5	42	79.2	121	2 D27888	Ig heavy chain V r
6	42	79.2	124	2 C27888	Ig heavy chain V r
7	40	75.5	40	2 S33406	Ig heavy chain V r
8	40	75.5	83	2 C25913	Ig heavy chain V r
9	40	75.5	98	2 S26891	Ig heavy chain V r
10	40	75.5	108	2 PL0248	Ig heavy chain V r
11	40	75.5	107	2 PH1006	Ig heavy chain V r
12	40	75.5	117	1 HWS84	Ig heavy chain pre
13	40	75.5	117	2 PL0249	Ig heavy chain V r
14	40	75.5	117	2 PL0252	Ig heavy chain V r
15	40	75.5	119	2 E27888	Ig heavy chain V r
16	40	75.5	122	2 E27888	Ig heavy chain V r
17	40	75.5	138	2 S9258	Ig heavy chain V r
18	40	75.5	138	2 I47205	Ig heavy chain V r
19	39	73.6	92	2 S56009	Ig heavy chain var
20	39	73.6	92	2 S56008	Ig heavy chain var
21	39	73.6	97	1 HWS91	Ig heavy chain V r
22	39	73.6	97	2 PH0872	Ig heavy chain V r
23	39	73.6	98	2 S26889	Ig heavy chain V r
24	39	73.6	100	2 D48223	Ig heavy chain V r
25	39	73.6	102	2 S14581	Ig heavy chain V r
26	39	73.6	108	2 PH1648	Ig heavy chain V r
27	39	73.6	108	2 PH1011	Ig heavy chain V r
28	39	73.6	109	2 PH1649	Ig heavy chain V r
29	39	73.6	111	2 PH1659	Ig heavy chain V r

30	39	73.6	111	2 S40090	Ig heavy chain - m
31	39	73.6	111	2 PH1007	Ig heavy chain V r
32	39	73.6	112	2 S26327	Ig heavy chain V r
33	39	73.6	112	2 PH1647	Ig heavy chain V r
34	39	73.6	113	2 S25571	Ig heavy chain V r
35	39	73.6	117	1 H3H026	Ig heavy chain pre
36	39	73.6	117	2 A45953	Ig heavy chain pre
37	39	73.6	117	2 B34964	Ig heavy chain pre
38	39	73.6	117	2 S34012	Ig heavy chain V r
39	39	73.6	118	2 S31121	Ig heavy chain - h
40	39	73.6	119	2 C36005	Ig heavy chain V r
41	39	73.6	119	2 D36005	Ig heavy chain V r
42	39	73.6	119	2 S31107	Ig heavy chain - h
43	39	73.6	119	2 S31108	Ig heavy chain - h
44	39	73.6	120	2 S48798	Ig heavy chain V r
45	39	73.6	120	2 S55538	Ig heavy chain V r

ALIGNMENTS

RESULT 1

S14580
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
R:Chen, Q.; Stenzel-Poore, M.; Rittenberg, M.B.
submitted to the EMBL Data Library, March 1991
A:Description: Natural polyreactive antibodies differ from Ag-Induced antibodies in V
A:Reference number: S14484
A:Accession: S14580
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-94 <CHE>
A:Cross-references: EMBL:X58652; NID:g51293; PIDN:CAA41509.1; PID:g51294
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:7-90/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 88.7%; Score 47; DB 2; Length 94;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10

Db 18 GFTFLSYDMS 27

RESULT 2

S26890
Ig heavy chain V region (DP-48) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S26890
R:Tominson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups o
A:Reference number: S26885; MUID:93021117; PMID:1404388
A:Accession: S26890
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-97 <TOM>
A:Cross-references: EMBL:Z12348; NID:g32916; PIDN:CAA78218.1; PID:g32917
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:15-97/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 81.1%; Score 43; DB 2; Length 97;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFLSYDM 9

Db 26 GFTFSSYDM 34
|||||

RESULT 3

S26468 Ig heavy chain V region - mouse

C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C:Accession: S26468

R:Kavaler, J.

submitted to the EMBL Data Library, April 1991

A:Reference number: S26459

A:Accession: S26468

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-113 <KAV>

A:Cross-references: EMBL:X59107; NID:951944; PIDN:CAA41833.1; PID:951945

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:11-94/Domain: immunoglobulin homology <IMM>

Query Match 79.2%; Score 42; DB 2; Length 113;

Best Local Similarity 80.0%; Pred. No. 0.32;

Matches 8; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 GFTFSLSYDMS 10

|||||

Db 22 GFAPSSYDMS 31

RESULT 4

HVMS34

Ig heavy chain precursor V region (345) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 31-Mar-1997

C:Accession: JT0502

R:Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.

J. Exp. Med. 169, 2007-2019, 1989

A:Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary

A:Reference number: JT0501; MUID:89279149; PMID:2499654

A:Accession: JT0502

A>Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-117 <LEV>

A:Experimental source: strain BALB/cJ

A:Note: this sequence belongs to the VH7183 subfamily

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-117/Product: Ig heavy chain V region (345) #status predicted <MAT>

F:34-117/Domain: immunoglobulin homology <IMM>

F:41-115/Disulfide bonds: #status predicted

Query Match 79.2%; Score 42; DB 1; Length 117;

Best Local Similarity 80.0%; Pred. No. 0.33;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GFTFSLSYDMS 10

|||||

Db 45 GFAPSSYDMS 54

RESULT 5

D27888

Ig heavy chain V region (H37-60) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996

C:Accession: D27888

R:Catton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.

EMBO J. 5, 1577-1587, 1986

A:Title: Structural and functional implications of a restricted antibody response to a

A:Reference number: A91043; MUID:86300658; PMID:2427335

A:Accession: D27888

A:Molecule type: DNA

A:Residues: 1-121 <CAT>

A:Experimental source: strain Balb/c

A:Note: this sequence was determined from the germline gene

C:Comment: This chain was isolated from a hybridoma protein that binds influenza viru

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 79.2%; Score 42; DB 2; Length 121;

Best Local Similarity 80.0%; Pred. No. 0.34;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GFTFSLSYDMS 10

|||||

Db 26 GFAPSSYDMS 35

RESULT 6

C27888

Ig heavy chain V region (H37-62) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996

C:Accession: C27888

R:Catton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.

EMBO J. 5, 1577-1587, 1986

A:Title: Structural and functional implications of a restricted antibody response to

A:Reference number: A91043; MUID:86300658; PMID:2427335

A:Accession: C27888

A:Molecule type: DNA

A:Residues: 1-124 <CAT>

A:Experimental source: strain Balb/c

A:Note: this sequence was determined from the germline gene

C:Comment: This chain was isolated from a hybridoma protein that binds influenza viru

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 79.2%; Score 42; DB 2; Length 124;

Best Local Similarity 80.0%; Pred. No. 0.35;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GFTFSLSYDMS 10

|||||

Db 26 GFAPSSYDMS 35

RESULT 7

S33406

Ig heavy chain V region - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 19-Mar-1997 #sequence_revision 24-Jul-1997 #text_change 17-Jul-1998

C:Accession: S33406

R:Kettleborough, C.A.; Saldanha, J.; Ansell, K.H.; Bendig, M.M.

Eur. J. Immunol. 23, 206-211, 1993

A:Title: Optimization of primers for cloning libraries of mouse immunoglobulin genes

A:Reference number: S33391; MUID:93122092; PMID:8419173

A:Accession: S33406

A:Molecule type: mRNA

A:Residues: 1-40 <KET>

A:Cross-references: EMBL:X73009

A:Experimental source: strain BALB/c

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-40/Domain: immunoglobulin homology (fragment) <IMM>

Query Match 75.5%; Score 40; DB 2; Length 40;

Best Local Similarity 80.0%; Pred. No. 0.26;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GFTFSLSYDMS 10

|||||

Db 26 GFTFSSYDMS 35

RESULT 8

C25913 Ig heavy chain V region (BF114) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 16-Aug-1998 #sequence_revision 16-Aug-1998 #text_change 16-Aug-1996

C:Accession: C25913

R:Lawler, A.M.; Lin, P.S.; Gearhart, P.J.

Proc. Natl. Acad. Sci. U.S.A. 84, 2454-2458, 1987

A:Title: Adult B-cell repertoire is biased toward two heavy-chain variable-region genes

A:Reference number: A94148; MUID:87175692; PMID:3104915

A:Accession: C25913

A:Molecule type: DNA

A:Residues: 1-83 <LAW>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 75.5%; Score 40; DB 2; Length 83;

Best Local Similarity 80.0%; Pred. No. 0.58;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GFTFLSYDMS 10

||||| ||| ||

Db 11 GFTFSSYDMS 20

RESULT 9

S26891 Ig heavy chain V region (DP-58) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C:Accession: S26891

R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.

J. Mol. Biol. 227, 776-798, 1992

A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V

A:Reference number: S26895; MUID:93021117; PMID:1404388

A:Accession: S26891

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-98 <TOW>

A:Cross-references: EMBL:Z12358; NID:932935; PID:CAA78228.1; PID:932936

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 75.5%; Score 40; DB 2; Length 98;

Best Local Similarity 70.0%; Pred. No. 0.69;

Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GFTFLSYDMS 10

||||| ||| ||

Db 26 GFTFSSYDMS 35

RESULT 10

PL0248

Ig heavy chain V region (anti-DNA, DP12VH) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996

C:Accession: PL0248

R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A

J. Exp. Med. 171, 265-297, 1990

A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic

A:Reference number: PL0231; MUID:90111618; PMID:2104919

A:Accession: PL0248

A:Molecule type: mRNA

A:Residues: 1-108 <SHL>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-24/Region: framework 1

F:9-92/Domain: immunoglobulin homology <IMM>

Query Match 75.5%; Score 40; DB 1; Length 117;

Best Local Similarity 80.0%; Pred. No. 0.83;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GFTFLSYDMS 10

||||| ||| ||

F:25-29/Region: complementarity-determining 1
F:30-43/Region: framework 2
F:44-60/Region: complementarity-determining 2
F:61-92/Region: framework 3
F:93-99/Region: complementarity-determining 3
F:100-108/Region: framework 4

Query Match 75.5%; Score 40; DB 2; Length 108;

Best Local Similarity 80.0%; Pred. No. 0.77;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GFTFLSYDMS 10

||||| ||| ||

Db 20 GFTFSSYDMS 29

RESULT 11

PH1006

Ig heavy chain V region (clone 202.33) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C:Accession: PH1006

R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marlon, T.N.

J. Exp. Med. 176, 761-779, 1992

A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective

A:Reference number: PH0971; MUID:92381444; PMID:1512540

A:Accession: PH1006

A>Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-108 <TIL>

A:Experimental source: B cell, strain [NZB x NZW]FI

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:10-93/Domain: immunoglobulin homology <IMM>

Query Match 75.5%; Score 40; DB 2; Length 108;

Best Local Similarity 80.0%; Pred. No. 0.77;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GFTFLSYDMS 10

||||| ||| ||

Db 21 GFTFSSYDMS 30

RESULT 12

HVMS84

Ig heavy chain precursor V region (5-84) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 31-Mar-1997

C:Accession: JT0505

R:Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.

J. Exp. Med. 169, 2007-2019, 1989

A:Title: Early onset of somatic mutation in immunoglobulin VH genes during the primar

A:Reference number: JT0501; MUID:89279149; PMID:2499654

A:Accession: JT0505

A>Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-117 <LEV>

A:Experimental source: strain BALB/cJ

A:Note: This sequence belongs to the VH7183 subfamily

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-117/product: Ig heavy chain V region (5-84) #status predicted <MAT>

F:34-117/Domain: immunoglobulin homology <IMM>

F:41-115/Disulfide bonds: #status predicted

Query Match 75.5%; Score 40; DB 1; Length 117;

Best Local Similarity 80.0%; Pred. No. 0.83;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GFTFLSYDMS 10

||||| ||| ||

DB 45 GFTFSSYTMS 54

RESULT 13

Ig heavy chain V region (anti-DNA, 3E12VH) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996

C:Accession: PL0249

R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A

J. Exp. Med. 171, 265-297, 1990

A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic

A:Reference number: PL0231; MUID:9011618; PMID:2104919

A:Accession: PL0249

A:Molecule type: mRNA

A:Residues: 1-117 <SHL>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-30/Region: framework 1

F:15-98/Domain: immunoglobulin homology <IMM>

F:31-35/Region: complementarity-determining 1

F:36-49/Region: framework 2

F:50-66/Region: complementarity-determining 2

F:67-98/Region: framework 3

F:99-108/Region: complementarity-determining 3

F:109-117/Region: framework 4

Query Match 75.5%; Score 40; DB 2; Length 117;

Best Local Similarity 80.0%; Pred. No. 0.83;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GFTFLSYDMS 10

||||| || ||

Db 26 GFTFSSYTMS 35

RESULT 14

PL0252

Ig heavy chain V region (anti-DNA, clones 2E3VH, 6B8VH, and 3G9VH) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996

C:Accession: PL0252; PL0251

R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A

J. Exp. Med. 171, 265-297, 1990

A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic

A:Reference number: PL0231; MUID:9011618; PMID:2104919

A:Accession: PL0252

A:Molecule type: mRNA

A:Residues: 1-117 <SHL>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-30/Region: framework 1

F:15-98/Domain: immunoglobulin homology <IMM>

F:31-35/Region: complementarity-determining 1

F:36-49/Region: framework 2

F:50-66/Region: complementarity-determining 2

F:67-98/Region: framework 3

F:99-108/Region: complementarity-determining 3

F:109-117/Region: framework 4

Query Match 75.5%; Score 40; DB 2; Length 117;

Best Local Similarity 80.0%; Pred. No. 0.83;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GFTFLSYDMS 10

||||| || ||

Db 26 GFTFSSYTMS 35

RESULT 15

F27888

Ig heavy chain V region (H158-89H4) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996

C:Accession: F27888

R:Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.

EMBO J. 5, 1577-1587, 1986

A:Title: Structural and functional implications of a restricted antibody response to

A:Reference number: A91043; MUID:86300658; PMID:2427335

A:Accession: F27888

A:Molecule type: DNA

A:Residues: 1-119 <CAT>

A:Experimental source: strain Balb/c

A:Note: this sequence was determined from the germline gene

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 75.5%; Score 40; DB 2; Length 119;

Best Local Similarity 80.0%; Pred. No. 0.85;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GFTFLSYDMS 10

||||| || ||

Db 26 GFTFSSYTMS 35

Search completed: November 18, 2002, 17:47:00

Job time : 4.90196 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model
Run on: November 18, 2002, 17:22:00 : Search time 2.45098 Seconds
(without alignments)
169.223 Million cell updates/sec

Title: US-09-016-061-52
Perfect score: 53
Sequence: 1 GFTFLSYDMS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	ID	Description
1	42	79.2	117	1 HV55_MOUSE	P18526 mus musculus
2	40	75.5	117	1 HV54_MOUSE	P18525 mus musculus
3	39	73.6	97	1 HV56_MOUSE	P18527 mus musculus
4	39	73.6	117	1 HV3C_HUMAN	P01764 homo sapien
5	38	71.7	117	1 HV52_MOUSE	P06327 mus musculus
6	38	71.7	117	1 HV53_MOUSE	P18524 mus musculus
7	37	69.8	117	1 HV59_MOUSE	P18530 mus musculus
8	36	67.9	3106	1 LMA2_MOUSE	Q60675 mus musculus
9	35	66.0	115	1 HV3D_HUMAN	P01765 homo sapien
10	35	66.0	117	1 HV17_MOUSE	P01786 mus musculus
11	34	64.2	117	1 HV58_MOUSE	P18529 mus musculus
12	34	64.2	289	1 ROC1_ARATH	Q92uu4 arabidopsis
13	34	64.2	326	1 Y808_SCHPO	O13805 schizosacch
14	34	64.2	398	1 O59B_DROME	Q9wlp8 drosophila
15	34	64.2	451	1 ARP2_PLAFA	P13824 plasmodium
16	33	62.3	114	1 HV00_MOUSE	P01741 mus musculus
17	33	62.3	114	1 HV01_CANFA	P01784 canis famil
18	33	62.3	116	1 HV1A_RABIT	P01826 oryctolagus
19	33	62.3	117	1 HV2B_RABIT	P01828 oryctolagus
20	33	62.3	120	1 HV3E_HUMAN	P01766 homo sapien
21	33	62.3	121	1 HV3J_HUMAN	P01771 homo sapien
22	33	62.3	300	1 CYPE_DROME	Q9v3g3 drosophila
23	33	62.3	396	1 EFTU_STIAU	P42479 stigmatella
24	33	62.3	706	1 VGLH_EBV	P03231 epstein-bar
25	33	62.3	928	1 PM11_CHLPN	O86164 chlamydia p
26	33	62.3	1578	1 NX3A_RAT	Q07310 rattus norv
27	32	60.4	95	1 Y131_MYCPN	Q9exdl mycoplasma
28	32	60.4	114	1 HV3B_HUMAN	P01763 homo sapien
29	32	60.4	117	1 HV14_MOUSE	P01758 mus musculus
30	32	60.4	122	1 HV3G_HUMAN	P01768 homo sapien
31	32	60.4	136	1 HV16_MOUSE	P01783 mus musculus
32	32	60.4	247	1 ATP6_ACACA	Q37385 acanthamoeb
33	32	60.4	281	1 Y373_MYCGE	P47613 mycoplasma

34	32	60.4	281	1 Y373_MYCPN	P75227 mycoplasma
35	32	60.4	293	1 ROC1_HUMAN	O60812 homo sapien
36	32	60.4	465	1 Y093_RHIME	O87394 rhizobium m
37	32	60.4	550	1 INV1_HANAN	P40912 hansenula a
38	32	60.4	747	1 FHUA_ECOLI	P06971 escherichia
39	32	60.4	975	1 PMPA_CHLTR	O84417 chlamydia t
40	31	58.5	111	1 HV35_MOUSE	P01804 mus musculus
41	31	58.5	113	1 HV27_MOUSE	P01796 mus musculus
42	31	58.5	113	1 HV28_MOUSE	P01797 mus musculus
43	31	58.5	113	1 HV29_MOUSE	P01798 mus musculus
44	31	58.5	113	1 HV30_MOUSE	P01799 mus musculus
45	31	58.5	113	1 HV31_MOUSE	P01800 mus musculus

ALIGNMENTS

RESULT 1
HV55_MOUSE STANDARD; PRT; 117 AA.
AC P18526;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 345 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Mallapiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RT the primary immune response";
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; JT0502; HVMS34.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IG; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 345.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12902 MW; 49380EA627ACA99A CRC64;
Query Match 79.2%; Score 42; DB 1; Length 117;
Best Local Similarity 80.0%; Pred. No. 0.22;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GFTFLSYDMS 10
|||
Db 45 GFAFSSYDMS 54
RESULT 2
HV54_MOUSE STANDARD; PRT; 117 AA.
ID HV54_MOUSE
AC P18525;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 5-84 precursor.

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OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR: JTO505; HVMS84.
DR HSSP: P01810; 2FBJ.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117
FT DOMAIN 20 49
FT DOMAIN 50 54
FT DOMAIN 55 68
FT DOMAIN 69 85
FT DOMAIN 86 117
FT DISULFID 41 115
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12872 MW; 234055CB6A469861 CRC64;

Query Match 75.5%; Score 40; DB 1; Length 117;
Best Local Similarity 80.0%; Pred. No. 0.53;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
DB 45 GFTFSSYMS 54

RESULT 3
HV56_MOUSE
ID HV56_MOUSE STANDARD; PRT; 97 AA.
AC P18527;
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 914.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR: JTO504; HVMS91.
DR HSSP: P01810; 2FBJ.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT NON_TER 97
FT NON_TER 97
SQ SEQUENCE 97 AA; 10661 MW; C23CB33FF55DA893 CRC64;

Query Match 73.6%; Score 39; DB 1; Length 97;
Best Local Similarity 80.0%; Pred. No. 0.68;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
DB 45 GFTFSSYMS 54

RESULT 4
HV52_MOUSE
ID HV52_MOUSE STANDARD; PRT; 117 AA.
AC P06327;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region VH558 A1/A4 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

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Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
DB 26 GFTFSSYMS 35

RESULT 4
HV3C_HUMAN
ID HV3C_HUMAN STANDARD; PRT; 117 AA.
AC P01764;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-III region VH26 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81101090; PubMed=6450418;
RA Matthysens G., Rabbitts T.H.;
RT "Structure and multiplicity of genes for the human immunoglobulin
heavy chain variable region.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).
CC -----
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CC -----
DR EMBL; J00236; AAA53516.1; -
DR EMBL; M35415; AAA58735.1; -
DR PIR; A02047; H3HU26.
DR HSSP: P01772; 2FB4.
DR Genew; HGNC:5545; IGHV@.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117
FT NON_TER 117 117
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12582 MW; E826733F1A3CB0F1 CRC64;

Query Match 73.6%; Score 39; DB 1; Length 117;
Best Local Similarity 80.0%; Pred. No. 0.83;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
DB 45 GFTFSSYMS 54

RESULT 5
HV52_MOUSE
ID HV52_MOUSE STANDARD; PRT; 117 AA.
AC P06327;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region VH558 A1/A4 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

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RX MEDLINE=85099340; PubMed=2578321;
RA Yancopoulos G.D., Alt F.W.;
RT "Developmentally controlled and tissue-specific expression of
RL rearranged VH gene segments.";
RL Cell 40:271-281(1985).
CC -----
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CC -----
DR EMBL; M13787; AAA38499.1; -.
DR PIR; A02029; HVMSAL.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION VH558 A1/R4.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12971 MW; 850BC138856DFC9D CRC64;

Query Match 71.7%; Score 38; DB 1; Length 117;
Best Local Similarity 60.0%; Pred. No. 1.3;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
DB 45 GYFTSYDIN 54

RESULT 6
HV53_MOUSE STANDARD; PRT; 117 AA.
AC P18524;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region RF precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RL the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; JTO507; HVMS39.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Igv; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 7-39.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12972 MW; D5CA4167D0F1774F CRC64;

Query Match 69.8%; Score 37; DB 1; Length 117;
Best Local Similarity 70.0%; Pred. No. 2;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
DB 45 GFTFSNYGMS 54

RESULT 8
LMA2_MOUSE STANDARD; PRT; 3106 AA.
ID LMA2_MOUSE
AC Q60675; Q05003; Q64061;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Laminin alpha-2 chain precursor (Laminin M chain) (Merosin heavy

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FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12866 MW; 2CE3295F390F725B CRC64;

Query Match 71.7%; Score 38; DB 1; Length 117;
Best Local Similarity 80.0%; Pred. No. 1.3;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
DB 45 GFTFSYMS 54

RESULT 7
HV59_MOUSE STANDARD; PRT; 117 AA.
ID HV59_MOUSE
AC P18530;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 7-39 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RL the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; JTO507; HVMS39.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Igv; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 7-39.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12972 MW; D5CA4167D0F1774F CRC64;

Query Match 69.8%; Score 37; DB 1; Length 117;
Best Local Similarity 70.0%; Pred. No. 2;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
DB 45 GFTFSNYGMS 54

RESULT 8
LMA2_MOUSE STANDARD; PRT; 3106 AA.
ID LMA2_MOUSE
AC Q60675; Q05003; Q64061;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Laminin alpha-2 chain precursor (Laminin M chain) (Merosin heavy

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DE chain).

GN LAMA2.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=FVB/N; TISSUE=Embryo, and Heart;

RX MEDLINE=95316259; PubMed=7795883;

RA Bernier S.M., Utani A., Sugiyama S., Doi T., Polistina C.,

RA Yamada Y.;

RT "Cloning and expression of laminin alpha 2 chain (M-chain) in the

RT mouse.";

RL Matrix Biol. 14:447-455(1995).

RL [2]

RN SEQUENCE OF 2162-2279 FROM N.A.

RP STRAIN=C57BL/6; TISSUE=Thymus;

RC MEDLINE=93346725; PubMed=8345183;

RA Chang A.C., Wadsworth S., Colligan J.E.;

RX "Expression of merosin in the thymus and its interaction with

RT thymocytes.";

RL J. Immunol. 151:1789-1801(1993).

RN [3]

RP SEQUENCE OF 64-281 FROM N.A.

RX MEDLINE=95179178; PubMed=7874173;

RA Xu H., Wu X.R., Wewer U.M., Engvall E.;

RT "Murine muscular dystrophy caused by a mutation in the laminin alpha

RT 2 (Lama2) gene.";

RL Nat. Genet. 8:297-302(1994).

RL [4]

RP X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF 2932-3106.

RX MEDLINE=20085745; PubMed=10619025;

RA Hohenester E., Tisi D., Talts J.F., Timpl R.;

RT "The crystal structure of a laminin G-like module reveals the

RT molecular basis of alpha-dystroglycan binding to laminins, perlecan,

RT and agrin.";

RL Mol. Cell 4:783-792(1999).

CC -1- FUNCTION: Binding to cells via a high affinity receptor, laminin

CC is thought to mediate the attachment, migration, and organization

CC of cells into tissues during embryonic development by interacting

CC with other extracellular matrix components.

CC -1- SUBUNIT: Laminin is a complex glycoprotein, consisting of three

CC different polypeptide chains (alpha, beta, gamma), which are bound

CC to each other by disulfide bonds into a cross-shaped molecule

CC comprising one long and three short arms with globules at each

CC end.

CC THE ALPHA-2 CHAIN IS A SUBUNIT OF LAMININ-2 (MEROSIN) AND LAMININ-

CC 4 (S-MEROSIN).

CC -1- SUBCELLULAR LOCATION: Extracellular.

CC -1- TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES (MAJOR

CC COMPONENT).

CC -1- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT

CC WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.

CC -1- DOMAIN: DOMAINS VI, IV AND G ARE GLOBULAR.

CC -1- DISEASE: DEFECTS IN LAMA2 ARE A CAUSE OF MURINE MUSCULAR DYSTROPHY

CC (DY2J).

CC -1- SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).

CC -1- SIMILARITY: CONTAINS 17 LAMININ EGF-LIKE DOMAINS.

CC -1- SIMILARITY: CONTAINS 2 LAMININ DOMAINS IV.

CC -1- SIMILARITY: CONTAINS 5 LAMININ G-LIKE DOMAINS.

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CC EMBL; U12147; AAC52165.1; -

CC EMBL; X69869; CAA49502.1; -

CC EMBL; S75315; AAB33573.1; -

DR

DR PDB; 1QU0; 03-DEC-99.

DR MGD; MGI:99912; Lama2.

DR InterPro; IPR000561; EGF-like.

DR InterPro; IPR001886; Laminin.

DR InterPro; IPR000034; Laminin_B.

DR InterPro; IPR002049; Laminin_EGF.

DR InterPro; IPR001791; Laminin_G.

DR Pfam; PF00052; laminin_B; 2.

DR Pfam; PF00053; laminin_EGF; 15.

DR Pfam; PF00054; laminin_G; 5.

DR Pfam; PF00055; laminin_Nterm; 1.

DR PRINTS; PR00011; EGF_LAMININ.

DR ProDom; PD002082; LamNT; 1.

DR ProDom; PD003031; Laminin_B; 2.

DR SMART; SM00180; EGF_Lam; 15.

DR SMART; SM00001; EGF-like; 1.

DR SMART; SM00281; LamB; 2.

DR SMART; SM00282; LamG; 5.

DR SMART; SM00136; LamNT; 1.

DR PROSITE; PS00022; EGF_1; 11.

DR PROSITE; PS01186; EGF_2; 3.

DR PROSITE; PS01248; LAMININ_TYPE_EGF; 14.

DR PROSITE; PS00025; LAM_G_DOMAIN; 5.

DR Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;

DR Laminin EGF-like domain; Cell adhesion; Repeat; Signal; 3D-structure.

FT SIGNAL 1 22 POTENTIAL.

FT CHAIN 23 3106 LAMININ ALPHA-2 CHAIN.

FT DOMAIN 23 282 LAMININ N-TERMINAL (DOMAIN VI).

FT DOMAIN 283 339 LAMININ EGF-LIKE 1.

FT DOMAIN 340 409 LAMININ EGF-LIKE 2.

FT DOMAIN 410 464 LAMININ EGF-LIKE 3.

FT DOMAIN 465 513 LAMININ EGF-LIKE 4.

FT DOMAIN 514 523 LAMININ EGF-LIKE 5 (N-TERMINAL).

FT DOMAIN 524 719 LAMININ DOMAIN IV 1 (DOMAIN IV B).

FT DOMAIN 720 752 LAMININ EGF-LIKE 5 (C-TERMINAL).

FT DOMAIN 753 802 LAMININ EGF-LIKE 6.

FT DOMAIN 803 860 LAMININ EGF-LIKE 7.

FT DOMAIN 861 913 LAMININ EGF-LIKE 8.

FT DOMAIN 914 962 LAMININ EGF-LIKE 9.

FT DOMAIN 963 1009 LAMININ EGF-LIKE 10.

FT DOMAIN 1010 1055 LAMININ EGF-LIKE 11.

FT DOMAIN 1056 1101 LAMININ EGF-LIKE 12.

FT DOMAIN 1102 1161 LAMININ EGF-LIKE 13.

FT DOMAIN 1162 1171 LAMININ EGF-LIKE 14 (N-TERMINAL).

FT DOMAIN 1172 1375 LAMININ DOMAIN IV 2 (DOMAIN IV A).

FT DOMAIN 1376 1415 LAMININ EGF-LIKE 14 (C-TERMINAL).

FT DOMAIN 1416 1464 LAMININ EGF-LIKE 15.

FT DOMAIN 1465 1522 LAMININ EGF-LIKE 16.

FT DOMAIN 1523 1569 LAMININ EGF-LIKE 17.

FT DOMAIN 1570 2140 DOMAIN II AND I.

FT DOMAIN 2141 2324 LAMININ G-LIKE 1.

FT DOMAIN 2325 2517 LAMININ G-LIKE 2.

FT DOMAIN 2522 2706 LAMININ G-LIKE 3.

FT DOMAIN 2759 2930 LAMININ G-LIKE 4.

FT DOMAIN 2929 3106 LAMININ G-LIKE 5.

FT DOMAIN 1662 1863 COILED COIL (POTENTIAL).

FT DOMAIN 1923 2146 COILED COIL (POTENTIAL).

FT DISULFID 283 292 BY SIMILARITY.

FT DISULFID 285 303 BY SIMILARITY.

FT DISULFID 305 314 BY SIMILARITY.

FT DISULFID 317 337 BY SIMILARITY.

FT DISULFID 340 349 BY SIMILARITY.

FT DISULFID 374 386 BY SIMILARITY.

FT DISULFID 377 386 BY SIMILARITY.

FT DISULFID 389 407 BY SIMILARITY.

FT DISULFID 410 422 BY SIMILARITY.

FT DISULFID 412 438 BY SIMILARITY.

FT DISULFID 440 449 BY SIMILARITY.

FT DISULFID 452 462 BY SIMILARITY.

FT DISULFID 465 478 BY SIMILARITY.

FT DISULFID 467 482 BY SIMILARITY.

FT DISULFID 484 493 BY SIMILARITY.

FT DISULFID 496 511 BY SIMILARITY.

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FT DISULFID 753 762 BY SIMILARITY.
FT DISULFID 755 769 BY SIMILARITY.
FT DISULFID 772 781 BY SIMILARITY.
FT DISULFID 784 800 BY SIMILARITY.
FT DISULFID 803 818 BY SIMILARITY.
FT DISULFID 805 828 BY SIMILARITY.
FT DISULFID 831 840 BY SIMILARITY.
FT DISULFID 843 858 BY SIMILARITY.
FT DISULFID 861 875 BY SIMILARITY.
FT DISULFID 863 882 BY SIMILARITY.
FT DISULFID 885 894 BY SIMILARITY.
FT DISULFID 897 911 BY SIMILARITY.
FT DISULFID 914 926 BY SIMILARITY.
FT DISULFID 916 933 BY SIMILARITY.
FT DISULFID 935 944 BY SIMILARITY.
FT DISULFID 947 960 BY SIMILARITY.
FT DISULFID 963 975 BY SIMILARITY.
FT DISULFID 965 981 BY SIMILARITY.
FT DISULFID 983 992 BY SIMILARITY.
FT DISULFID 995 1007 BY SIMILARITY.
FT DISULFID 1010 1019 BY SIMILARITY.
FT DISULFID 1012 1026 BY SIMILARITY.
FT DISULFID 1028 1037 BY SIMILARITY.
FT DISULFID 1040 1053 BY SIMILARITY.
FT DISULFID 1056 1068 BY SIMILARITY.
FT DISULFID 1058 1075 BY SIMILARITY.
FT DISULFID 1077 1086 BY SIMILARITY.
FT DISULFID 1089 1099 BY SIMILARITY.
FT DISULFID 1416 1425 BY SIMILARITY.
FT DISULFID 1418 1432 BY SIMILARITY.
FT DISULFID 1435 1444 BY SIMILARITY.
FT DISULFID 1447 1462 BY SIMILARITY.
FT DISULFID 1465 1480 BY SIMILARITY.
FT DISULFID 1467 1490 BY SIMILARITY.
FT DISULFID 1493 1502 BY SIMILARITY.
FT DISULFID 1505 1520 BY SIMILARITY.
FT DISULFID 1523 1535 BY SIMILARITY.
FT DISULFID 1525 1542 BY SIMILARITY.
FT DISULFID 1544 1553 BY SIMILARITY.
FT DISULFID 1556 1567 BY SIMILARITY.
FT DISULFID 1570 1577 INTERCHAIN (PROBABLE).
FT DISULFID 1574 1574 INTERCHAIN (PROBABLE).
FT CARBOHYD 51 51 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 85 85 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 299 299 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 359 359 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 376 376 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 466 466 N-LINKED (GLCNAC. . .) (POTENTIAL).

Query Match 67.9%; Score 36; DB 1; Length 3106;
Best Local Similarity 66.7%; Pred. No. 87;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTFLSYDM 9
DB 2817 GFPPFSYDL 2825

RESULT 9
HV3D_HUMAN STANDARD; PRT; 115 AA.
AC P01765;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-III region TIL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
ON NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=78005528; PubMed=409716;
```

```
RA Wang A.-C., Wang I.Y., Fudenberg H.H.;
RT "Immunoglobulin structure and genetics. Identity between variable
RL J. Biol. Chem. 252:7192-7199(1977).
CC -I- MISCELLANEOUS: THE SEQUENCES OF THE V REGIONS OF THE HEAVY CHAINS
CC OF IGM AND IGG2 ISOLATED FROM A SINGLE PATIENT WITH BICLONAL
CC GAMMOPATHY ARE IDENTICAL. THEIR LIGHT CHAINS ARE APPARENTLY ALSO
CC IDENTICAL.
DR PIR: A02048; H3HUTL.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region.
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12356 MW; 4DCC67D179F62326 CRC64;

Query Match 66.0%; Score 35; DB 1; Length 115;
Best Local Similarity 70.0%; Pred. No. 4.9;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
DB 26 GFTFTDYVMS 35

RESULT 10
HV17_MOUSE STANDARD; PRT; 117 AA.
AC P01786;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region MOPC 47A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=80049769; PubMed=115869;
RT Robinson E.A., Appella E.;
RT "Amino acid sequence of a mouse myeloma immunoglobulin heavy chain
RT (MOPC 47 A) with a 100-residue deletion.";
RL J. Biol. Chem. 254:11418-11430(1979).
CC -I- MISCELLANEOUS: THIS ALPHA CHAIN WAS ISOLATED FROM A MYELOMA
CC PROTEIN THAT CONTAINS ONE LIGHT AND ONE HEAVY CHAIN PER MOLECULE,
CC LINKED BY A DISULFIDE BOND. IN CONTRAST, NORMAL MOUSE IGA
CC MOLECULES CONTAIN TWO LIGHT AND TWO HEAVY CHAINS AND LACK A
CC LIGHT-HEAVY CHAIN DISULFIDE BOND.
DR PIR: A02069; AIMS47.
DR HSSP; P01789; LMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12975 MW; 0C74BE8BBI54BDF4 CRC64;

Query Match 66.0%; Score 35; DB 1; Length 117;
Best Local Similarity 70.0%; Pred. No. 5;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
DB 26 GFTFTDYVMS 35

RESULT 11
HV58_MOUSE STANDARD; PRT; 117 AA.
ID HV58_MOUSE
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AC P18529;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain v region 5-76 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BAUB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RT Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RT the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; J0506; HVMS57.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 5-76.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12991 MW; 93A04782B78B8FA0 CRC64;

Query Match 64.2%; Score 34; DB 1; Length 117;
Best Local Similarity 70.0%; Pred. No. 7.8;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GFTFLSYDMS 10
Db 45 GFTFNKYAMS 54

RESULT 12
ROCI_ARATH
ID ROCI_ARATH STANDARD; PRT; 289 AA.
AC Q9ZU04;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative ribonucleoprotein At5g37220, chloroplast precursor.
GN AT5G37220 OR F365.1.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
RA Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
RA Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
RA Goodman H.M., Smerville C.R., Copenhagen G.P., Preuss D.,
RA Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
RA Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT thaliana.";

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RL Nature 402:761-768(1999).
CC -!- FUNCTION: COULD BE INVOLVED IN SPLICING AND/OR PROCESSING OF
CC CHLOROPLAST RNA'S (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Chloroplast (Potential).
CC -!- SIMILARITY: CONTAINS 2 RNA RECOGNITION MOTIFS (RRM).
CC -----
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CC -----
DR EMBL; AC005896; AAC98043.1; -
DR HSSP; P09651; LUPL.
DR SWISS-2DPAGE; Q9ZU04; ARATH.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF00076; rtm; 2.
DR SMART; SM00360; RRM; 2.
DR PROSITE; PS0102; RRM; 2.
DR PROSITE; PS00030; RRM_RNP_1; 2.
KW RNA-binding; Ribonucleoprotein; Repeat; mRNA processing; Chloroplast;
KW Transit peptide.
FT TRANSIT 1 61 CHLOROPLAST (POTENTIAL).
FT CHAIN 62 289 PUTATIVE RIBONUCLEOPROTEIN AT2G37220.
FT DOMAIN 91 169 RNA-BINDING (RRM) 1.
FT DOMAIN 170 203 LINKER (GLY-RICH).
FT DOMAIN 204 282 RNA-BINDING (RRM) 2.
FT DOMAIN 4 57 SER-RICH.
FT DOMAIN 168 171 POLY-PRO.
SQ SEQUENCE 289 AA; 30718 MW; E500C3C0518369AD CRC64;

Query Match 64.2%; Score 34; DB 1; Length 289;
Best Local Similarity 60.0%; Pred. No. 19;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GFTFLSYDMS 10
Db 246 GFGFVIYDSS 255

RESULT 13
YE08_SCHPO
ID YE08_SCHPO STANDARD; PRT; 326 AA.
AC O13805;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Putative mitochondrial carrier Cl17H9.08.
GN SPAC17H9.08.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Williams R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Felwell T., Fraser A.,
RA Gentes S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odeell C.,
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skellton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grynoprez B.,

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RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Leirach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Carlson A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsberg S.L.,
RA Cerrutti L., Lowe T., McComble W.R., Paulsen I., Potashkin J.,
RA Shpakowski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane (Potential).
CC -!- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC
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CC EMBL; Z98597; CAB1217.1; -.
CC InterPro; IPR002067; MitocCarrier.
CC InterPro; IPR001993; MitocCarrier.
CC Pfam; PF00153; mito.cart; 3.
CC PRINTS; PR00926; MITOCARRIER.
CC PROSITE; PS00215; MITOCARRIER; 2.
CC Hypothetical protein; Mitochondrion; Inner membrane; Repeat;
KW Transmembrane; Transport.
FT TRANSMEM 16 36 POTENTIAL.
FT TRANSMEM 120 140 POTENTIAL.
FT TRANSMEM 191 211 POTENTIAL.
FT TRANSMEM 240 260 POTENTIAL.
FT TRANSMEM 294 314 POTENTIAL.
SQ SEQUENCE 326 AA; 37059 MW; 12163A73260F35D2 CRC64;
Query Match 64.2%; Score 34; DB 1; Length 326;
Best Local Similarity 50.0%; Pred. No. 22;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 1 GFTFLSYDMS 10
I :||:|:
Db 203 GNSFLAYDLA 212
RESULT 14
OS 059B.DROME STANDARD; PRT; 398 AA.
AC Q9W1P8.
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative odorant receptor 59b.
GN OR59B OR CG3569.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Berkeley;
RC MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,
RA April J.P., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
RA Ballaw R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
CC -!- FUNCTION: PROBABLE ROLE IN THE ODORANT RESPONSE, BEING AN ODORANT
CC RECEPTOR.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: BELONGS TO FAMILY DR-OR OF G-PROTEIN COUPLED
CC RECEPTORS.
CC
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CC
CC EMBL; AE003460; AAF47008.1; -.
CC FlyBase; FBgn0034865; Or59b.
CC InterPro; IPR004117; 7tm_6.
CC Pfam; PF02949; 7tm_6; 1.
CC
CC KW Hypothetical protein; Transmembrane; G-protein coupled receptor;
CC Glycoprotein; Olfaction; Multigene family.
FT DOMAIN 1 46 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 47 67 1 (POTENTIAL).
FT DOMAIN 68 84 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 85 105 2 (POTENTIAL).
FT DOMAIN 106 141 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 142 162 3 (POTENTIAL).
FT DOMAIN 163 179 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 180 200 4 (POTENTIAL).
FT DOMAIN 201 269 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 270 290 5 (POTENTIAL).
FT DOMAIN 291 293 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 294 314 6 (POTENTIAL).
FT DOMAIN 315 348 7 (POTENTIAL).
FT TRANSMEM 349 369 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 370 398 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 124 124 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 398 AA; 46164 MW; DF631070C9BAC002 CRC64;
Query Match 64.2%; Score 34; DB 1; Length 398;
Best Local Similarity 70.0%; Pred. No. 27;

Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GFTFLSYDMS 10
| | | | | : |
Db 154 GSTFLSYALS 163

RESULT 15

ARP2_PLAFA
ID ARP2_PLAFA STANDARD; PRT; 451 AA.
AC P13824;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Clustered-asparagine-rich protein (Fragment).
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86206015; PubMed=3517875;
RA Wahlgren M., Aaslund L., Franzen L., Sundvall M., Waahlén B.,
RA Berzins K., McNicol L.A., Bjoerkman A., Wigzell H., Perlmann P.,
RA Pettersson U.;
RT "A Plasmodium falciparum antigen containing clusters of asparagine
RT residues.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:2677-2681(1986)
CC -!- SIMILARITY: CONTAINS 2 RNA RECOGNITION MOTIFS (RRM).
CC -----
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DR EMBL; M13021; AAA29485.1; -;
DR PIR; A23535; A23535.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF00076; rrm; 2.
DR SMART; SM00360; RRM; 2.
DR PROSITE; PS0102; RRM; 2.
DR PROSITE; PS00030; RRM_RNP.1; FALSE_NEG.
KW RNA-binding; Repeat; Malaria.
FT NON_TER 1
FT DOMAIN 24 114 RNA-BINDING (RRM) 1.
FT DOMAIN 350 443 RNA-BINDING (RRM) 2.
FT DOMAIN 119 128 POLY-ASN.
FT DOMAIN 175 180 POLY-ASN.
FT DOMAIN 195 210 POLY-ASN.
FT DOMAIN 237 245 POLY-ASN.
FT DOMAIN 264 285 POLY-ASN.
SQ SEQUENCE 451 AA; 52204 MW; B686354D85F8C293 CRC64;

Query Match 64.2%; Score 34; DB 1; Length 451;
Best Local Similarity 75.0%; Pred. No. 30;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GFTFLSYD 8
| | | | |
Db 407 GFGFVSVD 414

Search completed: November 18, 2002, 17:33:20
Job time : 3.45098 secs

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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:01 ; Search time 10.4412 Seconds
(without alignments)
197.341 Million cell updates/sec

Title: US-09-016-061-52

Perfect score: 53

Sequence: 1 GFTFLSYDMS 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL21.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	83.0	486	11 Q91Z07	Q91Z07 mus musculus
2	40	75.5	119	11 Q920E7	Q920E7 mus musculus
3	39	73.6	437	11 Q9RIA4	Q9RIA4 mus musculus
4	39	73.6	487	11 Q99KA4	Q99KA4 mus musculus
5	38	71.7	118	4 Q9UL91	Q9UL91 homo sapien
6	38	71.7	471	4 Q8TC77	Q8TC77 homo sapien
7	38	71.7	497	4 Q8WK24	Q8WK24 homo sapien
8	38	71.7	1376	17 Q97AU9	Q97AU9 thermoplasm
9	37	69.8	95	4 Q9ULB6	Q9ULB6 homo sapien
10	37	69.8	147	4 Q9Y509	Q9Y509 homo sapien
11	37	69.8	1379	17 Q9HL55	Q9HL55 thermoplasm
12	36	67.9	76	2 Q9AFQ9	Q9AFQ9 shigella fl
13	36	67.9	113	4 Q9UL90	Q9UL90 homo sapien
14	36	67.9	140	10 Q9ARP0	Q9ARP0 oryza sativ
15	36	67.9	149	12 Q8QXX8	Q8QXX8 garlic late
16	36	67.9	312	12 Q67551	Q67551 garlic late

17	36	67.9	613	4 Q8WUK1	Q8WUK1 homo sapien
18	36	67.9	1924	12 Q67654	Q67654 garlic late
19	36	67.9	1924	12 Q8QXY8	Q8QXY8 garlic late
20	36	67.9	1967	12 Q85652	Q85652 blueberry s
21	36	67.9	2183	12 Q64962	Q64962 apple stem
22	36	67.9	2185	12 Q9E948	Q9E948 apple stem
23	35	66.0	116	4 Q9UL93	Q9UL93 homo sapien
24	35	66.0	314	10 Q9ZQR7	Q9ZQR7 arabidopsis
25	35	66.0	363	10 Q9ZU66	Q9ZU66 arabidopsis
26	35	66.0	363	10 Q94C63	Q94C63 arabidopsis
27	35	66.0	404	10 Q9FGJ5	Q9FGJ5 arabidopsis
28	35	66.0	431	10 Q8VZ63	Q8VZ63 arabidopsis
29	35	66.0	469	11 Q8R3V9	Q8R3V9 mus musculu
30	35	66.0	484	11 Q8VEA0	Q8VEA0 mus musculu
31	35	66.0	588	16 Q8ZGB8	Q8ZGB8 yersinia pe
32	35	66.0	594	5 P91823	P91823 caenorhabdl
33	34	64.2	112	4 Q9HCC1	Q9HCC1 homo sapien
34	34	64.2	275	2 Q8VSN4	Q8VSN4 shigella fl
35	34	64.2	310	12 Q91QV4	Q91QV4 grapevine b
36	34	64.2	324	3 Q96X08	Q96X08 candida gla
37	34	64.2	347	8 Q34096	Q34096 crithidia f
38	34	64.2	349	12 Q85125	Q85125 african swi
39	34	64.2	364	10 Q9LIR8	Q9LIR8 arabidopsis
40	34	64.2	405	2 Q9AFX2	Q9AFX2 shigella fl
41	34	64.2	412	16 Q92VB2	Q92VB2 rhizobium m
42	34	64.2	452	16 Q98IN8	Q98IN8 rhizobium l
43	34	64.2	475	5 Q9XWR7	Q9XWR7 caenorhabdl
44	34	64.2	690	10 Q9LIB7	Q9LIB7 arabidopsis
45	34	64.2	690	10 Q94OD0	Q94OD0 arabidopsis

ALIGNMENTS

RESULT 1

Q91Z07
ID Q91Z07 PRELIMINARY; PRT; 486 AA.
AC Q91Z07;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Hypothetical 52.7 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC010324; AAH10324.1; -
DR InterPro; IPR003598; Ig_C2.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_4.
DR SMART; SM00408; Igc2; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein; Immunoglobulin domain.
SQ SEQUENCE 486 AA; 52682 MW; 4FEF835125DA870B CRC64;

Query Match 83.0%; Score 44; DB 11; Length 486;
Best Local Similarity 80.0%; Pred. No. 2;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
DB 45 GFSFTSYDMS 54

RESULT 2

Q920E7
ID Q920E7 PRELIMINARY; PRT; 119 AA.
AC Q920E7;
DT 01-DEC-2001 (TREMBLrel. 19, Created)

```

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Pterin-mimicking anti-idiotope heavy chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Atkin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.;
RT "Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed
in Mammalian Cells.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307937; AAL09421.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig; 1.
FT NON_TER 1
FT NON_TER 119
SQ SEQUENCE 119 AA; 13025 MW; F6E904044381CA7C CRC64;

Query Match 75.5%; Score 40; DB 11; Length 119;
Best Local Similarity 80.0%; Pred. No. 3;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
D 11111111
Db 26 GFTFSYGS 35

RESULT 3
Q9R1A4 PRELIMINARY; PRT; 437 AA.
AC Q9R1A4;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Gamma1 heavy chain of Mab7 (Fragment).
GN IGH-4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
antibody (Mab 7, its light and heavy chains) and construction of a
single chain antibody (scFv).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF152372; AAD40243.1; -.
DR HSSP; P01842; 7FAB.
DR MGD; MGI:96446; Igh-4.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 4.
DR SMART; SM00406; Igv; 1.
DR SMART; SM00410; IG_like; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 437
SQ SEQUENCE 437 AA; 5C3A7BB3E7D697C CRC64;

Query Match 73.6%; Score 39; DB 11; Length 437;
Best Local Similarity 80.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
D 11111111
Db 25 GFTFSYGS 34

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RESULT 4
Q99KA4 PRELIMINARY; PRT; 487 AA.
AC Q99KA4;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Hypothetical 52.6 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC004786; AAH04786.1; -.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 4.
DR SMART; SM00409; IG; 3.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; Igv; 1.
DR SMART; SM00410; IG_like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 487 AA; 52554 MW; 7DC8E96DB33077B CRC64;

Query Match 73.6%; Score 39; DB 11; Length 487;
Best Local Similarity 80.0%; Pred. No. 19;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
D 11111111
Db 45 GFTFSYGS 54

RESULT 5
Q9UL91 PRELIMINARY; PRT; 118 AA.
AC Q9UL91;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035023; AAD56259.1; -.
DR HSSP; P01772; 2FBA.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; Igv; 1.
FT NON_TER 1
FT NON_TER 118
SQ SEQUENCE 118 AA; 12843 MW; D0633949F2AC149D CRC64;

Query Match 71.7%; Score 38; DB 4; Length 118;

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Best Local Similarity 70.0%; Pred. No. 7.2;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10

Db 26 GFTFSSYSMN 35

RESULT 6

Q8TC77 PRELIMINARY; PRT; 471 AA.

AC Q8TC77;

DT 01-JUN-2002 (TReMBLrel. 21, Created)

DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)

DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)

DE Hypothetical 51.8 kDa protein.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RP [1]

RN SEQUENCE FROM N.A.

RC TISSUE=SPLEN;

RA Strausberg R.;

RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC024289; AAH24289.1; -

KW Hypothetical protein.

SQ SEQUENCE 471 AA; 51791 MW; 388F7F4CF588660E CRC64;

Query Match

Best Local Similarity 71.7%; Score 38; DB 4; Length 471;

Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10

Db 45 GFTFSSYSMN 54

RESULT 7

Q8WY24 PRELIMINARY; PRT; 497 AA.

AC Q8WY24;

DT 01-MAR-2002 (TReMBLrel. 20, Created)

DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)

DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)

DE SNC66 protein.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Zheng S., Shao X., Cao J., Geng L., Fang Y., Dong Q.;

RT "Identification and characterization of SNC66, a Ig-like gene which is

down-regulated in colorectal cancer.";

RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF283666; AAL36987.1; -

DR InterPro; IPR003599; Ig.

DR InterPro; IPR003597; Ig-cl.

DR InterPro; IPR003596; Ig_MHC.

DR Pfam; PF00047; Ig; 4.

DR SMART; SM00409; IG; 4.

DR SMART; SM00407; IGcl; 2.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.

SQ SEQUENCE 497 AA; 53665 MW; F24D08DFA5A663E5 CRC64;

Query Match

Best Local Similarity 71.7%; Score 38; DB 4; Length 497;

Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10

Db 45 GFTFSSYSMN 54

Db 45 GYTFIAYDIN 54

RESULT 8

Q97AU9

ID Q97AU9

AC Q97AU9;

DT 01-OCT-2001 (TReMBLrel. 18, Created)

DT 01-OCT-2001 (TReMBLrel. 18, Last sequence update)

DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)

DE Hypothetical protein TV0710.

GN TV0710 OR TVG0719175

OS Thermoplasma volcanium.

OC Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;

OC Thermoplasmataceae; Thermoplasma.

OX NCBI_TaxID=50339;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=GSSI / DSM 4299 / JCM 9571;

RX MEDLINE=20570466; PubMed=11121031;

RA Kawashima T., Amano N., Koike H., Makino S.-I., Higuchi S.,

RA Kawashima T., Watanabe K., Yamazaki M., Kanehori K., Kawamoto T.,

RA Nunoshima T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.;

RT "Archaeal adaptation to higher temperatures revealed by genomic

sequence of Thermoplasma volcanium.";

RL Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000).

DR EMBL; AP000993; BAB59852.1; -

DR InterPro; IPR00209; Peptidase_S8.

DR PRINTS; PR00723; SUBTILISIN.

DR PROSITE; PS00138; SUBTILASE_SER; UNKNOWN_1.

KW Hypothetical protein; Complete proteome.

SQ SEQUENCE 1376 AA; 147895 MW; 430384BC49873FDD CRC64;

Query Match

Best Local Similarity 71.7%; Score 38; DB 17; Length 1376;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFLSYDM 9

Db 1113 GFATISYDI 1121

RESULT 9

Q9ULB6

ID Q9ULB6

AC Q9ULB6;

DT 01-MAY-2000 (TReMBLrel. 13, Created)

DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)

DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)

DE Immunoglobulin heavy chain (Fragment).

GN VH.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Tange Y., Kayano H.;

RT "Human VH gene sequence.";

RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB035268; BAA87067.1; -

DR HSSP; P01772; 2FB4.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_v.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IGV; 1.

FT NON_TER 1

FT NON_TER 95

SQ SEQUENCE 95 AA; 10527 MW; 90A8C6D16D22574A CRC64;

Query Match

Best Local Similarity 69.8%; Score 37; DB 4; Length 95;

Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GFTFLSYDMS 10
 ||||| : ||
 Db 25 GFTFSSYWMS 34

RESULT 10

ID Q9Y509 PRELIMINARY; PRT; 147 AA.
 AC Q9Y509;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE VH3 protein (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96071149; PubMed=7475288;
 RA Cao J., Vescio R.A., Rettig M.B., Hong C.H., Kim A., Lee J.C.,
 RA Lichtenstein A.K., Berenson J.R.;
 RT "A CD10-positive subset of malignant cells is identified in multiple
 RT myeloma using PCR with patient-specific immunoglobulin gene primers.";
 RL Leukemia 9:1548-1553(1995).
 DR EMBL; S80860; AAD14339.1; -.
 DR HSSP; P01772; 2FB4.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; Igv; 1.
 FT NON_TER
 SQ SEQUENCE 147 AA; 15768 MW; 8489FCAAA7BC925C CRC64;

Query Match 69.8%; Score 37; DB 4; Length 147;

Best Local Similarity 70.0%; Pred. No. 14;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GFTFLSYDMS 10

||||| : ||
 Db 26 GFTFSTYGMS 35

RESULT 11

ID Q9HL55 PRELIMINARY; PRT; 1379 AA.
 AC Q9HL55;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Lymphoethelial protein.
 OS TA0376.
 OS Thermoplasma acidophilum.
 OC Archaea; Euryarchaeota; Thermoplasmatata; Thermoplasmatatales;
 OC Thermoplasmatataceae; Thermoplasma.
 OX NCBI_TaxID=2303;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DSM 1728;
 RX MEDLINE=20479972; PubMed=11029001;
 RA Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C.,
 RA Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.;
 RT "The genome sequence of the thermoacidophilic scavenger Thermoplasma
 RT acidophilum.";
 RL Nature 407:508-513(2000).
 DR EMBL; AL445064; CAC11520.1; -.
 DR InterPro; IPR000209; Peptidase_S8.
 DR PROSITE; PS00138; SUBTILASE_SER; UNKNOWN_1.
 KW Complete proteome.
 SQ SEQUENCE 1379 AA; 147449 MW; 9177B2EBB765A540 CRC64;

Query Match 69.8%; Score 37; DB 17; Length 1379;

Best Local Similarity 66.7%; Pred. No. 1.4e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GFTFLSYDM 9

||||| : ||
 Db 1115 GFTFIYDI 1123

RESULT 12

ID Q9AFQ9 PRELIMINARY; PRT; 76 AA.
 AC Q9AFQ9;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Putative transposase (Transposase-like protein).
 GN S0183 OR CP0174.
 OS Shigella flexneri, and
 OS Shigella flexneri 2a.
 OC Plasmid virulence plasmid pWR501, and Plasmid pCP301.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Shigella.
 OX NCBI_TaxID=623, 42897;
 [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=S.flexneri; PLASMID=VIRULENCE PLASMID PWR501;
 RX MEDLINE=21189246; PubMed=11292750;
 RA Venkatesan M.M., Goldberg M.B., Rose D.J., Grothbeck E.J., Burland V.,
 RA Blattner F.R.;
 RT "Complete DNA sequence and analysis of the large virulence plasmid of
 RT Shigella flexneri.";
 RL Infect. Immun. 69:3271-3285(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=S.flexneri 2a; STRAIN=PCP301; PLASMID=PCP301;
 RA Jin O., Zhang J.Y., Liu H., Yang J., Yang F., Zhang X.B., Wang J.H.,
 RA Yang G.W., Wu H.T., Dong J., Sun L.L., Xue Y., Zhao A.L., Gao Y.S.,
 RA Zhu J.P., Kan B., Chen S.X., Yao Z.J., He B.K., Chen R.S., Ma D.L.,
 RA Yuan Z.H., Xu J.G., Wang Y., Shen Y., Lu W.C., Qiang B.Q., Wen Y.M.,
 RA Hou Y.D.;
 RT "Complete DNA sequence and analysis of the large virulence plasmid
 RT pCP301 of Shigella flexneri.";
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF348706; AAK18493.1; -.
 DR EMBL; AF386526; AAL72511.1; -.
 DR InterPro; IPR002560; Transposase_12.
 DR Pfam; PF01610; Transposase_12; 1.
 KW Plasmid.

SQ SEQUENCE 76 AA; 9010 MW; 206A0C5A58CCE93 CRC64;

Query Match 67.9%; Score 36; DB 2; Length 76;

Best Local Similarity 70.0%; Pred. No. 11;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GFTFLSYDMS 10

||||| : ||
 Db 16 GFKFLSMDMN 25

RESULT 13

ID Q9UL90 PRELIMINARY; PRT; 113 AA.
 AC Q9UL90;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Myosin-reactive immunoglobulin heavy chain variable region
 DE (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035024; AAD56260.1; -;
DR HSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12437 MW; ED57FDD19086D07F CRC64;

Query Match 67.9%; Score 36; DB 4; Length 113;
Best Local Similarity 77.8%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTFLSYDM 9
Db 26 GFTFSYGM 34
|||||

RESULT 14

ID Q9ARPO PRELIMINARY; PRT; 140 AA.
AC Q9ARPO;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE P0024G09.20 protein.
GN P0024G09.20.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC clone:P0024G09.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AP003311; BAB40128.1; -;
SQ SEQUENCE 140 AA; 15782 MW; 222CB6E0CA6FCBDD CRC64;

Query Match 67.9%; Score 36; DB 10; Length 140;
Best Local Similarity 66.7%; Pred. No. 21;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFLSYDM 9
Db 131 GFTFSYEL 139
|||||

RESULT 15

ID Q8QXX8 PRELIMINARY; PRT; 149 AA.
AC Q8QXX8;
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE RNA-dependent RNA-polymerase (Fragment).
OS garlic latent virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Carlaviruses.
OX NCBI_TaxID=12458;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=YH3;
RX MEDLINE=21578618; PubMed=11722009;
RA Chen J., Chen J.P., Adams M.J.;
RT "Molecular characterisation of a complex mixture of viruses in garlic with mosaic symptoms in China.";
RL Arch. Virol. 146:1841-1853(2001).
DR EMBL; AJ292228; CAC83692.1; -;
FT NON_TER 1
FT NON_TER 149 149
SQ SEQUENCE 149 AA; 17307 MW; BE6E5747657A7F54 CRC64;

Query Match 67.9%; Score 36; DB 12; Length 149;
Best Local Similarity 66.7%; Pred. No. 23;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 FTFLSYDMS 10
Db 5 FTFLRYDLN 13
|||||

Search completed: November 18, 2002, 17:40:36
Job time : 11.4912 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:21:57 ; Search time 13.8235 Seconds
(without alignments)
96.394 Million cell updates/sec

Title: US-09-016-061-52

Perfect score: 53

Sequence: 1 GFTFLSYDMS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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- 1: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
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 - 14: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
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 - 16: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
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 - 19: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
 - 20: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
 - 21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
 - 22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
 - 23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	53	100.0	10	AAW76016	LM609 grafted anti
2	53	100.0	10	AAAB61374	Mutant VH CDR1 pep
3	47	88.7	10	AAW76007	LM609 grafted anti
4	47	88.7	10	AAAB61365	LM609 VH CDR1 pep
5	47	88.7	117	AAW76001	Vitaxin antibody h
6	47	88.7	117	AAAG63587	A heavy chain vari
7	47	88.7	117	AAAB61359	Vitaxin heavy chai
8	45	84.9	117	AAW86141	Protein sequence o
9	44	83.0	117	AAW86137	Protein sequence o
10	44	83.0	128	AAW54000	Anti-CD4 antibody

11	44	83.0	134	AAW24713	Sequence encoded b
12	44	83.0	225	AAW05710	TRY40. Mus muscul
13	44	83.0	225	AAW06478	TRY40. Mus muscul
14	44	83.0	225	AAW3675	Single chain polyp
15	44	83.0	225	AAW99645	Single chain bindi
16	44	83.0	236	AAW06479	TRY61. Mus muscul
17	44	83.0	236	AAW3676	Single chain polyp
18	44	83.0	236	AAW02188	TRY61 single chain
19	44	83.0	236	AAW99646	Single chain bindi
20	44	83.0	246	AAW06480	TRY59. Mus muscul
21	44	83.0	246	AAW3677	Single chain polyp
22	44	83.0	246	AAW02189	TRY59 single chain
23	44	83.0	246	AAW99647	Single chain bindi
24	44	83.0	250	AAW06481	TRY104b. Mus musc
25	44	83.0	250	AAW3678	Single chain polyp
26	44	83.0	250	AAW02190	TRY104b single cha
27	44	83.0	250	AAW99648	Single chain bindi
28	44	83.0	256	ABP45381	Human Buys binding
29	44	83.0	256	ABP46108	Human Buys binding
30	44	83.0	448	AAW06476	Heavy chain of ant
31	44	83.0	448	AAW3673	Mouse anti-bovine
32	44	83.0	448	AAW97376	Murine anti-BGH MA
33	44	83.0	448	AAW99643	Anti-BGH monoclonal
34	44	83.0	466	AAW24812	Sequence encoded b
35	43	81.1	97	AAW40112	Anti-hiL12 antibod
36	43	81.1	102	ABW39276	Peptide #6782 enco
37	43	81.1	102	AAW59940	Human brain expres
38	43	81.1	102	AAW72535	Human bone marrow
39	43	81.1	102	AAW32779	Peptide #6816 enco
40	43	81.1	102	ABG42355	Human peptide enco
41	43	81.1	139	AAW21652	Humanised reshaped
42	43	81.1	252	ABP45601	Human Buys binding
43	43	81.1	470	AAU74298	Anti-human AILIM m
44	43	81.1	470	AAU74300	Anti-human AILIM m
45	42	79.2	10	AAW76015	LM609 grafted anti

ALIGNMENTS

RESULT 1
AAW76016
ID AAW76016 standard; Protein; 10 AA.
XX AAW76016;
XX AC
XX DT 02-NOV-1998 (first entry)
XX DE LM609 grafted antibody V-H region CDR1 protein fragment #4.
XX KW Vitaxin; antibody; variable region; heavy chain; light chain; Integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
XX OS Mus sp.
XX PN WO9833919-A2.
XX PD 06-AUG-1998.
XX PF 30-JAN-1998; 98WO-US01826.
XX PR 30-JAN-1997; 97US-0791391.
XX PA (IXSY-) IXSYS INC.
XX PI Glaser SM, Huse WD;
XX WPI; 1998-437472/37.
XX DR N-PSDB; AAV49853.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
PS Claim 60; Page 41; 129pp; English.

XX AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
CC antibodies contain non-murine framework regions so are suitable for use
CC in humans. Enhanced types of LM609 have affinity more than 90 times
CC greater than that of parent the parent antibody.

XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 53; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00028;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTFLSYDMS 10
|||||
Db 1 GFTFLSYDMS 10
|||||

RESULT 2
AAB61374
ID AAB61374 standard; peptide: 10 AA.
XX
AC AAB61374;
XX
XX 03-APR-2001 (first entry)
XX
XX Mutant VH CDR1 peptide #3.
XX
XX LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
KW inflammatory; cancer; retina; restenosis; osteoporosis;
KW
XX
XX Unidentified.
XX
XX WO200078815-A1.
XX
XX 28-DEC-2000.
XX
XX 23-JUN-2000; 2000WO-US17454.
XX
XX 24-JUN-1999; 99US-0339922.
XX
XX (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX
XX Huse WD, Wu H;
XX
XX WPI; 2001-050110/06.
XX
XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
PT osteoporosis -
XX
XX Disclosure; Page 41; 132pp; English.
XX
XX The present invention relates to enhanced LM609 grafted antibodies
CC exhibiting selective binding affinity to alphavbeta_3 integrin or
CC their functional fragments. The antibodies or their functional
CC fragments, can be used in the diagnosis and treatment of
CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory

CC diseases (such as psoriasis and chronic articular rheumatism),
CC disorders associated with inappropriate or inopportune invasion of
CC vessels (such as diabetic retinopathy, neovascular glaucoma and
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
CC diseases (such as macular degeneration), restenosis and
CC osteoporosis.
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 53; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00028;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTFLSYDMS 10
|||||
Db 1 GFTFLSYDMS 10
|||||

RESULT 3
AAW76007
ID AAW76007 standard; Protein; 10 AA.
XX
AC AAW76007;
XX
XX 02-NOV-1998 (first entry)
XX
XX LM609 grafted antibody V-H region CDR1 protein fragment #1.
XX
XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
XX
XX Mus sp.
XX
XX WO9833919-A2.
XX
XX 06-AUG-1998.
XX
XX 30-JAN-1998; 98WO-US01826.
XX
XX 30-JAN-1997; 97US-0791391.
XX
XX (IXSY-) IXSYS INC.
XX
XX Glaser SM, Huse WD;
XX
XX WPI; 1998-437472/37.
XX
XX N-PSDB; AAV49844.
XX
XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
XX Disclosure; Page 40; 129pp; English.

AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
CC antibodies contain non-murine framework regions so are suitable for use
CC in humans. Enhanced types of LM609 have affinity more than 90 times
CC greater than that of parent the parent antibody.

XX
SQ Sequence 10 AA;

Query Match 88.7%; Score 47; DB 19; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.0046;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
 IIII IIIII
 Db 1 GFTFSSYDMS 10

RESULT 4
 AAB61365
 ID AAB61365 standard; peptide; 10 AA.
 XX AAB61365;
 AC
 XX
 DT 03-APR-2001 (first entry)
 DE LM609 VH CDR1 peptide.
 XX
 KW LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
 KW Inflammatory; cancer; retina; restenosis; osteoporosis.
 XX
 OS Unidentified.
 XX
 PN WO200078815-A1.
 XX
 PD 28-DEC-2000.
 XX
 PF 23-JUN-2000; 2000WO-US17454.
 XX
 PR 24-JUN-1999; 99US-0339922.
 XX
 PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
 XX
 PI Huse WD, Wu H;
 XX
 DR WPI; 2001-050110/06.
 XX
 PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -
 XX
 PS Claim 4; Page 39; 132pp; English.
 CC The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphavbeta_3 integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.
 XX
 SO Sequence 10 AA;

Query Match 88.7%; Score 47; DB 22; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.0046;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
 IIII IIIII
 Db 1 GFTFSSYDMS 10

RESULT 5
 AAW76001
 ID AAW76001 standard; Protein; 117 AA.
 XX

AC AAW76001;
 XX
 DT 02-NOV-1998 (first entry)
 XX
 DE Vitaxin antibody heavy chain variable region protein fragment.
 XX
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.
 XX
 OS Mus sp.
 XX
 PN WO9833919-A2.
 XX
 PD 06-AUG-1998.
 XX
 PF 30-JAN-1998; 98WO-US01826.
 XX
 PR 30-JAN-1997; 97US-0791391.
 XX
 PA (IXSY-) IXSYS INC.
 XX
 PI Glaser SM, Huse WD;
 XX
 DR WPI; 1998-437472/37.
 DR N-PSDB; AAV49820.
 XX
 PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 PS Claim 1; Fig 1a; 129pp; English.
 XX
 CC This sequence represents a fragment of the vitaxin antibody variable
 CC heavy chain region. Vitaxin and the antibody LM609 bind selectively to
 CC integrin alphavbeta3 and can be used to inhibit binding of alphavbeta3
 CC to a ligand and thus block integrin-mediated signal transduction. This is
 CC useful in the treatment, prevention and diagnosis of alphavbeta3-mediated
 CC disease, specifically angiogenesis and restenosis (but also e.g.
 CC (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,
 CC cancer, psoriasis, rheumatoid arthritis, macular degeneration,
 CC osteoporosis etc.). The antibodies contain non-murine framework regions
 CC so are suitable for use in humans. Enhanced types of LM609 have affinity
 CC more than 90 times greater than that of parent the parent antibody.
 XX
 SO Sequence 117 AA;

Query Match 88.7%; Score 47; DB 19; Length 117;
 Best Local Similarity 90.0%; Pred. No. 0.065;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
 IIII IIIII
 Db 26 GFTFSSYDMS 35

RESULT 6
 AAG63587
 ID AAG63587 standard; Protein; 117 AA.
 XX
 AC AAG63587;
 XX
 DT 15-OCT-2001 (first entry)
 XX
 DE A heavy chain variable region of LM609 grafted antibody.
 XX
 KW Grafted antibody; LM609; integrin; alphavbeta3; inflammatory disorder;
 KW chronic articular rheumatism; psoriasis; diabetic retinopathy;
 KW neovascular glaucoma; capillary proliferation; atherosclerotic plaque;
 KW cancer.

```

XX OS Synthetic.
XX OS Mus sp.
XX PN US2001011125-A1.
XX XX
XX PD 02-AUG-2001.
XX XX
XX PF 30-JAN-1997; 97US-0790540.
XX PR 30-JAN-1997; 97US-0790540.
XX PA (HUSE/) HUSE W D.
XX XX
XX PI Huse WD;
XX DR
XX DR WPI; 2001-496171/54.
XX DR N-PSDB; AAH74623.
XX PT
XX PT New LM609 grafted antibody exhibiting selective binding affinity to
XX PT alphavbeta3, comprising at least one LM609 grafted heavy and light
XX PT chain polypeptide, useful for diagnosing and treating e.g. inflammatory
XX PT disorders or cancer -
XX XX
XX PS Claim 1; Fig 1A; 25pp; English.
XX XX
XX CC The present sequence represents the heavy chain variable region of the
XX CC grafted monoclonal antibody LM609. LM609 is a murine antibody which
XX CC specifically recognises the integrin alphavbeta3, and inhibits its
XX CC functional activity. The LM609 grafted antibody has the
XX CC complementarity determining regions (CDRs) substituted into a non-murine
XX CC framework. Nucleic acids encoding LM609 grafted heavy and light chain
XX CC polypeptides and fragments are useful in diagnostic and therapeutic
XX CC purposes, such as in the production of LM609 grafted antibodies and
XX CC fragments having binding specificity and inhibitory activity against
XX CC the integrin alphavbeta3. The antibody can be used for the diagnosis
XX CC or treatment of alphavbeta3-mediated diseases (e.g. inflammatory
XX CC disorders, chronic articular rheumatism, psoriasis, disorders
XX CC associated with inappropriate or inopportune invasion of vessels such
XX CC as diabetic retinopathy, neovascular glaucoma and capillary
XX CC proliferation in atherosclerotic plaques, or cancers), and to inhibit
XX CC binding activity of alphavbeta3 that are necessary for progression of
XX CC an alphavbeta3-mediated disease.
XX SQ Sequence 117 AA;

Query Match 88.7%; Score 47; DB 22; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.065;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GFTFLSYDMS 10
Db ||||| |||||
26 GFTFSSYDMS 35

RESULT 7
AAB61359
ID AAB61359 standard; protein; 117 AA.
XX AC
XX AC AAB61359;
XX XX
XX DT 03-APR-2001 (first entry)
XX XX
XX DE Vitaxin heavy chain variable region protein.
XX XX
XX DE LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
XX KW inflammatory; cancer; retina; restenosis; osteoporosis.
XX KW
XX OS Unidentified.
XX OS
XX PN WO200078815-A1.
XX PD 28-DEC-2000.

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XX XX 23-JUN-2000; 2000WO-US17454.
XX XX
XX PR 24-JUN-1999; 99US-0339922.
XX XX
XX PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX XX
XX PI Huse WD, Wu H;
XX XX
XX DR WPI; 2001-050110/06.
XX XX
XX PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity
XX PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
XX PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
XX PT osteoporosis -
XX XX
XX PS Disclosure; Fig 1; 132pp; English.
XX XX
XX CC The present invention relates to enhanced LM609 grafted antibodies
XX CC exhibiting selective binding affinity to alphavbeta_3 integrin or
XX CC their functional fragments. The antibodies or their functional
XX CC fragments can be used in the diagnosis and treatment of
XX CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
XX CC diseases (such as psoriasis and chronic articular rheumatism),
XX CC disorders associated with inappropriate or inopportune invasion of
XX CC vessels (such as diabetic retinopathy, neovascular glaucoma and
XX CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
XX CC diseases (such as macular degeneration), restenosis and
XX CC osteoporosis.
XX SQ Sequence 117 AA;

Query Match 88.7%; Score 47; DB 22; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.065;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GFTFLSYDMS 10
Db ||||| |||||
26 GFTFSSYDMS 35

RESULT 8
AAW86141
ID AAW86141 standard; Protein; 117 AA.
XX AC
XX AC AAW86141;
XX XX
XX DT 03-MAR-1999 (first entry)
XX XX
XX DE Protein sequence of de-immunised murine A33 Vh.
XX XX
XX KW Non-immunogenic; epitope; T-cell; immunogenicity; immune system; SK;
XX KW immunogl bulin; therapeutic; streptokinase; murine; de-immunised.
XX XX
XX OS Mus sp.
XX XX
XX PN WO9852976-A1.
XX XX
XX PD 26-NOV-1998.
XX XX
XX PF 21-MAY-1998; 98WO-GB01473.
XX XX
XX PR 14-APR-1998; 98GB-0007751.
XX PR 21-MAY-1997; 97GB-0010480.
XX PR 31-JUL-1997; 97GB-0016197.
XX PR 28-NOV-1997; 97GB-0025270.
XX PR 02-DEC-1997; 97US-0067235.
XX XX
XX PA (BIOV-) BIOVATION LTD.
XX XX
XX PI Carr FJ;
XX XX
XX DR WPI; 1999-045301/04.

```

XX Reducing immunogenicity of proteins - by modifying the amino acid
 PT sequence of the protein to eliminate potential epitopes for T-cells
 PT of a given species
 XX
 XX Example 6; Fig 27; 77pp; English.
 PS
 CC The invention relates to a method for the production of non-immunogenic
 CC proteins. The method comprises determining at least part of the amino
 CC acid sequence of the protein; (b) identifying in the amino acid sequence
 CC one or more potential epitopes for T-cells (T-cell epitopes) of the given
 CC species; and (c) modifying the amino acid sequence to eliminate at least
 CC one of the T-cell epitopes identified in step (b) thereby to eliminate or
 CC reduce the immunogenicity of the protein when exposed to the immune
 CC system of the given species. A method of analysing a pre-existing protein
 CC to predict the basis for immunogenic responses is also provided. The
 CC methods can be used particularly for reducing the immunogenicity of
 CC immunoglobulins or therapeutic proteins, e.g. streptokinase (SK). The
 CC products can be used for diagnosis and therapy. The present sequence
 CC represents the protein sequence of de-immunised murine A33 Vh.
 XX
 SQ Sequence 117 AA;

Query Match 84.9%; Score 45; DB 20; Length 117;
 Best Local Similarity 80.0%; Pred. No. 0.16;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
 |||| :||||
 Db 26 GFTFTTYDMS 35

RESULT 9
 AAW86137
 ID AAW86137 standard; Protein; 117 AA.

XX AC AAW86137;
 XX DT 03-MAR-1999 (first entry)
 XX DE Protein sequence of de-immunised humanised A33 Vh.
 XX KW Non-immunogenic; epitope; T-cell; immunogenicity; immune system; SK;
 XX KW Immunogl bulin; therapeutic; streptokinase; humanised; de-immunised;
 XX OS Homo sapiens.
 XX PN WO9852976-A1.
 XX PD 26-NOV-1998.

XX PF 21-MAY-1998; 98WO-GB01473.
 XX PR 14-APR-1998; 98GB-0007751.
 XX PR 21-MAY-1997; 97GB-0010480.
 XX PR 31-JUL-1997; 97GB-0016197.
 XX PR 28-NOV-1997; 97GB-0025270.
 XX PR 02-DEC-1997; 97US-0067235.
 XX PA (BIOV-) BIOVATION LTD.
 XX PI Carr FJ;
 XX WPI; 1999-045301/04.
 XX
 PT Reducing immunogenicity of proteins - by modifying the amino acid
 PT sequence of the protein to eliminate potential epitopes for T-cells
 PT of a given species
 XX
 XX Example 5; Fig 25; 77pp; English.
 XX
 CC The invention relates to a method for the production of non-immunogenic
 CC proteins. The method comprises determining at least part of the amino

CC acid sequence of the protein; (b) identifying in the amino acid sequence
 CC one or more potential epitopes for T-cells (T-cell epitopes) of the given
 CC species; and (c) modifying the amino acid sequence to eliminate at least
 CC one of the T-cell epitopes identified in step (b) thereby to eliminate or
 CC reduce the immunogenicity of the protein when exposed to the immune
 CC system of the given species. A method of analysing a pre-existing protein
 CC to predict the basis for immunogenic responses is also provided. The
 CC methods can be used particularly for reducing the immunogenicity of
 CC immunoglobulins or therapeutic proteins, e.g. streptokinase (SK). The
 CC products can be used for diagnosis and therapy. The present sequence
 CC represents the protein sequence of de-immunised humanised A33 Vh.
 XX
 SQ Sequence 117 AA;

Query Match 83.0%; Score 44; DB 20; Length 117;
 Best Local Similarity 80.0%; Pred. No. 0.26;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
 |||| :||||
 Db 26 GFTFTTYDMS 35

RESULT 10
 AAW54000
 ID AAW54000 standard; Protein; 128 AA.

XX AC AAW54000;
 XX DT 29-JUL-1998 (first entry)
 XX DE Anti-CD4 antibody VH3 monkey clone 3-40.
 XX KW Anti-CD4 antibody; monkey; human; therapy; variable heavy domain;
 XX KW Old World monkey; constant domain; eczema; immuno-modulated disease;
 XX KW rheumatoid arthritis.
 XX OS Primate sp.

Key Location/Qualifiers
 FT Misc-difference 1..128
 ET /note= "Xaa= unspecified amino acid"

XX PN US5750105-A.
 XX PD 12-MAY-1998.
 XX PF 07-JUN-1995; 95US-0476349.
 XX PR 10-JUL-1992; 92US-0912292.
 XX PR 25-JUL-1991; 91US-0735064.
 XX PR 23-MAR-1992; 92US-0856281.
 XX PR 05-DEC-1995; 95US-0379072.
 XX PR 07-JUN-1995; 95US-0476349.
 XX PA (IDEC-) IDEC PHARM CORP.

XX PI Hanna N, Newman RA, Raab RW;
 XX WPI; 1998-296690/26.
 XX
 PT Improved method for antibody treatment - uses an antibody comprising
 PT an Old World monkey variable region and a human constant domain
 XX
 XX Example 1; Fig 9c; 84pp; English.

XX This sequence represents the VH3 domain of an anti-CD4 antibody
 CC (Ab). This sequence can be used in the method of the invention for
 CC treating a subject, where the treatment comprises administration of an
 CC Ab. The method comprises the administration of an antibody which has an
 CC Old World monkey (e.g. baboon or macaque) variable region which binds to
 CC an antigen (Ag) (or Ag binding portion), and a human constant domain. The
 CC method is useful for the treatment of eczema and immuno-modulated

CC diseases and especially rheumatoid arthritis. The recombinant antibodies
 CC used are sufficiently different from native monkey antibodies to allow
 CC human antigens to raise these antibodies, but similar enough to human
 CC antibody so there is no immune response to the antibodies in humans.
 CC Compared to antibodies used in therapy in prior art, these antibodies do
 CC not induce human anti-antibodies on repeated administration. They also
 CC have longer half-lives and do not have a lack of effector function with
 CC human cells.

XX Sequence 128 AA;

Query Match 83.0%; Score 44; DB 19; Length 128;
 Best Local Similarity 80.0%; Pred. No. 0.29;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
 |||||:|||||
 Db 26 GFTFSSYDMN 35

RESULT 11

AAR24713
 ID AAR24713 standard; Protein; 134 AA.

XX AAR24713;

XX 28-DEC-1992 (first entry)

XX Sequence encoded by the genomic chimeric heavy chain variable region
 (VFH) gene.

XX Chimeric monoclonal antibody; anti-fibrin antibody; PCR;
 XX antithrombotic agent; myocardial infarction therapy.

XX Mus musculus.

Key	Location/Qualifiers
FT Peptide	1..19
FT Region	/label= leader
FT Region	23..49
FT Region	/label= Framework Region (FR) 1
FT Region	50..54
FT Region	/label= Complementarity determining region(CDR)1
FT Region	55..68
FT Region	/label= FR-2
FT Region	69..84
FT Region	/label= CDR-2
FT Region	85..114
FT Region	/label= FR-3
FT Region	115..123
FT Region	/label= CDR-3
FT Region	124..134
FT Region	/label= FR-4

XX EP491351-A.

XX 24-JUN-1992.

XX 17-DEC-1991; 91EP-0121591.

XX 18-DEC-1990; 90JP-0413829.

XX 11-NOV-1991; 91JP-0294464.

XX (TAKE) TAKEDA CHEM IND LTD.

XX Iwasa-S, Taka H, Watanabe T, Tada H;

XX WPI; 1992-209528/26.

XX N-PSD#; AAQ25666.

XX Chimeric monoclonal antibodies - contain anti-human fibrin
 PT antibody light and heavy chain variable and constant for treating
 PT thrombotic conditions e.g. myocardial infarction

XX Example; Figure 4; 87pp; English.

CC PCR primers 5'mvh and 3'mvh were used to produce a VH gene-contg.
 CC fragment of about 330bp. The fragment was isolated and subcloned in
 CC pUC119. The fragment was found to be a functional VH structural
 CC gene, referred to as VFH, comprising a VH gene belonging to the
 CC subgroup III (VHIII) and the DSP2 and JH4 genes. Northern blot
 CC analysis using the whole RNA of F1B1-11 cells confirmed that VFH
 CC was the gene expressed in F1B1-11 cells. The sequence is given in
 CC AAQ25666.

SQ Sequence 134 AA;

Query Match 83.0%; Score 44; DB 13; Length 134;
 Best Local Similarity 80.0%; Pred. No. 0.3;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
 |||||:|||||
 Db 45 GFTFSSYDMS 54

RESULT 12

AAR05710
 ID AAR05710 standard; protein; 225 AA.

XX AAR05710;

XX 07-JAN-1991 (first entry)

XX TRV40.

XX Monoclonal antibody; variable chain anti-bovine growth hormone.

XX Mus musculus.

Key	Location/Qualifier
FT Region	4..126
FT Peptide	/label= LCVR(1-41)
FT Region	127..147
FT Region	/label= linker
FT Region	148..471
FT Peptide	/label= HCVR(8-115)
FT Peptide	472..483
FT Region	/label= linker
FT Region	484..678
FT Region	/label= LCVR(45-109)

XX US4946778-A.

XX 07-AUG-1990.

XX 19-JAN-1989; 89US-0299617.

XX 19-JAN-1989; 89US-0299617.

XX 02-SEP-1986; 86US-0902971.

XX 02-SEP-1987; 87US-0092110.

XX (GENE-) GENEX CORP.

XX Ladner RC, Bird RE, Hardman K;

XX WPI; 1990-260350/34.

XX N-PSDB; AAQ05710.

XX Single polypeptide chain binding molecules - having light chain
 PT variable region of antibody linked by peptide to heavy chain
 PT variable region.

XX Disclosure; Fig 24; 68pp; English.

XX The sequence was constructed from the variable regions of a MAb

CC produced by the cell line 3C2, an IgG1 with a gamma 1 heavy chain
 CC and kappa light chain. The sequence encodes a single chain binding
 CC molecule comprising the variable regions of heavy and light chains
 CC linked by a peptides. The variable region of each DNA chain was
 CC prep'd. by introducing a ClaI site and an initiation codon (atcgatg)
 CC prior to the first codon of the mature sequence and a HindIII site
 CC and termination codon (taagctt) after codon 123 (heavy chain) or
 CC 109 (light chain). The plasmids constructed to contain these
 CC portions were pGX3772 and pGX3773 (heavy and light resp.). TRY40
 CC Met-[LCVR(1-41)]-I-A-K-A-F-K-N-[HCVR(8-115)]-P-G-S-[LCVR(45-109)].
 CC See also AAQ05708-19.
 XX
 SQ Sequence 225 AA;
 Query Match 83.0%; Score 44; DB 11; Length 225;
 Best Local Similarity 80.0%; Pred. No. 0.53;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GFTFLSYDMS 10
 Db ||||:||||
 68 GFTFISYGMS 77
 RESULT 13
 AAR06478
 ID AAR06478 standard; protein; 225 AA.
 XX
 AC AAR06478;
 DT 07-JAN-1991 (first entry)
 XX
 DE TRY40.
 XX
 KW Monoclonal antibody; variable chain anti-bovine growth hormone.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifier
 FT misc_RNA 2..42
 FT /label= LCVR(1-41)
 FT Peptide 43..49
 FT /label= linker
 FT misc_RNA 50..157
 FT /label= HCVR(8-115)
 FT Peptide 158..160
 FT /label= linker
 FT misc_RNA 161..225
 FT /tag= e
 FT /label= LCVR(45-109)
 XX
 XX US4946778-A.
 PN
 PD 07-AUG-1990.
 XX
 PF 19-JAN-1989; 89US-0299617.
 XX
 PR 19-JAN-1989; 89US-0299617.
 PR 02-SEP-1986; 86US-0902971.
 PR 02-SEP-1987; 87US-0092110.
 XX
 XX (GENE-) GENEX CORP.
 PA
 XX
 XX Ladner RC, Bird RE, Hardman K;
 PI
 XX
 DR WPI; 1990-260350/34.
 DR N-PSDB; AAQ05710.
 XX
 PT Single polypeptide chain binding molecules - having light chain
 PT variable region of antibody linked by peptide to heavy chain
 PT
 XX
 PS Disclosure; Fig 24; 68pp; English.

XX The sequence was constructed from the variable regions of a MAb
 CC produced by the cell line 3C2, an IgG1 with a gamma 1 heavy chain
 CC and kappa light chain. The sequence encodes a single chain binding
 CC molecule comprising the variable regions of heavy and light chains
 CC linked by a peptides. The variable region of each DNA chain was
 CC prep'd. by introducing a ClaI site and an initiation codon (atcgatg)
 CC prior to the first codon of the mature sequence and a HindIII site
 CC and termination codon (taagctt) after codon 123 (heavy chain) or
 CC 109 (light chain). The plasmids constructed to contain these
 CC portions were pGX3772 and pGX3773 (heavy and light resp.). TRY40
 CC Met-[LCVR(1-41)]-I-A-K-A-F-K-N-[HCVR(8-115)]-P-G-S-[LCVR(45-109)].
 CC See also AAR06476-R06484.
 XX
 SQ Sequence 225 AA;
 Query Match 83.0%; Score 44; DB 11; Length 225;
 Best Local Similarity 80.0%; Pred. No. 0.53;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GFTFLSYDMS 10
 Db ||||:||||
 68 GFTFISYGMS 77
 RESULT 14
 AAR43675
 ID AAR43675 standard; Protein; 225 AA.
 XX
 AC AAR43675;
 XX
 DT 23-MAY-1994 (first entry)
 XX
 DE Single chain polypeptide with affinity for bovine growth hormone.
 XX
 KW Monoclonal antibody; MAB; affinity; binding; antigen; diagnostics;
 KW therapy; imaging; purification; 1; Mismatches 1; Indels 0; Gaps 0;
 XX
 OS Synthetic.
 XX
 PN US5260203-A.
 PD
 PD 09-NOV-1993.
 XX
 PF 02-SEP-1986; 86US-0902971.
 XX
 PR 02-SEP-1986; 86US-0902971.
 PR 02-SEP-1987; 87US-0092110.
 PR 19-JAN-1989; 89US-0299617.
 PR 25-APR-1990; 90US-0512910.
 XX
 XX (ENZO-) ENZON INC.
 PA
 XX
 XX Bird RE, Hardman K, Ladner RC;
 PI
 XX
 DR WPI; 1993-367875/46.
 DR N-PSDB; AAQ51536.
 XX
 PT Single chain polypeptide for binding antigen - comprising light
 PT and heavy chain antigen binding portions linked by peptide linker
 XX
 XX Example 1; Figure 24; 78pp; English.
 PS
 XX The single chain polypeptide is derived from the mature light and
 CC heavy chains of a mouse monoclonal antibody (MAB) and has affinity
 CC for a given antigen (Bovine growth hormone). It comprises a first
 CC polypeptide comprising the antigen binding portion of of the light
 CC chain variable region of an antibody and a second polypeptide
 CC comprising the antigen binding portion of the heavy chain variable
 CC region of an antibody and at least one peptide linker linking the
 CC first and second polypeptide chains. The resulting single chain

CC polypeptide can be used in diagnostics, therapy
 CC (in vivo and in vitro), imaging, purifications and biosensors.
 CC This particular single chain binding molecule was designated TRY40
 CC and contains two linker peptides.

SQ Sequence 225 AA;

Query Match 83.0%; Score 44; DB 14; Length 225;
 Best Local Similarity 80.0%; Pred. No. 0.53;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
 ||||:||||
 Db 68 GFTFISYGMS 77

RESULT 15

AAR99645
 ID AAR99645 standard; Protein; 225 AA.

XX AC

XX AC AAR99645;

DT 11-OCT-1996 (first entry)

XX Single chain binding molecule TRY40.

XX Antibody engineering; single polypeptide chain binding molecule;
 KW heavy chain; light chain; monoclonal antibody; Mab;
 KW bovine growth hormone; bGH; immunoaffinity purification; TRY40.

XX Chimeric Mus sp.;
 OS Chimeric synthetic.

XX Key Location/Qualifiers
 FT Domain 2..42

FT /label= L-chain
 FT /note= "Mab 3C2 VL amino acids 1-41"

FT Region 43..49

FT /label= Linker
 FT /note= "linker derived from MCPC-603"

FT Domain 50..157

FT /label= H-chain
 FT /note= "Mab 3C2 VH amino acids 8-105"

FT Region 158..160

FT /label= Linker
 FT /note= "linker derived from MCPC-603 Fv region"

FT Domain 161..225

FT /label= L-chain
 FT /note= "Mab 3C2 VL amino acids 45-109"

XX PN

XX US5534621-A.

XX PD

XX 09-JUL-1996.

XX PF

XX 02-SEP-1986; 86US-0902971.

XX PR

XX 19-JAN-1989; 89US-0299617.

XX PR

XX 02-SEP-1986; 86US-0902971.

XX PR

XX 02-SEP-1987; 87US-0092110.

XX PR

XX 25-APR-1990; 90US-0512910.

XX PR

XX 01-APR-1993; 93US-0040440.

XX PR

XX 06-JUN-1995; 95US-0468992.

XX PA

XX (ENZO-) ENZON LABS INC.

XX PI

XX Bird RE, Hardman K, Ladner RC;

XX DR

XX WPI; 1996-33309/33.

XX DR

XX N-PSDT; AAT13735.

XX PT

XX Immuno:purificn. using single binding chain molecule including
 PT antigen-binding parts of antibody light and heavy chain variable
 PT regions connected by a linker - is smaller, stabler and less

PT expensive than complete antibodies

XX

PS Example 1; Fig 24; 78pp; English.

XX

CC A novel single chain binding molecule (AAR99645), designated TRY40,
 CC is a 2-linker construction incorporating VL and VH regions from
 CC IgG1 anti-bovine growth hormone mouse IgG1 monoclonal antibody 3C2,
 CC and peptide linkers from the Fv region of the IgA anti-phosphoryl
 CC choline myeloma antibody MCPC-603. The single chain binding
 CC molecule was expressed in E.coli transformants carrying pCX3776,
 CC which incorporates encoding DNA (AAT13735), at a level of 7-2% of total
 CC cell protein. Single chain binding molecules (see also AAR99646-51)
 CC retain the binding specificity and affinity of the light and heavy
 CC chain aggregate variable region of the native antibody but have the
 CC advantages of smaller size, greater stability and reduced cost.

XX Sequence 225 AA;

Query Match 83.0%; Score 44; DB 17; Length 225;

Best Local Similarity 80.0%; Pred. No. 0.53;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10

||||:||||

Db 68 GFTFISYGMS 77

Search completed: November 18, 2002, 17:31:34

Job time : 13.8235 secs

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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:54:45 ; Search time 1.96078 Seconds
(without alignments)
76.811 Million cell updates/sec

Title: US-09-016-061-52
Perfect score: 53
Sequence: 1 GFTFLSYDMS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 97044 seqs, 15060890 residues

Total number of hits satisfying chosen parameters: 97044

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications,AA:*

- 1: /cgn2_5/ptodata/1/pubaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/1/pubaa/PC8_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubaa/PC7US_PUBCOMB.pep.*
- 8: /cgn2_6/ptodata/1/pubaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubaa/US09_NEW_PUB.pep.*
- 10: /cgn2_6/ptodata/1/pubaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/1/pubaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/1/pubaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	47	88.7	117	8	US-08-790-540A-2
2	47	88.7	117	8	US-08-791-391A-2
3	44	83.0	128	10	US-09-850-165-110
4	43	81.1	102	10	US-09-864-761-43848
5	43	81.1	470	10	US-09-859-053-32
6	43	81.1	470	10	US-09-859-053-36
7	42	79.2	117	8	US-08-790-540A-6
8	42	79.2	117	8	US-08-791-391A-6
9	41	77.4	123	10	US-09-850-165-112
10	40	75.5	87	10	US-09-840-459-53
11	40	75.5	89	10	US-09-840-459-48
12	40	75.5	98	10	US-09-840-459-38
13	40	75.5	98	10	US-09-840-459-39
14	40	75.5	98	10	US-09-840-459-44
15	40	75.5	98	10	US-09-840-459-45
16	40	75.5	98	12	US-10-066-895-4
17	40	75.5	118	9	US-09-423-800-46
18	40	75.5	118	9	US-09-423-800-56
19	40	75.5	137	9	US-09-423-800-76

20-	40	75.5	137	9	US-09-423-800-77	Sequence 77, Appl
21	40	75.5	140	10	US-09-286-240-4	Sequence 4, Appl
22	40	75.5	144	10	US-09-881-823-12	Sequence 12, Appl
23	39	73.6	88	10	US-09-840-459-51	Sequence 51, Appl
24	39	73.6	89	10	US-09-840-459-49	Sequence 49, Appl
25	39	73.6	98	10	US-09-822-698A-18	Sequence 18, Appl
26	39	73.6	98	10	US-09-840-459-40	Sequence 40, Appl
27	39	73.6	98	12	US-10-025-687-19	Sequence 19, Appl
28	39	73.6	113	10	US-09-056-160B-11	Sequence 11, Appl
29	39	73.6	116	10	US-09-840-459-80	Sequence 80, Appl
30	39	73.6	118	9	US-09-144-886-64	Sequence 64, Appl
31	39	73.6	118	9	US-09-144-886-65	Sequence 65, Appl
32	39	73.6	118	9	US-09-144-886-66	Sequence 66, Appl
33	39	73.6	118	9	US-09-144-886-67	Sequence 67, Appl
34	39	73.6	119	10	US-09-811-123-3	Sequence 3, Appl
35	39	73.6	120	10	US-09-840-459-85	Sequence 85, Appl
36	39	73.6	120	12	US-10-025-687-4	Sequence 4, Appl
37	39	73.6	121	10	US-09-840-459-92	Sequence 92, Appl
38	39	73.6	123	10	US-09-840-459-82	Sequence 82, Appl
39	39	73.6	124	10	US-09-840-459-81	Sequence 81, Appl
40	39	73.6	124	10	US-09-840-459-89	Sequence 89, Appl
41	39	73.6	125	10	US-09-840-459-76	Sequence 76, Appl
42	39	73.6	125	10	US-09-850-165-107	Sequence 107, Appl
43	39	73.6	127	10	US-09-811-737-1	Sequence 1, Appl
44	39	73.6	127	10	US-09-840-459-87	Sequence 87, Appl
45	39	73.6	128	10	US-09-840-459-77	Sequence 77, Appl

ALIGNMENTS

RESULT 1
US-08-790-540A-2
; Sequence 2, Application US/08790540A
; Patent No. US20010011125A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESS: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,540A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-790-540A-2

Query Match 88.7%; Score 47; DB 8; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.041;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GFTFLSYDMS 10
| | | | | | | | | |
Db 26 GFTFSSYDMS 35

RESULT 2

US-08-791-391A-2
; Sequence 2, Application US/08791391A
; Patent No. US20010016645A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791.391A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-391A-2

Query Match 88.7%; Score 47; DB 8; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.041;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GFTFLSYDMS 10
| | | | | | | | | |
Db 26 GFTFSSYDMS 35

RESULT 3

US-09-850-165-110
; Sequence 110, Application US/09850165
; Patent No. US20020150580A1
; GENERAL INFORMATION:
; APPLICANT: NEWMAN, ROLAND A.
; APPLICANT: HANNA, NABIL
; APPLICANT: RAAB, RONALD W.
; TITLE OF INVENTION: RECOMBINANT ANTIBODIES FOR HUMAN THERAPY
; FILE REFERENCE: 037003-0280614
; CURRENT APPLICATION NUMBER: US/09/850.165
; CURRENT FILING DATE: 2001-05-08
; PRIOR APPLICATION NUMBER: 09/082,472
; PRIOR FILING DATE: 1998-05-21
; PRIOR APPLICATION NUMBER: 08/476,237
; PRIOR FILING DATE: 1995-06-07

; PRIOR APPLICATION NUMBER: 08/397,072
; PRIOR FILING DATE: 1995-04-17
; PRIOR APPLICATION NUMBER: 07/912,292
; PRIOR FILING DATE: 1992-07-10
; PRIOR APPLICATION NUMBER: 07/856,281
; PRIOR FILING DATE: 1992-03-23
; PRIOR APPLICATION NUMBER: 07/735,064
; PRIOR FILING DATE: 1991-07-25
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 110
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: MonKey
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (12)
; OTHER INFORMATION: Ile or Val
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (23)
; OTHER INFORMATION: Ser, Val or Ala
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (49)
; OTHER INFORMATION: Any amino acid, preferably Gly, Ser or Ala
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (79)
; OTHER INFORMATION: Val, Ala or Leu
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (87)
; OTHER INFORMATION: Lys, Glu or Arg
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (88)
; OTHER INFORMATION: Thr, Pro or Ala
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (93)
; OTHER INFORMATION: Leu or Val
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (95)
; OTHER INFORMATION: Phe or Tyr
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (97)
; OTHER INFORMATION: Thr or Ala
US-09-850-165-110

Query Match 83.0%; Score 44; DB 10; Length 128;
Best Local Similarity 80.0%; Pred. No. 0.16;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GFTFLSYDMS 10
| | | | | | | | | |
Db 26 GFTFSSYDMS 35

RESULT 4

US-09-864-761-43848
; Sequence 43848, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO

; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Acomica-x-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 43848
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AB019440.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.84
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.89
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.95
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1
; OTHER INFORMATION: EST_HUMAN HIT: AW405458.1, EVALUATE 3.00e-43
; OTHER INFORMATION: SWISSPROT HIT: P01766, EVALUATE 2.00e-39
US-09-864-761-43848

Query Match 81.1%; Score 43; DB 10; Length 102;
Best Local Similarity 88.9%; Pred. No. 0.19;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GFTFLSYDM 9
| | | | |
Db 17 GFTFSSYDM 25

RESULT 5

US-09-859-053-32
; Sequence 32, Application US/09859053
; Patent No. US20020102658A1
; GENERAL INFORMATION:
; APPLICANT: Tsuji, Takashi

; APPLICANT: Tezuka, Katsunari
; APPLICANT: Hori, No. US20020102658A1uaki
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
; TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
; FILE REFERENCE: 06501-079001
; CURRENT APPLICATION NUMBER: US/09/859,053
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: JP 2001-99508
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-147116
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-859-053-32

Query Match 81.1%; Score 43; DB 10; Length 470;
Best Local Similarity 88.9%; Pred. No. 0.86;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GFTFLSYDM 9
| | | | |
Db 45 GFTFSSYDM 53

RESULT 6

US-09-859-053-36
; Sequence 36, Application US/09859053
; Patent No. US20020102658A1
; GENERAL INFORMATION:
; APPLICANT: Tsuji, Takashi
; APPLICANT: Tezuka, Katsunari
; APPLICANT: Hori, No. US20020102658A1uaki
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
; TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
; FILE REFERENCE: 06501-079001
; CURRENT APPLICATION NUMBER: US/09/859,053
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: JP 2001-99508
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-147116
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-859-053-36

Query Match 81.1%; Score 43; DB 10; Length 470;
Best Local Similarity 88.9%; Pred. No. 0.86;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GFTFLSYDM 9
| | | | |
Db 45 GFTFSSYDM 53

RESULT 7

US-08-790-540A-6
; Sequence 6, Application US/08790540A
; Patent No. US2001001125A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 24

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Campbell & Flores LLP
;; STREET: 4370 La Jolla Village Drive, Suite 700
;; CITY: San Diego
;; STATE: California
;; COUNTRY: United States
;; ZIP: 92122
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/790,540A
;; FILING DATE: 30-JAN-1997
;; CLASSIFICATION: 424
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Campbell, Cathryn A.
;; REGISTRATION NUMBER: 31,815
;; REFERENCE/DOCKET NUMBER: P-IX 2405
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (619) 535-9001
;; TELEFAX: (619) 535-8949
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 117 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-790-540A-6

Query Match 79.2%; Score 42; DB 8; Length 117;
Best Local Similarity 80.0%; Pred. No. 0.33;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GFTFLSYDMS 10
||| |||||
Db 26 GFAFSSYDMS 35

RESULT 8
US-08-791-391A-6
; Sequence 6, Application US/08791391A
; Patent No. US20010016645A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,391A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949

;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 117 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-791-391A-6

Query Match 79.2%; Score 42; DB 8; Length 117;
Best Local Similarity 80.0%; Pred. No. 0.33;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GFTFLSYDMS 10
||| |||||
Db 26 GFAFSSYDMS 35

RESULT 9
US-09-850-165-112
; Sequence 112, Application US/09850165
; Patent No. US20020150580A1
; GENERAL INFORMATION:
; APPLICANT: NEWMAN, ROLAND A.
; APPLICANT: HANNA, RONALD W.
; APPLICANT: RAAB, RONALD W.
; TITLE OF INVENTION: RECOMBINANT ANTIBODIES FOR HUMAN THERAPY
; FILE REFERENCE: 037003-0280614
; CURRENT APPLICATION NUMBER: US/09/850,165
; CURRENT FILING DATE: 2001-05-08
; PRIOR APPLICATION NUMBER: 09/082,472
; PRIOR FILING DATE: 1998-05-21
; PRIOR APPLICATION NUMBER: 08/476,237
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/397,072
; PRIOR FILING DATE: 1995-04-17
; PRIOR APPLICATION NUMBER: 07/912,292
; PRIOR FILING DATE: 1992-07-10
; PRIOR APPLICATION NUMBER: 07/856,281
; PRIOR FILING DATE: 1992-03-23
; PRIOR APPLICATION NUMBER: 07/735,064
; PRIOR FILING DATE: 1991-07-25
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 112
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Monkey
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (12)
; OTHER INFORMATION: Ile or Val
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (23)
; OTHER INFORMATION: Ser, Val or Ala
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (49)
; OTHER INFORMATION: Any amino acid, preferably Gly, Ser or Ala
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (74)
; OTHER INFORMATION: Asn or Asp
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (75)
; OTHER INFORMATION: Ala or Ser
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (78)
; OTHER INFORMATION: Met, Ser or Thr

FEATURE: *
NAME/KEY: MOD_RES
LOCATION: (79)
OTHER INFORMATION: Val, Ala or Leu
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (80)
OTHER INFORMATION: Phe or Tyr
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (84)
OTHER INFORMATION: Ser, Asp or Asn
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (87)
OTHER INFORMATION: Lys, Glu or Arg
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (88)
OTHER INFORMATION: Thr, Pro or Ala
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (93)
OTHER INFORMATION: Leu or Val
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (95)
OTHER INFORMATION: Phe or Tyr
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (97)
OTHER INFORMATION: Thr or Ala
US-09-850-165-112

Query Match 77.4%; Score 41; DB 10; Length 123;
Best Local Similarity 70.0%; Pred. No. 0.53;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
| | | | : | | :
Db 26 GFTFTYDMS 35

RESULT 10
US-09-840-459-53
; Sequence 53, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840.459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; SOFTWARE: FastSeq for Windows Version 3.0
; NUMBER OF SEQ ID NOS: 107
; SEQ ID NO 53
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Mus musculus

US-09-840-459-53
Query Match 75.5%; Score 40; DB 10; Length 87;
Best Local Similarity 80.0%; Pred. No. 0.58;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GFTFLSYDMS 10
| | | | | | | |
Db 15 GFTFSYDMS 24

RESULT 11
US-09-840-459-48
; Sequence 48, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840.459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 48
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-840-459-48

Query Match 75.5%; Score 40; DB 10; Length 89;
Best Local Similarity 80.0%; Pred. No. 0.59;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GFTFLSYDMS 10
| | | | | | | |
Db 17 GFTFSYDMS 26

RESULT 12
US-09-840-459-38
; Sequence 38, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840.459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193

; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 38
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-840-459-38

Query Match 75.5%; Score 40; DB 10; Length 98;
Best Local Similarity 80.0%; Pred. No. 0.65;
Matches 8; Conservative 0; Mismatches 2; Indels 2; Gaps 0;

Qy 1 GFTFLSYDMS 10
||||| ||| ||
Db 26 GFTFSSYTMS 35

RESULT 13
US-09-840-459-39
; Sequence 39, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 39
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-840-459-39

Query Match 75.5%; Score 40; DB 10; Length 98;
Best Local Similarity 80.0%; Pred. No. 0.65;
Matches 8; Conservative 0; Mismatches 2; Indels 2; Gaps 0;

Qy 1 GFTFLSYDMS 10
||||| ||| ||
Db 26 GFTFSSYTMS 35

RESULT 14
US-09-840-459-44
; Sequence 44, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND

; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 44
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-840-459-44

Query Match 75.5%; Score 40; DB 10; Length 98;
Best Local Similarity 80.0%; Pred. No. 0.65;
Matches 8; Conservative 0; Mismatches 2; Indels 2; Gaps 0;

Qy 1 GFTFLSYDMS 10
||||| ||| ||
Db 26 GFTFSSYTMS 35

RESULT 15
US-09-840-459-45
; Sequence 45, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 45
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-840-459-45

Query Match 75.5%; Score 40; DB 10; Length 98;
Best Local Similarity 80.0%; Pred. No. 0.65;
Matches 8; Conservative 0; Mismatches 2; Indels 2; Gaps 0;

Qy 1 GFTFLSYDMS 10
||||| ||| ||
Db 26 GFTFSSYTMS 35

Search completed: November 18, 2002, 18:45:13
Job time : 1.96078 secs

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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:01 : Search time 4.2402 Seconds
(without alignments)
69.390 Million cell updates/sec

Title: US-09-016-061-52

Perfect score: 53

Sequence: 1 GFTFLSYDMS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/1/iaa/5A-COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B-COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A-COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B-COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS-COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44	83.0	128	1	US-08-478-039-73
2	44	83.0	128	1	US-08-478-039-102
3	44	83.0	128	1	US-08-476-349A-73
4	44	83.0	128	1	US-08-476-349A-102
5	44	83.0	225	6	5455030-5
6	44	83.0	236	6	5455030-7
7	44	83.0	247	6	5455030-9
8	44	83.0	447	6	5455030-1
9	42	79.2	239	2	US-07-956-399-4
10	42	79.2	247	5	PCT-US94-07659-2
11	41	77.4	119	5	PCT-US94-07659-6
12	41	77.4	123	1	US-08-478-039-71
13	41	77.4	123	1	US-08-478-039-104
14	41	77.4	123	1	US-08-476-349A-71
15	41	77.4	123	1	US-08-476-349A-104
16	40	75.5	98	2	US-08-665-202-31
17	40	75.5	116	3	US-08-545-809A-101
18	40	75.5	116	4	US-08-983-607-36
19	40	75.5	122	1	US-08-276-852-80
20	40	75.5	122	1	US-08-899-575-80
21	40	75.5	122	1	US-08-899-575-80
22	40	75.5	122	5	PCT-US95-08743-80
23	40	75.5	123	2	US-08-665-202-30
24	40	75.5	124	4	US-08-983-607-47
25	40	75.5	239	2	US-08-553-497A-18
26	39	73.6	35	2	US-08-765-179B-1
27	39	73.6	98	2	US-08-428-197-48

28 39 73.6 98 5 PCT-US93-10555-48 Sequence 48, Appl
29 39 73.6 102 2 US-08-273-146-65 Sequence 65, Appl
30 39 73.6 110 1 US-08-211-202-117 Sequence 117, App
31 39 73.6 113 3 US-08-974-899-6 Sequence 6, Appl
32 39 73.6 116 2 US-08-428-197-2 Sequence 2, Appl
33 39 73.6 116 5 PCT-US93-10555-2 Sequence 2, Appl
34 39 73.6 117 3 US-08-545-809A-109 Sequence 109, App
35 39 73.6 117 4 US-08-983-607-46 Sequence 46, Appl
36 39 73.6 117 4 US-08-752-693A-3 Sequence 3, Appl
37 39 73.6 117 4 US-08-752-693A-4 Sequence 4, Appl
38 39 73.6 117 4 US-09-157-370-1 Sequence 1, Appl
39 39 73.6 118 2 US-08-652-816A-12 Sequence 12, Appl
40 39 73.6 118 4 US-08-487-761-15 Sequence 15, Appl
41 39 73.6 118 5 PCT-US93-08435-10 Sequence 10, Appl
42 39 73.6 120 4 US-09-025-769B-38 Sequence 38, Appl
43 39 73.6 120 4 US-09-025-769B-63 Sequence 63, Appl
44 39 73.6 121 1 US-08-339-582-2 Sequence 2, Appl
45 39 73.6 122 2 US-07-934-373C-21 Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-08-478-039-73
; Sequence 73, Application US/08478039
; Patent No. 5681722
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,039
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-160
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant

; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Monkey
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: VH3 clone 3-40
US-08-478-039-73

Query Match 83.0%; Score 44; DB 1; Length 128;
Best Local Similarity 80.0%; Pred. No. 0.29;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTFLSYDMS 10
DB 26 GTTFSSYDMN 35

RESULT 2

US-08-478-039-102
; Sequence 102, Application US/08478039
; Patent No. 5681722
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,039
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-160
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021

; INFORMATION FOR SEQ ID NO: 102:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Monkey
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: #40

US-08-478-039-102

Query Match 83.0%; Score 44; DB 1; Length 128;
Best Local Similarity 80.0%; Pred. No. 0.29;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTFLSYDMS 10
DB 26 GTTFSSYDMN 35

RESULT 3

US-08-476-349A-73
; Sequence 73, Application US/08476349A
; Patent No. 5750105
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,349A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-161
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021

; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Monkey
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: VH3 clone 3-40
US-08-476-349A-73

Query Match 83.0%; Score 44; DB 1; Length 128;
Best Local Similarity 80.0%; Pred. No. 0.29;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GFTFLSYDMS 10
|||||
Db 26 GFTFSSYDMN 35

RESULT 4
US-08-476-349A-102
; Sequence 102, Application US/08476349A
; Patent No. 5750105
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,349A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-161
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 102:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Monkey
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: #40
US-08-476-349A-102

Query Match 83.0%; Score 44; DB 1; Length 128;
Best Local Similarity 80.0%; Pred. No. 0.29;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GFTFLSYDMS 10
|||||
Db 26 GFTFSSYDMN 35

RESULT 5

5455030-5
; Patent No. 5455030
; APPLICANT: LADNER, ROBERT C.; BIRD, ROBERT E.; HARDMAN, KARL
; TITLE OF INVENTION: IMMUNOTHERAPY USING SINGLE CHAIN
; POLYPEPTIDE BINDING MOLECULES
; NUMBER OF SEQUENCES: 24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/40,440
; FILING DATE: 1-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 512,910
; FILING DATE: 25-APR-1990
; APPLICATION NUMBER: 299,617
; FILING DATE: 19-JAN-1989
; APPLICATION NUMBER: 92,110
; FILING DATE: 02-SEP-1987
; APPLICATION NUMBER: 902,971
; FILING DATE: 01-SEP-1986
; SEQ ID NO: 5;
; LENGTH: 225
5455030-5

Query Match 83.0%; Score 44; DB 6; Length 225;
Best Local Similarity 80.0%; Pred. No. 0.52;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GFTFLSYDMS 10
|||||
Db 68 GFTFISYGMS 77

RESULT 6
5455030-7
; Patent No. 5455030
; APPLICANT: LADNER, ROBERT C.; BIRD, ROBERT E.; HARDMAN, KARL
; TITLE OF INVENTION: IMMUNOTHERAPY USING SINGLE CHAIN
; POLYPEPTIDE BINDING MOLECULES
; NUMBER OF SEQUENCES: 24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/40,440
; FILING DATE: 1-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 512,910
; FILING DATE: 25-APR-1990
; APPLICATION NUMBER: 299,617
; FILING DATE: 19-JAN-1989
; APPLICATION NUMBER: 92,110
; FILING DATE: 02-SEP-1987
; APPLICATION NUMBER: 902,971
; FILING DATE: 01-SEP-1986
; SEQ ID NO: 7;
; LENGTH: 236
5455030-7

Query Match 83.0%; Score 44; DB 6; Length 236;
Best Local Similarity 80.0%; Pred. No. 0.54;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GFTFLSYDMS 10
|||||
Db 138 GFTFISYGMS 147

RESULT 7
5455030-9
; Patent No. 5455030
; APPLICANT: LADNER, ROBERT C.; BIRD, ROBERT E.; HARDMAN, KARL
; TITLE OF INVENTION: IMMUNOTHERAPY USING SINGLE CHAIN
; POLYPEPTIDE BINDING MOLECULES
; NUMBER OF SEQUENCES: 24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/40,440
; FILING DATE: 1-APR-1993

;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 512,910
; FILING DATE: 25-APR-1990
; APPLICATION NUMBER: 299,617
; FILING DATE: 19-JAN-1989
; APPLICATION NUMBER: 92,110
; FILING DATE: 02-SEP-1987
; APPLICATION NUMBER: 902,971
; FILING DATE: 01-SEP-1986
; SEQ ID NO:9
; LENGTH: 247
5455030-9

Query Match 83.0%; Score 44; DB 6; Length 247;
Best Local Similarity 80.0%; Pred. No. 0.57;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
|||:|:| |
Db 150 GFTFISYGMS 159

RESULT 8

5455030-1
; Patent No. 5455030
; APPLICANT: LADNER, ROBERT C.; BIRD, ROBERT E.; HARDMAN, KARL
; TITLE OF INVENTION: IMMUNOTHERAPY USING SINGLE CHAIN
; POLYPEPTIDE BINDING MOLECULES
; NUMBER OF SEQUENCES: 24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/40,440
; FILING DATE: 1-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 512,910
; FILING DATE: 25-APR-1990
; APPLICATION NUMBER: 299,617
; FILING DATE: 19-JAN-1989
; APPLICATION NUMBER: 92,110
; FILING DATE: 02-SEP-1987
; APPLICATION NUMBER: 902,971
; FILING DATE: 01-SEP-1986
; SEQ ID NO:1
; LENGTH: 447
5455030-1

Query Match 83.0%; Score 44; DB 6; Length 447;
Best Local Similarity 80.0%; Pred. No. 1.1;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
|||:|:| |
Db 25 GFTFISYGMS 34

RESULT 9

US-07-956-399-4
; Sequence 4, Application US/07956399
; Patent No. 5876717
; GENERAL INFORMATION:
; APPLICANT: SHIMAMURA, TOSHIRO
; APPLICANT: TAKI, SHINSURE
; APPLICANT: HAMURO, JUNJI
; TITLE OF INVENTION: POLYPEPTIDES CAPABLE OF BINDING TO HEAVY
; CHAINS OF IL-2 RECEPTORS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202

;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/956,399
; FILING DATE: 19921005
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NO. 5876717man P.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 10-586-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-956-399-4

Query Match 79.2%; Score 42; DB 2; Length 239;
Best Local Similarity 80.0%; Pred. No. 1.3;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
|||:|:| |
Db 148 GFAFSSYDMS 157

RESULT 10

PCT-US94-07659-2
; Sequence 2, Application PC/TUS9407659
; GENERAL INFORMATION:
; APPLICANT: Young, Peter
; APPLICANT: Gross, Mitchell
; APPLICANT: Jonak, Zdenka L.
; APPLICANT: Theisen, Timothy
; APPLICANT: Hurle, Mark
; APPLICANT: Jackson, Jeffrey R.
; TITLE OF INVENTION: Recombinant and Humanized IL-1 beta
; TITLE OF INVENTION: Antibodies for Treatment of IL-1 Mediated Inflammatory
; TITLE OF INVENTION: Disorders in Man
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation - Corp.
; ADDRESSEE: Intellectual Property
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07659
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/090,534
; FILING DATE: 09-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50171-1
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (610) 270-5024
TELEFAX: (610) 270-5090
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 247 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-07659-2

Query Match 79.2%; Score 42; DB 5; Length 247;
Best Local Similarity 80.0%; Pred. No. 1.3;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
Db 45 GFAFSSYDMS 54

RESULT 11
PCT-US94-07659-6
; Sequence 6, Application PC/TUS9407659
; GENERAL INFORMATION:
; APPLICANT: Young, Peter
; APPLICANT: Gross, Mitchell
; APPLICANT: Jonak, Zdenka L.
; APPLICANT: Theisen, Timothy
; APPLICANT: Hurie, Mark
; APPLICANT: Jackson, Jeffrey R.
; TITLE OF INVENTION: Recombinant and Humanized Il-1 beta
; TITLE OF INVENTION: Antibodies for Treatment of Il-1 Mediated Inflammatory
; TITLE OF INVENTION: Disorders in Man
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Smithline Beecham Corporation - Corp.
; ADDRESSEE: Intellectual Property
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07659
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/090,534
; FILING DATE: 09-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50171-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 270-5024
; TELEFAX: (610) 270-5090
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-07659-6

Query Match 77.4%; Score 41; DB 5; Length 119;
Best Local Similarity 80.0%; Pred. No. 0.97;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10

Db 26 GTFSSYDMS 35

RESULT 12
US-08-478-039-71
; Sequence 71, Application US/08478039
; Patent No. 5681722
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,039
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-160
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 123 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Monkey
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: VH3 clone 3-34
US-08-478-039-71

Query Match 77.4%; Score 41; DB 1; Length 123;
Best Local Similarity 70.0%; Pred. No. 1;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
Db 26 GFTFSTYDWT 35

RESULT 13
US-08-478-039-104

```
; Sequence 104, Application US/08478039
; Patent No. 5681722
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,039
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-160
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 123 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Monkey
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: #34
; US-08-478-039-104

Query Match 77.4%; Score 41; DB 1; Length 123;
Best Local Similarity 70.0%; Pred. No. 1;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
Db 26 GFTFTYDMT 35

RESULT 14
US-08-476-349A-71
; Sequence 71, Application US/08476349A
; Patent No. 5750105
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
```

```
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,349A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-161
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 123 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Monkey
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: VH3 clone 3-34
; US-08-476-349A-71

Query Match 77.4%; Score 41; DB 1; Length 123;
Best Local Similarity 70.0%; Pred. No. 1;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
Db 26 GFTFTYDMT 35

RESULT 15
US-08-476-349A-104
; Sequence 104, Application US/08476349A
; Patent No. 5750105
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
```

STATE: VA
COUNTRY: USA
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,349A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/379,072
FILING DATE: 25-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912,292
FILING DATE: 10-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Teskin Esq., Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-161
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Monkey
POSITION IN GENOME:
CHROMOSOME/SEGMENT: #34
US-08-476-349A-104

Query Match 77.4%; Score 41; DB 1; Length 123;
Best Local Similarity 70.0%; Pred. No. 1;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GFTFSLSDMS 10
| | | | : | | |
Db 26 GFTFSTYDMT 35

Search completed: November 18, 2002, 17:43:33
Job time : 4.2402 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:01 ; Search time 4.90196 Seconds
(without alignments)
196.114 Million cell updates/sec

Title: US-09-016-061-54
Perfect score: 55
Sequence: 1 WVAKVSGG 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR-73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	81.8	332	2 AH2593	cytochrome o ubiqu
2	45	81.8	377	2 B97376	cytochrome ba(3) (
3	44	80.0	118	2 S20641	Ig heavy chain v r
4	43	78.2	108	2 P10248	Ig heavy chain v r
5	43	78.2	138	2 S09258	Ig heavy chain v r
6	42	76.4	111	2 S40090	Ig heavy chain - m
7	42	76.4	111	2 P1007	Ig heavy chain v r
8	42	76.4	113	2 S26468	Ig heavy chain v r
9	42	76.4	117	1 HVMS34	Ig heavy chain pre
10	40	72.7	254	2 B31790	Ig heavy chain v r
11	39	70.9	108	2 P1006	Ig heavy chain v r
12	39	70.9	117	1 HVMS84	Ig heavy chain pre
13	39	70.9	121	2 H27888	Ig heavy chain v r
14	39	70.9	123	2 G27888	Ig heavy chain v r
15	39	70.9	391	2 B83203	alginate o-acetyl
16	39	70.9	408	2 D70549	hypothetical prote
17	38	69.1	92	2 S36009	Ig heavy chain var
18	38	69.1	92	2 S56008	Ig heavy chain var
19	38	69.1	97	1 HVMS91	Ig heavy chain v r
20	38	69.1	112	2 S26327	Ig heavy chain v r
21	38	69.1	121	2 H27887	Ig heavy chain v r
22	38	69.1	128	2 P10094	Ig heavy chain v r
23	38	69.1	128	2 P10095	Ig kappa chain v r
24	38	69.1	194	2 H83060	peptidyl-LRNA hydr
25	38	69.1	425	2 A87631	FMN oxidoreductase
26	38	69.1	509	2 A49094	methylmalonyl-CoA
27	37	67.3	83	2 C25913	Ig heavy chain v r
28	37	67.3	108	2 P1010	Ig heavy chain v r
29	37	67.3	108	2 P1011	Ig heavy chain v r

30	37	67.3	114	2 P11009	Ig heavy chain v r
31	37	67.3	117	1 HVMS57	Ig heavy chain pre
32	37	67.3	118	2 P10096	Ig heavy chain v r
33	37	67.3	118	2 P10097	Ig heavy chain v r
34	37	67.3	119	2 F27888	Ig heavy chain v r
35	37	67.3	120	2 S55336	Ig heavy chain v r
36	37	67.3	120	2 S55337	Ig heavy chain v r
37	37	67.3	121	2 B27888	Ig heavy chain v r
38	37	67.3	121	2 I27887	Ig heavy chain v r
39	37	67.3	121	2 D27888	Ig heavy chain v r
40	37	67.3	121	2 A27888	Ig heavy chain v r
41	37	67.3	122	2 E27888	Ig heavy chain v r
42	37	67.3	123	2 S63597	Ig heavy chain, v
43	37	67.3	124	2 C27888	Ig heavy chain v r
44	37	67.3	124	2 I27888	Ig heavy chain v r
45	37	67.3	137	2 S78054	Ig heavy chain pre

ALIGNMENTS

RESULT 1

AH2593
cytochrome o ubiquinol oxidase subunit II cyoa [imported] - Agrobacterium tumefaciens
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 03-Jun-2002
C:Accession: AH2593
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McCl
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; PMID:11743193
A:Accession: AH2593
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-332 <KUR>
A:Cross-references: GB:AE008688; PIDN:AA141166.1; PID:gl7738464; GSPDB:GN00186
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: cyoa
A:Map position: circular chromosome
C:Superfamily: bc-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase cha
C:Keywords: copper; electron transfer; membrane-associated complex; respiratory chain
Query Match 81.8%; Score 45; DB 2; Length 332;
Best Local Similarity 88.9%; Pred. No. 1.9;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 WVAKVSGG 9
IIIIIIII
Db 213 WVAKVREGG 221

RESULT 2

B97376
cytochrome ba(3) (X78196) [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
C:Species: Agrobacterium tumefaciens
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
C:Accession: B97376
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldm
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz,
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium
A:Reference number: A97359; PMID:11743194
A:Accession: B97376
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-377 <KUR>
A:Cross-references: GB:AE007869; PIDN:AAK85963.1; PID:gl515020; GSPDB:GN00169
C:Genetics:

A:Gene: AGR_C_230
A:Map position: circular chromosome
C:Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase chain
C:Keywords: copper; electron transfer; membrane-associated complex; respiratory chain

Query Match 81.8%; Score 45; DB 2; Length 377;
Best Local Similarity 88.9%; Pred. No. 2.1;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WVAVKSGG 9
|||||
Db 258 WVAVKEGG 266

RESULT 3
S20641
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C:Accession: S20641
R:Losman, M.; Fasy, T.M.; Novick, K.E.; Monestier, M.
submitted to the EMBL Data Library, February 1992
A:Description: Relationships among antinuclear antibodies from autoimmune MRL mice react
A:Reference number: S20639
A:Accession: S20641
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-118 <LOS>
A:Cross-references: EMBL:X65003; NID:952602; PIDN:CAA46136.1; PID:952603
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 80.0%; Score 44; DB 2; Length 118;
Best Local Similarity 70.0%; Pred. No. 1.1;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WVAVKSGGG 10
||| : ||||
Db 47 WVAITSSGGG 56

RESULT 4
PLO248
Ig heavy chain V region (anti-DNA, DP12VH) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996
C:Accession: PLO248
R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A
J. Exp. Med. 171, 265-297, 1990
A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
A:Reference number: PLO231; MUID:90111618; PMID:2104919
A:Accession: PLO248
A:Molecule type: mRNA
A:Residues: 1-108 <SHL>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-24/Region: framework 1
F:9-92/Domain: immunoglobulin homology <IMM>
F:23-29/Region: complementarity-determining 1
F:30-43/Region: framework 2
F:44-60/Region: complementarity-determining 2
F:61-92/Region: framework 3
F:93-99/Region: complementarity-determining 3
F:100-108/Region: framework 4

Query Match 78.2%; Score 43; DB 2; Length 108;
Best Local Similarity 70.0%; Pred. No. 1.5;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WVAVKSGGG 10
||| : ||||
Db 41 WVAITSSGGG 50

RESULT 5
S09258
Ig heavy chain V region precursor - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 23-Jul-1999
C:Accession: S09258
R:Hamada, H.; Maezawa, K.; Tsuruo, T.
Nucleic Acids Res. 18, 1900, 1990
A:Title: Nucleotide sequences of the variable regions of a mouse monoclonal antibody
A:Reference number: S09258; MUID:90245594; PMID:2110659
A:Accession: S09258
A:Molecule type: DNA
A:Residues: 1-138 <HAM>
A:Cross-references: EMBL:X51719; NID:953207; PIDN:CAA36012.1; PID:9297545
C:Genetics:
A:introns: 16/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 78.2%; Score 43; DB 2; Length 138;
Best Local Similarity 70.0%; Pred. No. 1.9;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WVAVKSGGG 10
||| : ||||
Db 66 WVAITSSGGG 75

RESULT 6
S40090
Ig heavy chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S40090
R:Maier, C.C.; Galin, F.S.; Jarpe, M.A.; Jackson, P.; Krishna, N.R.; Gautam, A.M.; Zh
submitted to the EMBL Data Library, December 1993
A:Description: A V-lambda x-bearing monoclonal antibody with similar specificity and
A:Reference number: S40090
A:Accession: S40090
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-111 <MAI>
A:Cross-references: EMBL:X76751; NID:9435680; PIDN:CAA54154.1; PID:g1334154
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:7-90/Domain: immunoglobulin homology <IMM>

Query Match 76.4%; Score 42; DB 2; Length 111;
Best Local Similarity 70.0%; Pred. No. 2.4;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WVAVKSGGG 10
||| : || ||
Db 39 WVAATKSNCG 48

RESULT 7
PH1007
Ig heavy chain V region (clone 163-cl) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PH1007
R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective
A:Reference number: PH0971; MUID:92381444; PMID:1512540
A:Accession: PH1007
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-111 <TIL>

A;Experimental source: B cell, strain [N2B x NZW]F1
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 76.4%; Score 42; DB 2; Length 113;
 Best Local Similarity 70.0%; Pred. No. 2.4;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WVAKVSGGG 10
 ||| : ||||
 Db 47 WVAYISSGGG 56

RESULT 8

S26468

Ig heavy chain V region - mouse

C;Species: Mus musculus (house mouse)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C;Accession: S26468

R;Kavaler, J.

submitted to the EMBL Data Library, April 1991

A;Reference number: S26459

A;Accession: S26468

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-113 <KAV>

A;Cross-references: EMBL:X59107; NID:g51944; PIDN:CAAM1833.1; PID:g51945

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;11-94/Domain: immunoglobulin homology <IMM>

Query Match 76.4%; Score 42; DB 2; Length 113;
 Best Local Similarity 70.0%; Pred. No. 2.4;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WVAKVSGGG 10
 ||| : ||||
 Db 43 WVAYISSGGG 52

RESULT 9

HVMS34

Ig heavy chain precursor V region (345) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 31-Mar-1997

C;Accession: JT0502

R;Levy, N.S.; Malpiero, U.V.; Lebecque, S.G.; Gearhart, P.J.

J. Exp. Med. 169, 2007-2019, 1989

A;Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary

A;Reference number: JT0501; MUID:89279149; PMID:2499654

A;Accession: JT0502

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-117 <LEV>

A;Experimental source: strain BALB/cJ

A;Note: this sequence belongs to the VH7183 subfamily

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;1-19/Domain: signal sequence #status predicted <SIG>

F;20-117/Product: Ig heavy chain V region (345) #status predicted <MAT>

F;34-117/Domain: immunoglobulin homology <IMM>

F;41-115/Disulfide bonds: #status predicted

Query Match 76.4%; Score 42; DB 1; Length 117;
 Best Local Similarity 70.0%; Pred. No. 2.5;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WVAKVSGGG 10
 ||| : ||||
 Db 66 WVAYISSGGG 75

RESULT 10

B31790

Ig heavy chain V region (17/9) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 23-May-1997

C;Accession: B31790

R;Schulze-Gahmen, U.; Rini, J.M.; Arevalo, J.; Stura, E.A.; Kenten, J.H.; Wilson, I.A.

J. Biol. Chem. 263, 17100-17105, 1988

A;Title: Preliminary crystallographic data, primary sequence, and binding data for an

A;Reference number: A92686; MUID:89034213; PMID:3182835

A;Accession: B31790

A;Molecule type: mRNA

A;Residues: 1-254 <SCH>

C;Superfamily: immunoglobulin C region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 72.7%; Score 40; DB 2; Length 254;
 Best Local Similarity 60.0%; Pred. No. 12;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WVAKVSGGG 10
 ||| : ||||
 Db 47 WVATISNGGG 56

RESULT 11

PH1006

Ig heavy chain V region (Clone 202.33) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C;Accession: PH1006

R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective

A;Reference number: PH0971; MUID:92381444; PMID:1512540

A;Accession: PH1006

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-108 <TIL>

A;Experimental source: B cell, strain [N2B x NZW]F1

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;10-93/Domain: immunoglobulin homology <IMM>

Query Match 70.9%; Score 39; DB 2; Length 108;
 Best Local Similarity 60.0%; Pred. No. 8.1;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 WVAKVSGGG 10
 ||| : ||||
 Db 42 WVATISNGGG 51

RESULT 12

HVMS84

Ig heavy chain precursor V region (5-84) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 31-Mar-1997

C;Accession: JT0505

R;Levy, N.S.; Malpiero, U.V.; Lebecque, S.G.; Gearhart, P.J.

J. Exp. Med. 169, 2007-2019, 1989

A;Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary

A;Reference number: JT0501; MUID:89279149; PMID:2499654

A;Accession: JT0505

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-117 <LEV>

A;Experimental source: strain BALB/cJ

A;Note: this sequence belongs to the VH7183 subfamily

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;1-19/Domain: signal sequence #status predicted <SIG>

F;20-117/Product: Ig heavy chain V region (5-84) #status predicted <MAT>
F;34-117/Domain: immunoglobulin homology <IMM>
F;41-115/Disulfide bonds: #status predicted

Query Match 70.9% Score 39; DB 1; Length 117;
Best Local Similarity 60.0%; Pred. No. 8.7; Indels 0; Gaps 0;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WVAKVSGG 10
| | | : | | |
Db 66 WVAISNGG 75

RESULT 13

H27888
Ig heavy chain V region (H37-40) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996
C:Accession: H27888
R:Catton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
EMBO J. 5, 1577-1587, 1986
A:Title: Structural and functional implications of a restricted antibody response to a d
A:Reference number: A91043; MUID:86300658; PMID:2427335
A:Accession: H27888

A:Molecule type: DNA
A:Residues: 1-121 <CAT>
A:Experimental source: strain Balb/c
A:Note: this sequence was determined from the germline gene
C:Comment: This chain was isolated from a hybridoma protein that binds influenza virus h
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 70.9% Score 39; DB 2; Length 121;
Best Local Similarity 66.7%; Pred. No. 8.9;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WVAKVSGG 9
| | | : | | |
Db 47 WVAEISSG 55

RESULT 14

G27888
Ig heavy chain V region (H28-A2) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996
C:Accession: G27888
R:Catton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
EMBO J. 5, 1577-1587, 1986
A:Title: Structural and functional implications of a restricted antibody response to a d
A:Reference number: A91043; MUID:86300658; PMID:2427335
A:Accession: G27888

A:Molecule type: DNA
A:Residues: 1-123 <CAT>
A:Experimental source: strain Balb/c
A:Note: this sequence was determined from the germline gene
C:Comment: This chain was isolated from a hybridoma protein that binds influenza virus h
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 70.9% Score 39; DB 2; Length 123;
Best Local Similarity 66.7%; Pred. No. 9.1;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WVAKVSGG 9
| | | : | | |
Db 47 WVAEISSG 55

RESULT 15
B83203

alginate O-acetyltransferase AlgJ PA3549 [imported] - Pseudomonas aeruginosa (strain
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: B83203
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.;
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L
; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: B83203
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-391 <STO>
A:Cross-references: GB:AE004775; GB:AE004091; NID:g9949692; PIDN:AAG06937.1; GSPDB:GN
A:Experimental source: strain PA01
C:Genetics:
A:Gene: algJ; PA3549

Query Match 70.9% Score 39; DB 2; Length 391;
Best Local Similarity 60.0%; Pred. No. 26;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WVAKVSGG 10
| | | : | | |
Db 371 WVAQLKASGG 380

Search completed: November 18, 2002, 17:47:00
Job time : 4.90196 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:00 ; Search time 2.45098 Seconds
(without alignments)
169.223 Million cell updates/sec

Title: US-09-016-061-54
Perfect score: 55
Sequence: 1 WVAKVSGGG 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	42	76.4	117	1 HV55_MOUSE
2	40	72.7	438	1 TRPE_AERPE
3	39	70.9	117	1 HV54_MOUSE
4	39	70.9	188	1 YLAL_LACAC
5	39	70.9	194	1 PTH_PASMU
6	38	69.1	97	1 HV56_MOUSE
7	38	69.1	194	1 PTH_PSEAE
8	37	67.3	117	1 HV58_MOUSE
9	37	67.3	256	1 CB4B_LYCES
10	36	65.5	37	1 THHS_HORVU
11	36	65.5	247	1 HS77_HUMAN
12	36	65.5	303	1 NORF_PHOPO
13	36	65.5	303	1 NORF_VIBMA
14	36	65.5	303	1 NORF_VIBPA
15	36	65.5	407	1 NORF_VIBAL
16	36	65.5	411	1 NORF_HAEIN
17	36	65.5	429	1 SYN_THEAC
18	36	65.5	429	1 SYN_THEVO
19	35.5	64.5	196	1 SODE_TETPY
20	35	63.6	140	1 RK16_CYACA
21	35	63.6	196	1 PTH_VIBCH
22	35	63.6	301	1 NORF_SHEPU
23	35	63.6	407	1 NORF_VIBHA
24	35	63.6	408	1 NORF_VIBCH
25	35	63.6	424	1 GUN1_RALSO
26	35	63.6	593	1 CSG_METFE
27	35	63.6	593	1 CSG_METSC
28	35	63.6	3432	1 POLG_JAEV1
29	35	63.6	3432	1 POLG_JAEV5
30	35	63.6	3432	1 POLG_JAEV3
31	34	61.8	121	1 NLTP_BOVIN
32	34	61.8	135	1 RM16_PROWI
33	34	61.8	202	1 P21_SOYBN

34 34 61.8 206 1 IAAT_MAIZE P13657 zea mays (m
35 34 61.8 227 1 ZEAM_MAIZE P33679 zea mays (m
36 34 61.8 301 1 YFEA_YEAST P43558 saccharomyc
37 34 61.8 311 1 BLAC_STRAU P10509 streptomyc
38 34 61.8 311 1 BLAC_STRCE Q06650 streptomyc
39 34 61.8 373 1 RFL_AERPE Q9yaf1 aeropyrum p
40 34 61.8 547 1 NLTP_CHICK Q07598 gallus gall
41 34 61.8 547 1 NLTP_HUMAN P22307 homo sapien
42 34 61.8 547 1 NLTP_MOUSE P32020 mus musculu
43 34 61.8 547 1 NLTP_RAT P11915 rattus norv
44 34 61.8 621 1 TRPX_ARATH P32069 arabidopsis
45 34 61.8 867 1 NIA_ASPNG P36858 aspergillus

ALIGNMENTS

RESULT 1
HV55_MOUSE STANDARD; PRT; 117 AA.
ID P18526;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 345 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebecqz S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response";
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; JTO502; HVMS34.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
KW SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 345.
FT DOMAIN 20 19 FRAMEWORK-1
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12902 MW; 49380E4627ACA99A CRC64;
Query Match 76.4%; Score 42; DB 1; Length 117;
Best Local Similarity 70.0%; Pred. No. 0.51;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 WVAKVSGGG 10
Db 66 WVAIVSGGG 75
III : IIII
RESULT 2
TRPE_AERPE STANDARD; PRT; 438 AA.
ID TRPE_AERPE
AC Q9Y8T0;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Anthranilate synthase component I (EC 4.1.3.27).

```
GN TRPE OR APE2553.
OS Aeropyrum pernix.
OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
OC Desulfurococaceae; Aeropyrum.
OX NCBI_TaxID=56636;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K1;
RX MEDLINE=99310339; PubMed=10382966;
RA Kawarabayashi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankal A., Kosugi H.,
RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
RA Yamazaki J., Kushiida N., Oguchi A., Aoki K.-I., Kubota K.,
RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
RT "Complete genome sequence of an aerobic hyper-thermophilic
RT crenarchaeon, Aeropyrum pernix K1."
RL DNA Res. 6:83-101(1999).
CC -|- CATALYTIC ACTIVITY: Chorismate + L-glutamine -> anthranilate +
CC pyruvate + L-glutamate.
CC -|- PATHWAY: Tryptophan biosynthesis: first step.
CC -|- SUBUNIT: Tetramer of two components I and two components II (by
CC similarity).
CC -|- MISCELLANEOUS: Component I catalyzes the formation of anthranilate
CC using ammonia rather than glutamine, whereas component II provides
CC glutamine amidotransferase activity.
CC -|- SIMILARITY: Belongs to the anthranilate synthase component I
CC family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF000064; BAA81570.1; ALT_INIT.
DR HSSP; Q06128; IQDL.
DR InterPro; IPR000350; Chorismate_bind.
DR Pfam; PF00425; chorismate_bind; 1.
DR PRINTS; PR00095; ANTSNTHASEI.
DR ProDom; PD000779; Chorismate_bind; 1.
DR Tryptophan biosynthesis; Lyase; Complete proteome.
KW Tryptophan biosynthesis; Lyase; Complete proteome.
SQ SEQUENCE 438 AA; 48309 MW; 16E59013EFDFAED CRC64;

Query Match 72.7%; Score 40; DB 1; Length 438;
Best Local Similarity 60.0%; Pred. No. 4.5;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WVAKVSGGG 10
Db 39 WIALESGGG 48

RESULT 3
HV54_MOUSE
ID HV54_MOUSE STANDARD; PRT; 117 AA.
AC FL8525;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 5-84 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
```

```
RT the primary immune response."
RL J. Exp. Med. 169:2007-2019(1989).
CC -|- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; J0505; HVMS84.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 5-84.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12872 MW; 234055CB6A469861 CRC64;

Query Match 70.9%; Score 39; DB 1; Length 117;
Best Local Similarity 60.0%; Pred. No. 1.9;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WVAKVSGGG 10
Db 66 WVAISNGGG 75

RESULT 4
YLAL_LACAC
ID YLAL_LACAC STANDARD; PRT; 188 AA.
AC P29470;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein in LAF 5' region (ORF1) (Fragment).
OS Lactobacillus acidophilus.
OC Plasmid pPRK160.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1579;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=11088;
RX MEDLINE=94113718; PubMed=8285694;
RA Frenaux C., Ahn C., Klaenhammer T.R.;
RT "Molecular analysis of the lactacin F operon."
RL Appl. Environ. Microbiol. 59:3906-3915(1993).
CC -----
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CC -----
CC EMBL; M57961; AAA16635.1; -.
DR Hypothetical protein; Plasmid.
FT NON_TER 1 1
SQ SEQUENCE 188 AA; 21073 MW; D7A1FABE073C1081 CRC64;

Query Match 70.9%; Score 39; DB 1; Length 188;
Best Local Similarity 70.0%; Pred. No. 3;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WVAKVSGGG 10
Db 70 WVAHVDGGG 79
```

```
RESULT 5
PTH_PASMU
ID PTH_PASMU STANDARD; PRT; 194 AA.
AC P57820;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Peptidyl-trna hydrolase (EC 3.1.1.29) (PTH).
GN PTH OR PM0164.
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Pasteurella.
OX NCBI_TaxID=747;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Pm70;
RX MEDLINE=21145866; PubMed=11248100;
RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
RT "Complete genomic sequence of Pasteurella multocida Pm70.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
CC -!- FUNCTION: THE NATURAL SUBSTRATE FOR THIS ENZYME MAY BE PEPTIDYL-
CC TRNAS WHICH DROP OFF THE RIBOSOME DURING PROTEIN SYNTHESIS (BY
CC SIMILARITY).
CC -!- CATALYTIC ACTIVITY: N-substituted aminoacyl-trna + H(2)O = N-
CC substituted amino acid + trna.
CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: BELONGS TO THE PTH FAMILY.
CC -----
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CC -----
CC EMBL; AE006051; AAK02248.1;
CC HSSP; P23932; 2PTH.
CC InterPro; IPR001328; Pept_trna_hydro.
CC Pfam; PF01195; Pept_trna_hydro; 1.
CC ProDom; PD005324; Pept_trna_hydro; 1.
CC TricRams; TIGR00447; pth; 1.
CC ProSITE; PS01195; PEPT_TRNA_HYDROL_1; FALSE_NEG.
CC ProSITE; PS01196; PEPT_TRNA_HYDROL_2; 1.
CC Hydrolase; Complete proteome.
KW HYDROLASE.
SQ SEQUENCE 194 AA; 21334 MW; P254C4D304243945 CRC64;

Query Match 70.9%; Score 39; DB 1; Length 194;
Best Local Similarity 77.8%; Pred. No. 3.1;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 VAKVSGGG 10
   |||: |||
DB 103 VAKIKGGG 111

RESULT 6
HV56_MOUSE
ID HV56_MOUSE STANDARD; PRT; 97 AA.
AC P18527;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 914.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE=89279149; PubMed=2499654;

Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
"Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response.";
J. Exp. Med. 169:2007-2019(1989).
-!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
PIR; JT0504; HVMS91.
HSSP; P01810; 2PBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT NON_TER 97
SQ SEQUENCE 97 AA; 10661 MW; C23CB33FF55DA893 CRC64;

Query Match 69.1%; Score 38; DB 1; Length 97;
Best Local Similarity 66.7%; Pred. No. 2.4;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WVAKVSGG 9
   |||: |||
DB 47 WVASISGG 55

RESULT 7
PTH_PSEAE
ID PTH_PSEAE STANDARD; PRT; 194 AA.
AC Q9HVC3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Peptidyl-trna hydrolase (EC 3.1.1.29) (PTH).
GN PTH OR PA4672.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
CC -!- FUNCTION: THE NATURAL SUBSTRATE FOR THIS ENZYME MAY BE PEPTIDYL-
CC TRNAS WHICH DROP OFF THE RIBOSOME DURING PROTEIN SYNTHESIS (BY
CC SIMILARITY).
CC -!- CATALYTIC ACTIVITY: N-substituted aminoacyl-trna + H(2)O = N-
CC substituted amino acid + trna.
CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: BELONGS TO THE PTH FAMILY.
CC -----
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CC -----
CC EMBL; AE004881; AAG08059.1;
CC HSSP; P23932; 2PTH.
CC InterPro; IPR001328; Pept_trna_hydro.
CC Pfam; PF01195; Pept_trna_hydro; 1.
CC ProDom; PD005324; Pept_trna_hydro; 1.
CC TricRams; TIGR00447; pth; 1.
```

DR PROSITE; PS01195; PEPT_TRNA_HYDROL_1; 1.
 DR PROSITE; PS01196; PEPT_TRNA_HYDROL_2; 1.
 KW Hydrolase; Complete proteome.
 SQ SEQUENCE 194 AA; 20804 MW; A6E14ECBF84B61AA CRC64;

Query Match 69.18; Score 38; DB 1; Length 194;
 Best Local Similarity 77.88; Pred. No. 4.8;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VAKVKS GG 10
 |||:||||
 Db 103 VAKLKTGG 111

RESULT 8
 HV58_MOUSE
 ID HV58_MOUSE STANDARD; PRT; 117 AA.
 AC P18529; 117 AA.
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V region 5-76 precursor.
 OS Mus musculus (Mouse)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALE/CJ;
 RX MEDLINE=89279149; PubMed=2499654;
 RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
 RT "Early onset of somatic mutation in immunoglobulin VH genes during
 the primary immune response.";
 RL J. Exp. Med. 169:2007-2019(1989).
 CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.

DR PIR; J05006; HVMS57.
 DR HSP; P01810; 2FBJ.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IgV; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION 5-76.
 FT DOMAIN 20 49 FRAMEWORK-1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 55 68 FRAMEWORK-2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 86 117 FRAMEWORK-3.
 FT DISULFID 41 115 BY SIMILARITY.
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12991 MW; 93A04782B78B8FA0 CRC64;
 Query Match 67.38; Score 37; DB 1; Length 117;
 Best Local Similarity 66.78; Pred. No. 4.5;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WVAKVKS GG 9
 |||:||||
 Db 66 WVAITSSGG 74

RESULT 9
 CB4B_LYCES
 ID CB4B_LYCES STANDARD; PRT; 256 AA.
 AC P27525;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Chlorophyll A-B binding protein CP24 10B, chloroplast precursor (CAB-10B) (LHCP).
 GN CAB10B.
 OS Lycopersicon esculentum (Tomato).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4081;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91355849; PubMed=2103430;
 RA Schwartz E., Pichersky E.;
 RT "Sequence of two tomato nuclear genes encoding chlorophyll
 a/b-binding proteins of CP24, a PSII antenna component.";
 RL Plant Mol. Biol. 15:157-160(1990).
 CC -!- SIMILARITY: BELONGS TO THE ELIP/PSBS FAMILY.

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 CC -----
 DR EMBL; M32606; AAA34146.1; -.
 DR PIR; S11878; S11878.
 DR InterPro; IPR001344; Chloro_Abbind.
 DR Pfam; PF00504; chloroa_b-bind; 1.
 DR ProDom; PD000275; Chloro_Abbind; 1.
 KW Chlorophyll; Photosynthesis; Photosystem II; Thylakoid;
 KW Chloroplast; Transit peptide; Multigene family; Transmembrane.
 FT TRANSIT 1 45
 FT CHAIN 46 256 CHLOROPHYLL A-B BINDING PROTEIN CP24 10B.
 SQ SEQUENCE 256 AA; 27470 MW; 33325E6486496726 CRC64;

Query Match 67.38; Score 37; DB 1; Length 256;
 Best Local Similarity 66.78; Pred. No. 9.8;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WVAKVKS GG 9
 I: |||||
 Db 55 WIPAVKSGG 63

RESULT 10
 THHS_HORVU
 ID THHS_HORVU STANDARD; PRT; 37 AA.
 AC P33045;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Antifungal protein S (Fragment).
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticeae; Hordeum.
 OX NCBI_TaxID=4513;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=CV. BOMI RISO 1508;
 RX MEDLINE=92037994; PubMed=1936240;
 RA Hejgaard J., Jacobsen S., Svendsen I.;
 RT "Two antifungal thaumatin-like proteins from barley grain.";
 RL FEBS Lett. 291:127-131(1991).
 CC -!- FUNCTION: HAS ANTIFUNGAL ACTIVITY. INHIBITS THE GROWTH OF
 CC -!- TRICHODERMA VIRIDAE AND CANDIDA ALBICANS.
 CC -!- SIMILARITY: BELONGS TO THE THAUMATIN FAMILY.
 DR PIR; S17684; S17684.
 DR HSP; P33679; 1DU5.
 DR InterPro; IPR001938; Thaumatin.
 DR Pfam; PF00314; thaumatin; 1.
 DR ProDom; PD001321; Thaumatin; 1.
 DR PROSITE; PS00316; THAUMATIN; PARTIAL.
 KW Plant defense; Fungicide.
 FT NON_TER 37 37
 SQ SEQUENCE 37 AA; 3871 MW; 7BE164CCBE8A9881 CRC64;


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Query Match      65.5%; Score 36; DB 1; Length 37;
Best Local Similarity 60.0%; Pred. No. 2.2;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WVKVSGGG 10
   | | | | |
Db 14 WAAVPCGG 23

RESULT 11
HS77_HUMAN
ID HS77_HUMAN STANDARD; PRT; 247 AA.
AC P48741; P19790;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Heat shock 70 kDa protein 7 (Heat shock 70 kDa protein B) (Fragment).
GN HSP70 OR HSP70B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85270444; PubMed=3927293;
RA Voellmy R., Ahmed A., Schiller P., Bromley P., Rungger D.;
RT "Isolation and functional analysis of a human 70,000-dalton heat
shock protein gene segment.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:4949-4953(1985).
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC -----
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CC -----
DR EMBL; M11236; AAA52696.1; -.
DR PIR; A25773; A25773.
DR HSP; P08107; IHJO.
DR Genew; HGNC:5240; HSP47.
DR MIN; 140556; -.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR ProDom; PD000089; Hsp70; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; PARTIAL.
KW ATP-binding; Heat shock; Multigene family.
FT NON_TER 247
FT SEQUENCE 247 AA; 26906 MW; 354EB237F6750DD7 CRC64;

Query Match      65.5%; Score 36; DB 1; Length 247;
Best Local Similarity 70.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WVKVSGGG 10
   | | | | |
Db 92 WPKVSGGG 101

RESULT 12
NQRF_POPO
ID NQRF_POPO STANDARD; PRT; 303 AA.
AC Q9LCJ1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Na(+)-translocating NADH-quinone reductase subunit F (EC 1.6.5.-)
DE Na(+)-translocating NQR subunit F (Na(+)-NQR subunit F) (NQR complex

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subunit F) (NQR-1 subunit F) (Fragment).
DE NQRF OR NQR6.
OS Photobacterium phosphoreum.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae;
OC Photobacterium.
OX NCBI_TaxID=659;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=IAM 12085;
RX MEDLINE=20242140; PubMed=10779868;
RA Kato S., Yumoto I.;
RT "Detection of the Na(+)-translocating NADH-quinone reductase in marine
bacteria using a PCR technique.";
RL Can. J. Microbiol. 46:325-332(2000).
CC -!- FUNCTION: NQR COMPLEX CATALYZES THE REDUCTION OF UBIQUINONE-1 TO
UBIQUINOL BY TWO SUCCESSIVE REACTIONS, COUPLED WITH THE TRANSPORT
OF NA(+) IONS FROM THE CYTOPLASM TO THE PERIPLASM. THE FIRST STEP
IS CATALYZED BY NQRF, WHICH ACCEPTS ELECTRONS FROM NADH AND
REDUCES UBIQUINONE-1 TO UBISEMIQUINONE BY A ONE-ELECTRON TRANSFER
PATHWAY.
CC -!- CATALYTIC ACTIVITY: NADH + ubiquinol + Na(+) (In) = NAD(+) +
ubiquinol + Na(+) (Out).
CC -!- COFACTOR: FAD AND A 2FE-2S CLUSTER (BY SIMILARITY).
CC -!- SUBUNIT: COMPOSED OF SIX SUBUNITS; NQRA, NQRB, NQRC, NQRD, NQRE
AND NQRF (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Inner membrane (Potential).
CC -!- SIMILARITY: BELONGS TO THE NQRF FAMILY.
CC -----
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CC -----
DR EMBL; AB024724; BAA83761.1; -.
DR InterPro; IPR000564; 2Fe2S_ferredoxin.
DR InterPro; IPR001834; Cyt_B5_reductase.
DR InterPro; IPR001041; Ferredoxin.
DR InterPro; IPR001433; Oxred_FAD/NAD(P).
DR Pfam; PF00111; fer2; 1.
DR Pfam; PF00175; NAD_binding_1.
DR Pfam; PF00970; FAD_binding_6; 1.
DR PROSITE; PS00197; 2FE2S_FERREDOXIN; PARTIAL.
KW Oxidoreductase; NAD; Ubiquinone; Transport; Sodium transport;
Flavoprotein; FAD; Iron-sulfur; Inner membrane.
FT NON_TER 1
FT DOMAIN <1 45 FERREDOXIN.
FT DOMAIN 201 >303 CATALYTIC.
FT METAL 4 4 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
FT METAL 7 7 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
FT METAL 39 39 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
FT NON_TER 303
FT SEQUENCE 303 AA; 34515 MW; 57396CC41F020FC5 CRC64;

Query Match      65.5%; Score 36; DB 1; Length 303;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 WVKSGGG 10
   | | | | |
Db 10 WVKSGGG 16

RESULT 13
NQRF_VIBMA
ID NQRF_VIBMA STANDARD; PRT; 303 AA.
AC Q9LCI9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Na(+)-translocating NADH-quinone reductase subunit F (EC 1.6.5.-)

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DE (Na(+)-translocating NOR subunit F) (Na(+)-NOR subunit F) (NOR complex
DE subunit F) (NOR-1 subunit F) (Fragment).
GN NQR6 OR NQR6.
OS Vibrio marinus (Moritella marina).
OC Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
OC Moritella.
OX NCBI_TaxID=90736;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15381;
RX MEDLINE=20242140; PubMed=10779868;
RA Kato S., Yumoto I.;
RT "Detection of the Na(+)-translocating NADH-quinone reductase in marine
RT bacteria using a PCR technique.";
RL Can. J. Microbiol. 46:325-332(2000).
CC -!- FUNCTION: NOR COMPLEX CATALYZES THE REDUCTION OF UBIQUINONE-1 TO
CC UBIQUINOL BY TWO SUCCESSIVE REACTIONS, COUPLED WITH THE TRANSPORT
CC OF NA(+) IONS FROM THE CYTOPLASM TO THE PERIPLASM. THE FIRST STEP
CC IS CATALYZED BY NQR6, WHICH ACCEPTS ELECTRONS FROM NADH AND
CC REDUCES UBIQUINONE-1 TO UBISEMIQUINONE BY A ONE-ELECTRON TRANSFER
CC PATHWAY.
CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone + Na(+)(In) = NAD(+) +
CC ubiquinol + Na(+)(Out).
CC -!- COFACTOR: FAD AND A 2FE-2S CLUSTER (BY SIMILARITY).
CC -!- SUBUNIT: COMPOSED OF SIX SUBUNITS; NORA, NORB, NQRC, NQRD, NQRE
CC AND NQRF (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Inner membrane (Potential).
CC -!- SIMILARITY: BELONGS TO THE NORF FAMILY.
CC
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CC -----
DR EMBL; AB024726; BAA83763.1; -
DR InterPro; IPR000564; 2Fe2S_ferredoxin.
DR InterPro; IPR001834; Cyt_B5_reductase.
DR InterPro; IPR001041; Ferredoxin.
DR InterPro; IPR001433; Oxred_FAD/NAD(P).
DR Pfam; PF00111; fer2; 1.
DR Pfam; PF00175; NAD_binding_1.
DR Pfam; PF00970; FAD_binding_6; 1.
DR PROSITE; PS00197; 2FE2S_FERREDOXIN; PARTIAL.
KW Oxidoreductase; NAD; Ubiquinone; Transport; Sodium transport;
KW Flavoprotein; FAD; Iron-sulfur; Inner membrane.
FT NON_TER 1
FT DOMAIN <1 45 FERREDOXIN.
FT CATALYTIC 201 >303 CATALYTIC.
FT METAL 4 4 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
FT METAL 7 7 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
FT METAL 39 39 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
FT NON_TER 303 303
SQ SEQUENCE 303 AA; 4DF643F69E9D44D5 CRC64;

Query Match 65.5%; Score 36; DB 1; Length 303;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KVKSGGG 10
Db 10 KVKSGGG 16

RESULT 14
NORF_VIBPA STANDARD; PRT; 303 AA.
AC Q9LJ0;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)

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DE (Na(+)-translocating NADH-quinone reductase subunit F (EC 1.6.5.-)
DE (Na(+)-translocating NQR subunit F) (Na(+)-NQR subunit F) (NQR complex
DE subunit F) (NQR-1 subunit F) (Fragment).
GN NQR6 OR NQR6.
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxID=670;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JCM 2147;
RX MEDLINE=20242140; PubMed=10779868;
RA Kato S., Yumoto I.;
RT "Detection of the Na(+)-translocating NADH-quinone reductase in marine
RT bacteria using a PCR technique.";
RL Can. J. Microbiol. 46:325-332(2000).
CC -!- FUNCTION: NOR COMPLEX CATALYZES THE REDUCTION OF UBIQUINONE-1 TO
CC UBIQUINOL BY TWO SUCCESSIVE REACTIONS, COUPLED WITH THE TRANSPORT
CC OF NA(+) IONS FROM THE CYTOPLASM TO THE PERIPLASM. THE FIRST STEP
CC IS CATALYZED BY NQRF, WHICH ACCEPTS ELECTRONS FROM NADH AND
CC REDUCES UBIQUINONE-1 TO UBISEMIQUINONE BY A ONE-ELECTRON TRANSFER
CC PATHWAY.
CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone + Na(+)(In) = NAD(+) +
CC ubiquinol + Na(+)(Out).
CC -!- COFACTOR: FAD AND A 2FE-2S CLUSTER (BY SIMILARITY).
CC -!- SUBUNIT: COMPOSED OF SIX SUBUNITS; NQRA, NORB, NQRC, NQRD, NQRE
CC AND NQRF (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Inner membrane (Potential).
CC -!- SIMILARITY: BELONGS TO THE NORF FAMILY.
CC
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CC
CC -----
DR EMBL; AB024725; BAA83762.1; -
DR InterPro; IPR000564; 2Fe2S_ferredoxin.
DR InterPro; IPR001834; Cyt_B5_reductase.
DR InterPro; IPR001709; FPN_cyt_reductase.
DR InterPro; IPR001041; Ferredoxin.
DR InterPro; IPR001433; Oxred_FAD/NAD(P).
DR Pfam; PF00111; fer2; 1.
DR Pfam; PF00175; NAD_binding_1.
DR Pfam; PF00970; FAD_binding_6; 1.
DR PRINTS; PR00371; FPNCR.
DR PROSITE; PS00197; 2FE2S_FERREDOXIN; PARTIAL.
KW Oxidoreductase; NAD; Ubiquinone; Transport; Sodium transport;
KW Flavoprotein; FAD; Iron-sulfur; Inner membrane.
FT NON_TER 1
FT DOMAIN <1 45 FERREDOXIN.
FT CATALYTIC 201 >303 CATALYTIC.
FT METAL 4 4 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
FT METAL 7 7 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
FT METAL 39 39 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
FT NON_TER 303 303
SQ SEQUENCE 303 AA; 506FDB1A489A6858 CRC64;

Query Match 65.5%; Score 36; DB 1; Length 303;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KVKSGGG 10
Db 10 KVKSGGG 16

RESULT 15
NORF_VIBAL STANDARD; PRT; 407 AA.
ID NQRF_VIBAL
AC Q56584;
DT 16-OCT-2001 (Rel. 40, Created)

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DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Na(+)-translocating NADH-quinone reductase subunit F (EC 1.6.5.-)
 DE (Na(+)-translocating NADH-quinone reductase subunit beta) (Na(+)-
 DE translocating NQR subunit F) (Na(+)-NQR subunit F) (NQR complex
 DE subunit F) (NQR-1 subunit F).
 GN NQR OR NQR6.
 OS Vibrio alginolyticus.
 OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
 OX NCBI_TaxID=663;
 RP [1]
 RP SEQUENCE FROM N.A.
 RP MEDLINE=95246889; PubMed=7729558;
 RA Hayashi M., Hirai K., Unemoto T.;
 RT "Sequencing and the alignment of structural genes in the nqr operon
 RT encoding the Na(+)-translocating NADH-quinone reductase from Vibrio
 RT alginolyticus.";
 RL FEBS Lett. 363:75-77(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RP MEDLINE=96230452; PubMed=8674503;
 RA Tan K., Beattie P., Leach D.R.F., Rich P.R., Coulson A.F.W.,
 RA Ward F.B.;
 RT "Expression and analysis of the gene for the catalytic beta subunit of
 RT the sodium-translocating NADH-ubiquinone oxidoreductase of Vibrio
 RT alginolyticus.";
 RL Biochem. Soc. Trans. 24:125-125(1996).
 RN [3]
 RP SEQUENCE OF 1-10.
 RP MEDLINE=98149659; PubMed=9490015;
 RA Nakayama Y., Hayashi M., Unemoto T.;
 RT "Identification of six subunits constituting Na+-translocating NADH-
 RT quinone reductase from the marine Vibrio alginolyticus.";
 RL FEBS Lett. 422:240-242(1998).
 RN [4]
 RP CHARACTERIZATION.
 RP STRAIN=DSM 2171;
 RC MEDLINE=98055703; PubMed=9395325;
 RA Steuber J., Krebs W., Dimroth P.;
 RT "The Na+-translocating NADH:ubiquinone oxidoreductase from Vibrio
 RT alginolyticus--redox states of the FAD prosthetic group and mechanism
 RT of Ag+ inhibition.";
 RL Eur. J. Biochem. 249:770-776(1997).
 RN [5]
 RP INHIBITION OF ENZYMATIC ACTIVITY.
 RP Unemoto T., Ogura T., Hayashi M.;
 RA "Modifications by Na+ and K+, and the site of Ag+ inhibition in the
 RT Na+-translocating NADH-quinone reductase from a marine Vibrio
 RT alginolyticus.";
 RL Biochim. Biophys. Acta 1183:201-205(1993).
 RN [6]
 RP INHIBITION OF ENZYMATIC ACTIVITY.
 RP MEDLINE=20016049; PubMed=10549856;
 RA Nakayama Y., Hayashi M., Yoshikawa K., Mochida K., Unemoto T.;
 RT "Inhibitor studies of a new antibiotic, koromicin, 2-n-heptyl-4-
 RT hydroxyquinoline N-oxide and Ag+ toward the Na+-translocating NADH-
 RT quinone reductase from the marine Vibrio alginolyticus.";
 RL Biol. Pharm. Bull. 22:1064-1067(1999).
 RN [7]
 RP REVIEW.
 RP MEDLINE=21145117; PubMed=11248187;
 RA Hayashi M., Nakayama Y., Unemoto T.;
 RT "Recent progress in the Na(+)-translocating NADH-quinone reductase
 RT from the marine Vibrio alginolyticus.";
 RL Biochim. Biophys. Acta 1505:37-44(2001).
 RN [8]
 RP REVIEW.
 RP MEDLINE=21145118; PubMed=11248188;
 RA Steuber J.;
 RT "Na(+)-translocation by bacterial NADH:quinone oxidoreductases: an
 RT extension to the complex-I family of primary redox pumps.";
 RL Biochim. Biophys. Acta 1505:45-56(2001).
 CC -!- FUNCTION: NQR COMPLEX CATALYZES THE REDUCTION OF UBIQUINONE-1 TO

CC UBIQUINOL BY TWO SUCCESSIVE REACTIONS, COUPLED WITH THE TRANSPORT
 CC OF NA(+) IONS FROM THE CYTOPLASM TO THE PERIPLASM. THE FIRST STEP
 CC IS CATALYZED BY NQRF, WHICH ACCEPTS ELECTRONS FROM NADH AND
 CC REDUCES UBIQUINONE-1 TO UBISEMIQUINONE BY A ONE-ELECTRON TRANSFER
 CC PATHWAY.
 CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone + Na(+)(In) -> NAD(+) +
 CC ubiquinol + Na(+)(Out).
 CC -!- COFACTOR: FAD AND A 2FE-2S CLUSTER (PROBABLE).
 CC -!- ENZYME REGULATION: ACTIVATED BY NA(+) OR K(+). INHIBITED BY
 CC SILVER.
 CC -!- SUBUNIT: COMPOSED OF SIX SUBUNITS; NQRA, NQRB, NQRC, NQRD, NQRE
 CC AND NQRF.
 CC -!- SUBCELLULAR LOCATION: Inner membrane (Potential).
 CC -!- PTM: THE N-TERMINUS IS BLOCKED.
 CC -!- SIMILARITY: BELONGS TO THE NQR FAMILY.
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 CC -----
 CC EMBL; AB008030; BAA22915.1; -;
 DR InterPro; IPR000564; 2Fe2S_ferredoxin.
 DR InterPro; IPR001834; Cyt_B5_reductase.
 DR InterPro; IPR001041; Ferredoxin.
 DR InterPro; IPR001433; Oxred_FAD/NAD(P).
 DR Pfam; PF00111; fer2; 1.
 DR Pfam; PF00175; NAD_binding_1.
 DR Pfam; PF00970; FAD_binding_6; 1.
 DR PROSITE; PS00197; 2FE2S_FERREDOXIN; FALSE_NEG.
 KW Oxidoreductase; NAD; Ubiquinone; Transport; Sodium transport;
 KW Flavoprotein; FAD; Iron-sulfur; Transmembrane; Inner membrane.
 FT TRANSMEM 5 24 POTENTIAL.
 FT DOMAIN 34 116 FERREDOXIN.
 FT DOMAIN 272 389 CATALYTIC.
 FT METAL 69 69 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
 FT METAL 75 75 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
 FT METAL 78 78 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
 FT METAL 110 110 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
 SQ SEQUENCE 407 AA; 45274 MW; A87BE89DFCA87346 CRC64;
 Query Match 65.5%; Score 36; DB 1; Length 407;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 KVKSGGG 10
 Db 81 KVKSGGG 87
 Search completed: November 18, 2002, 17:33:20
 Job time : 2.45098 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:01 ; Search time 10.4412 Seconds
(without alignments)
197.341 Million cell updates/sec

Title: US-09-016-061-54
Perfect score: 55
Sequence: 1 WAKVKSGG 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SPTEMBL21.*
2: sp_archaea.*
3: sp_bacteria.*
4: sp_fungi.*
5: sp_human.*
6: sp_invertebrate.*
7: sp_mammal.*
8: sp_mhc.*
9: sp_organella.*
10: sp_phase.*
11: sp_plant.*
12: sp_rodent.*
13: sp_virus.*
14: sp_vertebrate.*
15: sp_unclassified.*
16: sp_rvirus.*
17: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Length	ID	Description
1	45	81.8	377	16	Q8U129
2	41	74.5	352	12	Q9IR97
3	40	72.7	100	16	Q981Y3
4	39	70.9	134	8	Q9T232
5	39	70.9	342	12	Q55810
6	39	70.9	391	16	Q51393
7	39	70.9	408	16	Q06427
8	38	69.1	312	17	Q8TU18
9	38	69.1	425	16	Q9A3W8
10	38	69.1	509	2	Q57079
11	38	69.1	591	12	Q72120
12	38	69.1	907	3	Q00303
13	37	67.3	115	10	Q945T0
14	37	67.3	119	11	Q920E7
15	37	67.3	186	16	Q86545
16	37	67.3	198	10	Q8S5E2

17	37	67.3	238	10	O04364
18	37	67.3	289	2	Q9X2P4
19	37	67.3	345	12	O55828
20	37	67.3	409	2	O54496
21	37	67.3	462	16	Q8Y8L7
22	37	67.3	479	11	Q91WP5
23	37	67.3	1008	16	Q9X082
24	37	67.3	1217	10	Q94137
25	37	67.3	1350	10	O04013
26	37	67.3	1765	11	O88457
27	37	67.3	4318	5	Q27802
28	36.5	66.4	375	10	Q9XH01
29	36	65.5	71	10	P93234
30	36	65.5	171	16	Q9PMU1
31	36	65.5	175	10	O81927
32	36	65.5	194	16	Q9EWL8
33	36	65.5	225	5	P92048
34	36	65.5	233	10	Q946Y8
35	36	65.5	235	5	P92047
36	36	65.5	242	9	Q94WP6
37	36	65.5	282	17	Q9HRK0
38	36	65.5	331	17	Q8Z294
39	36	65.5	386	5	Q9VNY4
40	36	65.5	409	5	Q9GT69
41	36	65.5	443	10	Q9SB43
42	36	65.5	486	11	Q91Z07
43	36	65.5	521	5	Q9UIN6
44	36	65.5	558	17	Q8TWR0
45	36	65.5	616	10	O81533

ALIGNMENTS

RESULT 1

ID	Q8U129	PRELIMINARY;	PRT;	377 AA.
AC	Q8U129;			
DT	01-JUN-2002 (TrEMBLrel. 21, Created)			
DT	01-JUN-2002 (TrEMBLrel. 21, Last sequence update)			
DT	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)			
DE	Cytochrome o ubiquinol oxidase subunit II.			
GN	CyO OR ATU0142 OR AGR_C_230.			
OS	Agrobacterium tumefaciens (strain C58 / ATCC 33970).			
OC	Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;			
OC	Rhizobiaceae; Rhizobium.			
OX	NCBI_TaxID=176299;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21608550; PubMed=11743193;			
RA	Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,			
RA	Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F., Jr., Woo L.,			
RA	Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Boyee D. Sr.,			
RA	Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,			
RA	Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,			
RA	Raymond C., Rouse G., Saenphimachak C., Wu Z., Romero P., Gordon D.,			
RA	Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,			
RA	Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,			
RA	Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,			
RA	Nester E.W.;			
RT	"The genome of the natural genetic engineer Agrobacterium tumefaciens C58."			
RL	Science 294:2317-2323(2001).			
RN	[2]			
RX	SEQUENCE FROM N.A.			
RP	MEDLINE=21608551; PubMed=11743194;			
RA	Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,			
RA	Quorillo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,			
RA	Houmlet K., Gordon J., Vaudin M., Tartchouk O., Epp A., Liu F.,			
RA	Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,			
RA	Flanagan C., Crowell C., Gursion J., Lomo C., Sear C., Strub G.,			
RT	"Genome sequence of the plant pathogen and biotechnology agent			

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RT Agrobacterium tumefaciens C58.;
RL Science 294:2323-2328(2001);
DR EMBL; AE008988; AA411666.1; ALT_INIT.
DR EMBL; AE007955; AA85963.1; -.
KW Complete proteome.
SQ SEQUENCE 377 AA; 41560 MW; A1BF53FED8BA04AD CRC64;

Query Match 81.8%; Score 45; DB 16; Length 377;
Best Local Similarity 88.9%; Pred. No. 4.1;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WVAKVKSGG 9
Db 258 WVAKVKEGG 266
|||||

RESULT 2
ID Q9IR97 PRELIMINARY; PRT; 352 AA.
AC Q9IR97;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Capsid protein (p38).
OS Japanese iris necrotic ring virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Tombusviridae;
OC Carmovirus.
OX NCBI_TaxID=77344;
RN [1]
RP SEQUENCE FROM N.A.
RA Takemoto Y.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20254547; PubMed=10795530;
RA Takemoto Y., Kanehira T., Shinohara M., Yamashita S., Hibi T.;
RT "The nucleotide sequence and genome organization of Japanese iris
RT necrotic ring virus, a new species in the genus Carmovirus.";
RL Arch. Virol. 145:651-657(2000).
DR EMBL; D86123; BAA92796.1; -.
DR HSP; P11795; 2TBV.
DR InterPro; IPR000937; Viral_coat.
DR Pfam; PF00729; Viral_coat; 1.
DR PRINTS; PR00233; ICOSAHEDRAL.
DR SEQUENCE 352 AA; 37683 MW; 7A34087A0AEF2CE8 CRC64;

Query Match 74.5%; Score 41; DB 12; Length 352;
Best Local Similarity 60.0%; Pred. No. 21;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WVAKVKSGG 10
Db 19 WVKLRSKGG 28
|||||

RESULT 3
ID Q981Y3 PRELIMINARY; PRT; 100 AA.
AC Q981Y3;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein msr9401.
GS MSR9401.
OS Rhizobium loti (Mesorhizobium loti).
OG Plasmid pMLa.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAFF303099;
RX MEDLINE=21082930; PubMed=11214968;

RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpō S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti.";
RL DNA Res. 7:331-338(2000).
DR EMBL; AP003015; BAB54576.1; -.
KW Plasmid; Hypothetical protein; Complete proteome.
SQ SEQUENCE 100 AA; 11111 MW; 1E225AE42936C77 CRC64;

Query Match 72.7%; Score 40; DB 16; Length 100;
Best Local Similarity 70.0%; Pred. No. 8.7;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WVAKVKSGG 10
Db 87 WVAKVKSGG 96
|||||

RESULT 4
ID Q9T232 PRELIMINARY; PRT; 134 AA.
AC Q9T232;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Ribosomal protein L16 (RPL16 protein).
GN RPL16.
OS Phytophthora infestans (Potato late blight fungus).
OG Mitochondrion.
OC Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
OC Phytophthora.
OX NCBI_TaxID=4787;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WEST VIRGINIA 4;
RA Lang B.F., Forget L.;
RT "The mitochondrial genome of Phytophthora infestans.";
RL (In) O'Brien S.J. (eds.);
RL Genetic Maps, pp.3:133-135, Cold Spring Harbor Laboratory Press,
RL NY (1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=WEST VIRGINIA 4;
RA Paquin B., Roewer I., Wang Z., Lang B.F.;
RT "A robust fungal phylogeny using the mitochondrially encoded nad5
RT protein sequence.";
RL Can. J. Bot. 73:S180-S185(1995).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=WEST VIRGINIA 4;
RX MEDLINE=97306266; PubMed=9162109;
RA Paquin B., Laforest M.J., Forget L., Roewer I., Wang Z., Longcore J.,
RA Lang B.F.;
RT "The fungal mitochondrial genome project: evolution of fungal
RT mitochondrial genomes and their gene expression.";
RL Curr. Genet. 31:380-395(1997).
DR EMBL; U17009; AAF24799.1; -.
DR InterPro; IPR000114; Ribosomal_L16.
DR Pfam; PF00252; Ribosomal_L16; 1.
DR PRINTS; PR00060; RIBOSOMALL16.
DR TIGRFAMs; TIGR01164; rplP_bact; 1.
DR PROSITE; PS00701; RIBOSOMAL_L16_2; 1.
DR Mitochondrion; Ribosomal protein.
SQ SEQUENCE 134 AA; 15364 MW; 63CC5239B51095EA CRC64;

Query Match 70.9%; Score 39; DB 8; Length 134;
Best Local Similarity 87.5%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WVAKVKSG 8

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Db	93	WVAKVKGG 100		
RESULT 5				
ID	O55810	PRELIMINARY;	PRT;	342 AA.
AC	O55810;			
DT	01-JUN-1998	(TREMBLrel. 06, Created)		
DT	01-JUN-1998	(TREMBLrel. 06, Last sequence update)		
DT	01-DEC-2001	(TREMBLrel. 19, Last annotation update)		
DE	NS5	protein (Fragment).		
GN	NS5.			
OS	Meaban virus.			
OC	Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;			
OC	Flavivirus.			
OX	NCBI_TaxID=35279;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BREST ART707;			
RX	MEDLINE=98080391; PubMed=9420202;			
RA	Kuno G., Chang G.J., Tsuchiya K.R., Karabatsos N., Cropp C.B.;			
RT	"Phylogeny of the genus Flavivirus.";			
RL	J. Virol. 72:73-83(1998).			
DR	EMBL; AF013386; AAC58774.1; -;			
DR	InterPro; IPR00208; Flavi_NS5.			
DR	Pfam; PF00972; Flavi_NS5; 1.			
FT	NON_TER	1		
FT	NON_TER	342		
SQ	SEQUENCE	342 AA; 38615 MW; D06D642B4CFEE7CC	CRC64;	
Query Match		70.9%;	Score 39; DB 12; Length 342;	
Best Local Similarity		60.0%;	Pred. No. 47;	
Matches	6; Conservative	2; Mismatches	2; Indels	0; Gaps
0;				
Qy	1	WVAKVKSGG 10		
Db	37	WASREKSGG 46		
RESULT 6				
ID	Q51393	PRELIMINARY;	PRT;	391 AA.
AC	Q51393;			
DT	01-NOV-1996	(TREMBLrel. 01, Created)		
DT	01-NOV-1996	(TREMBLrel. 01, Last sequence update)		
DT	01-OCT-2001	(TREMBLrel. 18, Last annotation update)		
DE	ALGJ	(Algininate O-acetyltransferase ALGJ).		
GN	ALGJ OR PA3549.			
OS	Pseudomonas aeruginosa.			
OC	Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;			
OC	Pseudomonas.			
OX	NCBI_TaxID=287;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=FRD1;			
RA	Franklin M.J., Ohman D.E.;			
RL	J. Bacteriol. 178:0-0(0).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=ATCC 15692 / PA01;			
RX	MEDLINE=20437337; PubMed=10984043;			
RA	Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warraner P.,			
RA	Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,			
RA	Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,			
RA	Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,			
RA	Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,			
RA	Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;			
RT	"Complete genome sequence of Pseudomonas aeruginosa PA01, an			
RT	opportunistic pathogen.";			
RL	Nature 406:959-964(2000).			
DR	EMBL; U50202; AAB09782.1; -;			
DR	EMBL; AE004775; AAC06937.1; -;			
KW	Transferase; Complete proteome.			
SQ	SEQUENCE	391 AA; 43106 MW; AE048823947D5503	CRC64;	
Query Match		70.9%;	Score 39; DB 16; Length 391;	
Best Local Similarity		60.0%;	Pred. No. 54;	
Matches	6; Conservative	3; Mismatches	1; Indels	0; Gaps
0;				
Qy	1	WVAKVKSGG 10		
Db	371	WVAQLXASGG 380		
RESULT 7				
ID	O06427	PRELIMINARY;	PRT;	408 AA.
AC	O06427;			
DT	01-JUL-1997	(TREMBLrel. 04, Created)		
DT	01-JUL-1997	(TREMBLrel. 04, Last sequence update)		
DT	01-JUN-2002	(TREMBLrel. 21, Last annotation update)		
DE	Hypothetical 43.8 kDa protein (Monooxygenase, FAD-binding,			
DE	putative).			
GN	RV0561C OR MTCY25D10.40C OR MT0587.			
OS	Mycobacterium tuberculosis.			
OC	Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;			
OC	Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.			
OX	NCBI_TaxID=1773;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=H37RV;			
RX	MEDLINE=98295987; PubMed=9634230;			
RA	Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,			
RA	Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekalia F.,			
RA	Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,			
RA	Davies K., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,			
RA	Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,			
RA	Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,			
RA	Rutter S., Seeger K., Skelton S., Squares S., Squares R.,			
RA	Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;			
RT	"Deciphering the biology of Mycobacterium tuberculosis from the			
RT	complete genome sequence.";			
RL	Nature 393:537-544(1998).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=CDC 1551 / OSHKOSH;			
RA	Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,			
RA	Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,			
RA	Kolony J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,			
RA	Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,			
RA	Bishai W.;			
RT	"Whole genome comparison of Mycobacterium tuberculosis clinical and			
RT	laboratory strains.";			
RL	Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; Z95558; CAB08972.1; -;			
DR	EMBL; AE006956; AAK44810.1; -;			
DR	TIGR; MT0587; -;			
DR	Tuberculist; Rv0561c; -;			
DR	InterPro; IPR00205; NAD_binding.			
KW	Hypothetical protein; Complete proteome.			
SQ	SEQUENCE	408 AA; 43869 MW; B2F61E46A656EA8C	CRC64;	
Query Match		70.9%;	Score 39; DB 16; Length 408;	
Best Local Similarity		70.0%;	Pred. No. 56;	
Matches	7; Conservative	1; Mismatches	2; Indels	0; Gaps
0;				
Qy	1	WVAKVKSGG 10		
Db	386	WVARVWRGGG 395		
RESULT 8				
ID	Q8TU18	PRELIMINARY;	PRT;	312 AA.
AC	Q8TU18;			

Query Match	69.1%;	Score 38;	DB 16;	Length 425;
Best Local Similarity	60.0%;	Pred. No. 90;		
Matches	6;	Conservative	1;	Mismatches 3; Indels 0; Gaps
QY	1	WVAKVSGGG 10		
DB	92	WAKEKSGGG 101		
		: :		
RESULT 10				
Q57079		PRELIMINARY;	PRT;	509 AA.
AC	Q57079;			
DT	01-NOV-1996 (TrEMBLrel. 01, Created)			
DT	01-NOV-1996 (TrEMBLrel. 01, Last sequence update)			
DT	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)			
DE	Alpha-subunit,methylmalonyl-CoA decarboxylase.			
OS	Veillonella parvula.			
OC	Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;			
OC	Clostridiales; Acidaminococcaceae; Veillonella.			
OX	NCBI_TaxID=29466;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Huder J.B.; Dimroth P.;			
RL	J. Biol. Chem. 0:0-0(1993).			
[2]				
RP	SEQUENCE FROM N.A.			
RA	MEDLINE=94043308; PubMed=8227015;			
RL	Huder J.B.; Dimroth P.;			
RT	"Sequence of the sodium ion pump methylmalonyl-CoA decarboxylase from			
RT	Veillonella parvula.";			
RL	J. Biol. Chem. 268:24564-24571(1993).			
DR	EMBL; Z24754; CAA80872.1; -.			
DR	EMBL; L22208; AAC36820.1; -.			
DR	InterPro; IPR000022; Carboxyl_trans.			
DR	InterPro; IPR002203; Intein.			
DR	Pfam; PF01039; Carboxyl_trans; 1.			
DR	TIGRFAMS; TIGR01117; mmdA; 1.			
DR	PROSITE; PS00881; PROTEIN_SPLICING; UNKNOWN_1.			
SQ	SEQUENCE 509 AA; 55100 MW; B9F85266A422B03B CRC64;			
Query Match	69.1%;	Score 38;	DB 2;	Length 509;
Best Local Similarity	77.8%;	Pred. No. 1.1e+02;		
Matches	7;	Conservative	2;	Mismatches 0; Indels 0; Gaps
QY	2	VAKVSGGG 10		
DB	15	LAKVKAGGG 23		
		: :		
RESULT 11				
Q72120		PRELIMINARY;	PRT;	691 AA.
ID	Q72120			
AC	Q72120;			
DT	01-AUG-1998 (TrEMBLrel. 07, Created)			
DT	01-AUG-1998 (TrEMBLrel. 07, Last sequence update)			
DT	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)			
DE	Capsid protein.			
GN	ORF2.			
OS	Canine calicivirus.			
OC	Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;			
OC	Vesivirus.			
OX	NCBI_TaxID=74724;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=NO. 48;			
RA	MEDLINE=99226944; PubMed=10211962;			
RL	Roerink F.; Hashimoto M.; Tohya Y.; Mochizuki M.;			
RT	"Organization of the canine calicivirus genome from the RNA polymerase			
RT	gene to the poly(A) tail.";			
RL	J. Gen. Virol. 80:929-935(1999).			
[2]				
RP	SEQUENCE FROM N.A.			

RA Matsuura Y., Tohya Y.;
RT "Complete nucleotide sequence of canine calicivirus genome."
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF053720; AAC16446.1; -
DR EMBL; AB070225; BAB83602.1; -
DR InterPro; IPR004005; Calici_coat.
DR Pfam; PF00915; Calici_coat; 1.
SQ SEQUENCE 691 AA; 76181 MW; FIC9774C9217AEF4 CRC64;

Query Match 69.1%; Score 38; DB 12; Length 691;
Best Local Similarity 60.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WVAKVSGGG 10
I : : : : :
Db 549 WIAKEQSAGG 558

RESULT 12
Q00303 PRELIMINARY; PRT; 907 AA.
AC Q00303;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Nitrate reductase.
GN NIAD.
OS Botrytis cinerea (Botryotinia fuckelliana).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
OC Helotiales; Sclerotiniaceae; Botryotinia.
OX NCBI_TaxID=40559;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TA;
RA Lewis C., Dutertre M., Fortini D., Brygoo Y.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U43783; AAC02633.1; -
DR HSP; P17571; ICNE.
DR InterPro; IPR001199; Cyt_B5.
DR InterPro; IPR001834; Cyt_B5_reductase.
DR InterPro; IPR000572; Euk_Mb_oxred.
DR InterPro; IPR005066; Mo-co dimer.
DR InterPro; IPR001433; Oxred_FAD/NAD(P).
DR Pfam; PF00970; FAD_binding_6; 1.
DR Pfam; PF00173; heme_1; 1.
DR Pfam; PF03404; Mo-co dimer; 1.
DR Pfam; PF00175; NAD_binding; 1.
DR Pfam; PF00174; oxidored_molyb; 1.
DR PRINTS; PR00406; CYTB5RDTHASE.
DR PRINTS; PR00363; CYTOCHROME_B5.
DR PRINTS; PR00407; EUOPTERIN.
DR PRODOM; PD000612; Cyt_B5; 1.
DR PROSITE; PS00191; CYTOCHROME_B5_1; UNKNOWN_1.
DR PROSITE; PS0255; CYTOCHROME_B5_2; 1.
DR PROSITE; PS00559; MOLYBDOPTERIN_EUK; 1.
KW Heme.
SQ SEQUENCE 907 AA; 101897 MW; 9E04BA54B5084FAD CRC64;

Query Match 69.1%; Score 38; DB 3; Length 907;
Best Local Similarity 60.0%; Pred. No. 2e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WVAKVSGGG 10
I : : : : :
Db 494 WMERVKSAGG 503

RESULT 13
Q945T0 PRELIMINARY; PRT; 115 AA.
AC Q945T0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE RALF.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21532999; PubMed=11675511;
RA Pearce G., Moura D.S., Stratmann J., Ryan C.A. Jr.;
RT "RALF, a 5-kDa ubiquitous polypeptide in plants, arrests root growth
and development".
RL Proc. Natl. Acad. Sci. U.S.A. 98:12843-12847(2001).
DR EMBL; AF407278; AAL26478.1; - RALF.
FT CHAIN 67 115
SQ SEQUENCE 115 AA; 12203 MW; 7089DDF3EC1CE346 CRC64;

Query Match 67.3%; Score 37; DB 10; Length 115;
Best Local Similarity 60.0%; Pred. No. 36;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 WVAKVSGGG 10
I : : : : :
Db 31 WWPARGSGG 40

RESULT 14
Q920E7 PRELIMINARY; PRT; 119 AA.
AC Q920E7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE pterin-mimicking anti-idiotope heavy chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Atkin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.;
RT "Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed
in Mammalian Cells".
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307937; AAL09421.1; -
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR NON_TER 1 1
FT NON_TER 119 119
SQ SEQUENCE 119 AA; 13025 MW; F6E904044381CA7C CRC64;

Query Match 67.3%; Score 37; DB 11; Length 119;
Best Local Similarity 66.7%; Pred. No. 37;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WVAKVSGG 9
I : : : : :
Db 47 WWTISSGG 55

RESULT 15
O86545 PRELIMINARY; PRT; 186 AA.
AC O86545;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical protein SC06611.
GN SC06611 OR SCIF2.08C.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2) / M145;
 RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
 RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete Streptomyces
 coelicolor A3(2).";
 RL Nature 417:141-147(2002).
 DR EMBL; AL031350; CAA20499.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 186 AA; 19874 MW; A32B4FE734D48FB2 CRC64;

Query Match 67.3%; Score 37; DB 16; Length 186;
 Best Local Similarity 60.0%; Pred. No. 59;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 WAKVKGGG 10
 |||
 Db 51 WTTVRPGG 60

Search completed: November 18, 2002, 17:40:37
 Job time : 11.4912 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:21:57 : Search time 13.8235 Seconds
(without alignments)
96.394 Million cell updates/sec

Title: US-09-016-061-54
Perfect score: 55
Sequence: 1 WAKVKS GGG 10

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : A_Geneseq_101002.*
- 1: /SID22/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
 - 2: /SID22/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
 - 3: /SID22/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
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 - 5: /SID22/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
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 - 7: /SID22/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
 - 8: /SID22/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
 - 9: /SID22/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
 - 10: /SID22/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
 - 11: /SID22/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
 - 12: /SID22/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
 - 13: /SID22/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
 - 14: /SID22/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
 - 15: /SID22/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
 - 16: /SID22/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
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 - 18: /SID22/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
 - 19: /SID22/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
 - 20: /SID22/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
 - 21: /SID22/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
 - 22: /SID22/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
 - 23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	55	100.0	10	AAW76017	LM609 grafted anti
2	55	100.0	10	AAW76017	Mutant VH CDR2 pep
3	50	90.9	10	AAW76008	LM609 grafted anti
4	50	90.9	10	AAW76008	LM609 VH CDR2 pep
5	50	90.9	117	AAW76001	Vitaxin antibody h
6	50	90.9	117	AAW76003	LM609 antibody hea
7	50	90.9	117	AAW06381	Murine monoclonal
8	50	90.9	117	AAW06381	A heavy chain vari
9	50	90.9	117	AAW06381	A heavy chain vari
10	50	90.9	117	AAW06381	Vitaxin heavy chai

11	50	90.9	117	22	AAW76017	Antibody LM609 hea
12	50	90.9	130	20	AAW06379	Murine monoclonal
13	43	78.2	98	22	AAW06379	Mouse germline hea
14	43	78.2	119	19	AAW69322	15D3 antibody hea
15	43	78.2	119	20	AAW32832	15D3 VH chain prot
16	43	78.2	119	20	AAW73503	Antibody 15D3 hea
17	43	78.2	138	13	AAW20064	MRK16-H chain. Ch
18	43	78.2	140	23	AAU76122	Mouse monoclonal a
19	43	78.2	140	23	AAU76132	Mouse mAb 26-2F he
20	43	78.2	140	23	AAU76133	Mouse mAb 26-2F he
21	42	76.4	119	16	AAW11919	Humanised MAB SK48
22	42	76.4	123	19	AAW66099	anti-CD22 monoclon
23	42	76.4	247	16	AAW11917	Murine MAB SK48-E2
24	41	74.5	110	18	AAW06207	Rat antibody heavy
25	41	74.5	118	18	AAW06208	Xenograft antibody
26	41	74.5	140	18	AAW06205	Xenograft antibody
27	40	72.7	255	23	ABP45615	Human Blys binding
28	40	72.7	256	23	ABP46108	Human Blys binding
29	39	70.9	87	22	AAW06990	Mouse germline hea
30	39	70.9	98	22	AAW06978	Mouse germline hea
31	39	70.9	119	14	AAW32240	Humanised MAB hea
32	39	70.9	119	14	AAW32243	Humanised MAB hea
33	39	70.9	119	14	AAW32244	Humanised MAB hea
34	39	70.9	119	18	AAW27144	Mature heavy chain
35	39	70.9	119	21	AAW87570	Humanised ABL 364
36	39	70.9	120	17	AAW00240	EGF receptor chime
37	39	70.9	120	22	AAW65570	Amino acid sequenc
38	39	70.9	122	13	AAW25722	Humanised VH regio
39	39	70.9	122	22	AAW69663	Murine Fd79 antio
40	39	70.9	122	22	AAW69664	Humanised Fd79 ant
41	39	70.9	131	16	AAW70466	VH sequence of ant
42	39	70.9	131	22	AAW84293	Amino acid sequenc
43	39	70.9	138	14	AAW32242	Chimeric MAB heavy
44	39	70.9	138	14	AAW32246	BR55-2 murine IgG3
45	39	70.9	139	14	AAW31588	BR55-2 heavy chain

ALIGNMENTS

- RESULT 1
- AAW76017
- ID AAW76017 standard; Protein; 10 AA.
- XX AAW76017;
- XX
- AC AAW76017;
- DT 02-NOV-1998 (first entry)
- XX
- DE LM609 grafted antibody V-H region CDR2 protein fragment #3.
- XX
- KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
- KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
- KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
- KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
- KW macular degeneration; osteoporosis; primer; V-H region; CDR;
- KW complementarity determining region.
- XX
- OS Mus sp.
- XX
- PN W09833919-A2.
- XX
- PD 06-AUG-1998.
- XX
- PF 30-JAN-1998; 98WO-US01826.
- XX
- PR 30-JAN-1997; 97US-0791391.
- XX
- PA (IXSV-) IXSVS INC.
- XX
- PI Glaser SM, Huse WD;
- XX
- DR WPI; 1998-437472/37.
- DR N-PSDB; AAV49854.

XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
PS Claim 61; Page 41; 129pp; English.
XX
CC AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
CC antibodies contain non-murine framework regions so are suitable for use
CC in humans. Enhanced types of LM609 have affinity more than 90 times
CC greater than that of parent the parent antibody.
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 55; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0048;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVAKVSGGG 10
| | | | | | | | | |
Db 1 WVAKVSGGG 10
| | | | | | | | | |

RESULT 2
AAB61375
ID AAB61375 standard; peptide; 10 AA.
XX
AC AAB61375;
XX
XX 03-APR-2001 (first entry)
XX
XX Mutant VH CDR2 peptide #1.
XX
XX LM609; grafted antibody; alphaVbeta_3 integrin; angiogenesis;
KW inflammatory; cancer; retina; restenosis; osteoporosis.
XX
XX Unidentified.
XX
XX WO200078815-A1.
PN
XX
XX 28-DEC-2000.
PD
XX
XX 23-JUN-2000; 2000WO-US17454.
PF
XX
XX 24-JUN-1999; 99US-0339922.
PR
XX
XX (MOLE-) APPLIED MOLECULAR EVOLUTION.
PA
XX
XX Huse WD, Wu H;
PI
XX
XX WPI; 2001-050110/06.
DR
XX
XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
PT osteoporosis -
XX
XX Disclosure; Page 41; 132pp; English.
PS
XX
XX The present invention relates to enhanced LM609 grafted antibodies
CC exhibiting selective binding affinity to alphaVbeta_3 integrin or
CC their functional fragments. The antibodies or their functional
CC fragments can be used in the diagnosis and treatment of
CC alphaVbeta_3-mediated diseases such as angiogenesis, inflammatory

CC diseases (such as psoriasis and chronic articular rheumatism),
CC disorders associated with inappropriate or inopportune invasion of
CC vessels (such as diabetic retinopathy, neovascular glaucoma and
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
CC diseases (such as macular degeneration), restenosis and
CC osteoporosis.
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 55; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0048;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVAKVSGGG 10
| | | | | | | | | |
Db 1 WVAKVSGGG 10
| | | | | | | | | |

RESULT 3
AAW76008
ID AAW76008 standard; Protein; 10 AA.
XX
XX AAW76008;
AC AAW76008;
XX
XX 02-NOV-1998 (first entry)
DT
XX
XX LM609 grafted antibody V-H region CDR2 protein fragment #1.
DE
XX
XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
XX
XX Mus sp.
OS
XX
XX WO9833919-A2.
PN
XX
XX 06-AUG-1998.
PD
XX
XX 30-JAN-1998; 98WO-US01826.
PF
XX
XX 30-JAN-1997; 97US-0791391.
PR
XX
XX (IXSY-) IXSYS INC.
PA
XX
XX Glaser SM, Huse WD;
PI
XX
XX WPI; 1998-437472/37.
DR
XX
XX N-PSDB; AAV49845.
DR
XX
XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
XX Disclosure; Page 40; 129pp; English.
PS
XX
XX AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
CC antibodies contain non-murine framework regions so are suitable for use
CC in humans. Enhanced types of LM609 have affinity more than 90 times
CC greater than that of parent the parent antibody.
XX
XX Sequence 10 AA;
SQ

Query Match 90.9%; Score 50; DB 19; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.034;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WVAKVSGGG 10
 ||||| ||||
 Db 1 WVAKVSSGGG 10

RESULT 4

AAB61366
 ID AAB61366 standard; peptide; 10 AA.

XX XX
 AC AAB61366;

DT 03-APR-2001 (first entry)

XX XX
 DE LM609 VH CDR2 peptide.

XX LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis.

XX Unidentified.

XX WO200078815-A1.

XX 28-DEC-2000.

XX 23-JUN-2000; 2000WO-US17454.

XX 24-JUN-1999; 99US-0339922.

XX (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX Huse WD, Wu H;

XX WPI; 2001-050110/06.

XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -

XX Disclosure; Page 39; 132pp; English.

XX The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphavbeta_3 integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.

XX Sequence 10 AA;

Query Match 90.9%; Score 50; DB 22; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.034;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WVAKVSGGG 10
 ||||| ||||
 Db 1 WVAKVSSGGG 10

RESULT 5

AAW76001
 ID AAW76001 standard; Protein; 117 AA.

XX

AC AAW76001;
 XX 02-NOV-1998 (first entry)
 DT XX
 DE Vitaxin antibody heavy chain variable region protein fragment.
 XX XX
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.
 XX Mus sp.
 OS WO9833919-A2.
 PN 06-AUG-1998.
 PD 30-JAN-1998; 98WO-US01826.
 PF 30-JAN-1997; 97US-0791391.
 XX (IXSY-) IXSYS INC.
 PA Glaser SM, Huse WD;
 PI WPI; 1998-437472/37.
 XX N-PSDB; AAV49820.
 DR Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 XX integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX Claim 1; Fig 1a; 129pp; English.
 PS This sequence represents a fragment of the vitaxin antibody variable
 CC heavy chain region. Vitaxin and the antibody LM609 bind selectively to
 CC integrin alphavbeta3 and can be used to inhibit binding of alphavbeta3
 CC to a ligand and thus block integrin-mediated signal transduction. This is
 CC useful in the treatment, prevention and diagnosis of alphavbeta3-mediated
 CC disease, specifically angiogenesis and restenosis (but also e.g.
 CC (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,
 CC cancer, psoriasis, rheumatoid arthritis, macular degeneration,
 CC osteoporosis etc.). The antibodies contain non-murine framework regions
 CC so are suitable for use in humans. Enhanced types of LM609 have affinity
 CC more than 90 times greater than that of parent the parent antibody.
 XX Sequence 117 AA;
 SQ Query Match 90.9%; Score 50; DB 19; Length 117;
 Best Local Similarity 90.0%; Pred. No. 0.41;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 WVAKVSGGG 10
 ||||| ||||
 Db 47 WVAKVSSGGG 56
 RESULT 6
 AAW76003
 ID AAW76003 standard; Protein; 117 AA.
 XX XX
 AC AAW76003;
 XX 02-NOV-1998 (first entry)
 DT XX
 DE LM609 antibody heavy chain variable region protein fragment.
 XX XX
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;

KW macular degeneration; osteoporosis.
 OS Mus sp.
 XX WO9833919-A2.
 PN
 XX
 XX 06-AUG-1998.
 PD
 XX 30-JAN-1998; 98WO-US01826.
 XX 30-JAN-1997; 97US-0791391.
 PR (JXSY-) IXSYS INC.
 PA
 XX Glaser SM, Huse WD;
 PI
 XX WPI: 1998-437472/37.
 DR N-PSDB; AAV49822.
 DR
 XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 PS Claim 43; Fig 2a; 129pp; English.
 XX
 CC This sequence represents the LM609 antibody variable heavy chain region.
 CC LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3
 CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus
 CC block integrin-mediated signal transduction. This is useful in the
 CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,
 CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
 CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
 CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
 CC etc.). The antibodies contain non-murine framework regions so are
 CC suitable for use in humans. Enhanced types of LM609 have affinity more
 CC than 90 times greater than that of parent the parent antibody.
 XX
 SQ Sequence 117 AA;
 Query Match 90.9%; Score 50; DB 19; Length 117;
 Best Local Similarity 90.0%; Pred. No. 0.41;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 WVAKVSGGG 10
 Db | | | | | | | |
 47 WVAKVSSGGG 56
 RESULT 7
 AAY06381
 ID AAY06381 standard; Protein; 117 AA.
 XX
 AC AAY06381;
 XX
 XX 06-SEP-1999 (first entry)
 DT
 XX Murine monoclonal antibody LM609 VH region.
 DE
 XX Humanised antibody; antibody humanisation; antibody engineering;
 KW LM609; monoclonal antibody; complementarity determining region;
 KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
 KW cancer; therapy; diagnosis.
 XX
 OS Mus musculus.
 XX
 PN WO9929888-A1.
 XX
 PD 17-JUN-1999.
 XX
 PF 04-DEC-1998; 98WO-US25828.
 XX
 PR 05-DEC-1997; 97US-0986016.

XX (SCKI) SCRIPES RES INST.
 PA
 XX Barbas CF, Rader C;
 PI
 XX WPI: 1999-394979/33.
 DR
 XX Production of humanized mouse monoclonal antibodies
 PT
 XX Disclosure; Page 52-53; 55pp; English.
 PS
 XX This sequence represents the heavy chain variable region of murine
 CC monoclonal antibody LM609. LM609 is directed to integrin
 CC alpha-v beta-3. It selectively promotes apoptosis of vascular
 CC cells that have been stimulated to undergo angiogenesis, making it
 CC a tool for cancer diagnosis and therapy. The invention provides
 CC humanised antibodies, especially humanised LM609. In such humanized
 CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
 CC grafted onto a human light chain, and a heavy chain CDR from a mouse
 CC antibody is grafted onto a human antibody heavy chain to produce
 CC libraries from which a humanised murine antibody having the desired
 CC specificity is selected. By preserving the original CDR sequences
 CC such as the HCDR3 and LCDR3 sequences of LM609 (see AAY06371-72), the
 CC humanisation strategy ensures epitope conservation.
 XX
 SQ Sequence 117 AA;
 Query Match 90.9%; Score 50; DB 20; Length 117;
 Best Local Similarity 90.0%; Pred. No. 0.41;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 WVAKVSGGG 10
 Db | | | | | | | |
 47 WVAKVSSGGG 56
 RESULT 8
 AAG63587
 ID AAG63587 standard; Protein; 117 AA.
 XX
 AC AAG63587;
 XX
 XX 15-OCT-2001 (first entry)
 DT
 XX A heavy chain variable region of LM609 grafted antibody.
 DE
 XX Grafted antibody; LM609; integrin; alphavbeta3; inflammatory disorder;
 KW chronic articular rheumatism; psoriasis; diabetic retinopathy;
 KW neovascular glaucoma; capillary proliferation; atherosclerotic plaque;
 KW cancer.
 XX
 OS Synthetic.
 OS Mus sp.
 XX
 XX US2001011125-A1.
 PN
 XX 02-AUG-2001.
 PD
 XX 30-JAN-1997; 97US-0790540.
 PF
 XX 30-JAN-1997; 97US-0790540.
 PR
 XX (HUSE/) HUSE W D.
 PA
 XX Huse WD;
 PI
 XX WPI: 2001-496171/54.
 DR N-PSDB; AAH74623.
 DR
 XX New LM609 grafted antibody exhibiting selective binding affinity to
 PT alphavbeta3, comprising at least one LM609 grafted heavy and light
 PT chain polypeptide, useful for diagnosing and treating e.g. inflammatory
 PT disorders or cancer

CC osteoporosis.
XX
SQ Sequence 117 AA;

Query Match 90.9%; Score 50; DB 22; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.41;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WVAKVSGG 10
|||||
Db 47 WVAKVSSGG 56

RESULT 11

AAB61361
ID AAB61361 standard; protein; 117 AA.

XX
AC AAB61361;

XX
DT 03-APR-2001 (first entry)

XX Antibody LM609 heavy chain variable region protein.

XX LM609; grafted antibody; alphaVbeta₃ integrin; angiogenesis;
KW inflammatory; cancer; retina; restenosis; osteoporosis.

XX Unidentified.

XX WO200078815-A1.

XX 28-DEC-2000.

XX 23-JUN-2000; 2000WO-US17454.

XX 24-JUN-1999; 99US-0339922.

XX (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX Huse WD, Wu H;

XX WPI; 2001-050110/06.

XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
PT to alpha(V)beta₃ integrin, useful in the diagnosis and treatment of
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
PT osteoporosis.

XX Disclosure; Fig 2; 132pp; English.

XX The present invention relates to enhanced LM609 grafted antibodies
CC exhibiting selective binding affinity to alphaVbeta₃ integrin or
CC their functional fragments. The antibodies or their functional
CC fragments can be used in the diagnosis and treatment of
CC alphaVbeta₃-mediated diseases such as angiogenesis, inflammatory
CC diseases (such as psoriasis and chronic articular rheumatism),
CC disorders associated with inappropriate or inopportune invasion of
CC vessels (such as diabetic retinopathy, neovascular glaucoma and
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
CC diseases (such as macular degeneration), restenosis and
CC osteoporosis.

XX
SQ Sequence 117 AA;

Query Match 90.9%; Score 50; DB 22; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.41;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WVAKVSGG 10
|||||
Db 47 WVAKVSSGG 56

RESULT 12

AAE06981
ID AAE06981 standard; protein; 98 AA.

XX

AAV06379
ID AAV06379 standard; Protein; 130 AA.

XX
AC AAV06379;

XX
DT 06-SEP-1999 (first entry)

XX Murine monoclonal antibody LM609 V kappa.

XX Humanised antibody; antibody humanisation; antibody engineering;
KW LM609; monoclonal antibody; complementarity determining region;
KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
KW cancer; therapy; diagnosis.

XX Mus musculus.

XX Key Location/Qualifiers

FT Peptide 1..2 /note= "vector-encoded residues"

FT Region 28..32 /note= "CDR1"

FT Region 47..63 /note= "CDR2"

FT Region 96..103 /note= "CDR3"

XX WO9929888-A1.

XX 17-JUN-1999.

XX 04-DEC-1998; 98WO-US25828.

XX 05-DEC-1997; 97US-0986016.

XX (SCRI) SCRIPPS RES INST.

XX Barbas CF, Rader C;

XX WPI; 1999-394979/33.

XX Production of humanized mouse monoclonal antibodies

XX Disclosure; Page 49-50; 55pp; English.

XX This sequence represents the light chain V kappa region of murine
CC monoclonal antibody LM609. LM609 is directed to integrin
CC alpha-v beta-3. It selectively promotes apoptosis of vascular
CC cells that have been stimulated to undergo angiogenesis, making it
CC a tool for cancer diagnosis and therapy. The invention provides
CC humanised antibodies, especially humanised LM609. In such humanized
CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
CC grafted onto a human light chain, and a heavy chain CDR from a mouse
CC antibody is grafted onto a human antibody heavy chain to produce
CC libraries from which a humanised murine antibody having the desired
CC specificity is selected. By preserving the original CDR sequences
CC such as the HCDR3 and LCDR3 sequences of LM609 (see AAV06371-72), the
CC humanisation strategy ensures epitope conservation.

XX
SQ Sequence 130 AA;

Query Match 90.9%; Score 50; DB 20; Length 130;
Best Local Similarity 90.0%; Pred. No. 0.45;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WVAKVSGG 10
|||||

Db 44 WVAKVSSGG 53

AC	AAE01681;	
XX	16-OCT-2001 (first entry)	
DT		
XX	Mouse germline heavy chain variable (VH) region, VH283.	
DE		
XX		
KW	Mouse; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic; neuroprotective; immunosuppressive; human immunodeficiency virus; HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy; inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock; multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma; anaphylaxis; malignancy; inflammation; stenosis; allograft rejection; fibrotic disease; angioplasty; acquired immune deficiency syndrome; AIDS; inflammatory glomerulopathy; vascular intervention; neointimal hyperplasia; VH; heavy chain variable region.	
XX		
OS	Mus sp.	
XX		
XX	WO200157226-A1.	
PN		
XX		
XX	09-AUG-2001.	
PD		
XX		
PF	02-FEB-2001; 2001WO-US03537.	
XX		
PR	03-FEB-2000; 2000US-0497625.	
XX		
XX	(MILL-) MILLENNIUM PHARM INC.	
XX		
PI	Larosa GJ, Horvath C, Newman W, Jones ST, O'Brien S, O'Keefe T;	
XX	WPI; 2001-488888/53.	
DR		
XX		
PT	Humanized immunoglobulin for treating a CC-chemokine receptor	
PT	2-mediated disorder in a patient, comprises a binding specificity for	
PT	CCR2, and a non-human antigen binding region and human immunoglobulin	
PT		
XX		
XX	Disclosure; Page 156; 183pp; English.	
PS		
XX		
CC	The patent discloses a humanised antibody or its antigen-binding	
CC	fragment, having binding specificity for CC-chemokine receptor 2	
CC	(CCR2), comprising an antigen binding region of non-human origin	
CC	and at least a portion of an immunoglobulin of human origin. The	
CC	humanised antibodies are useful for inhibiting the interaction of	
CC	a cell expressing CCR2. They are useful for inhibiting or treating	
CC	HIV infection. The proteins of the invention are useful for inhibiting	
CC	leukocyte trafficking, for treating CCR2-mediated disorders such as	
CC	inflammatory disorder, autoimmune disorders such as rheumatoid	
CC	arthritis and multiple sclerosis, atherogenesis and atherosclerosis,	
CC	and for inhibiting restenosis. They are useful in therapy or diagnosis,	
CC	and in the manufacture of a medicament for treating CCR-2 mediated	
CC	disease. They are also useful for treating allergy, anaphylaxis,	
CC	malignancy, chronic and acute inflammation, histamine and IgE-	
CC	mediated allergic reaction, shock, stenosis, allograft rejection,	
CC	fibrotic disease, asthma, inflammatory glomerulopathies, acquired	
CC	immune deficiency syndrome (AIDS), restenosis associated with vascular	
CC	intervention, including angioplasty and/or stent placement in a mammal.	
CC	Humanised antibodies are also useful for inhibiting narrowing of the	
CC	lumen of a vessel in a mammal, and inhibiting neointimal hyperplasia of	
CC	a vessel in a mammal, preferably associated with vascular intervention.	
CC	The present sequence is mouse germline heavy chain variable (VH)	
CC	region, VH283.	
XX		
SQ	Sequence 98 AA;	
	Query Match 78.2%; Score 43; DB 22; Length 98;	
	Best Local Similarity 70.0%; Pred. No. 5.3;	
	Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;	
QY	1 WVAKVSGGG 10	
Db	47 WVAISGGG 56	

RESULT 14	
AAW69322	
ID	AAW69322 standard; Protein; 119 AA.
XX	
AC	AAW69322;
XX	
DT	19-NOV-1998 (first entry)
DE	15D3 antibody heavy chain.
XX	
KW	Hybridoma 15D3; 15D3 antibody; complementarity-determining region; scFv;
KW	single-chain antibody molecule; multidrug-resistant human tumour cell;
KW	MDR tumour; CDR; therapy; heavy chain.
XX	
OS	Homo sapiens.
XX	
XX	
FH	Key
FT	Region
FT	Location/Qualifiers
FT	1..30
FT	/note= "HFR1"
FT	31..35
FT	/note= "HCDR1"
FT	36..49
FT	/note= "HFR2"
FT	50..66
FT	/note= "HCDR2"
FT	67..98
FT	/note= "HFR3"
FT	99..108
FT	/note= "HCDR3"
FT	109..119
FT	/note= "HFR4"
XX	
PN	US5811267-A.
XX	
XX	
PD	22-SEP-1998.
XX	
XX	
PF	07-JUN-1995; 95US-0475000.
XX	
PR	07-JUN-1995; 95US-0475000.
PR	29-OCT-1990; 90US-0605399.
PR	22-OCT-1993; 93US-0141375.
PR	17-OCT-1994; 94US-0323566.
XX	
PA	(CHIR) CHIRON CORP.
XX	
PI	Ring DB;
XX	
DR	WPI; 1998-530873/45.
DR	N-PSDB; AAV44997.
XX	
PT	DNA encoding single-chain antibody molecule - specific for
PT	multidrug-resistant tumour cells, useful in diagnosis or therapy
XX	
PS	Disclosure; Fig 1; 26pp; English.
XX	
CC	This sequence represents the VH chain of the antibody
CC	produced by hybridoma cell line 15D3. It is part of the nucleic acid of
CC	the invention which encodes a single-chain antibody molecule (scFv)
CC	comprising the heavy-chain complementarity-determining regions (CDRs) of
CC	the monoclonal antibody produced by hybridoma cell line 15D3, where the
CC	monoclonal antibody and scFv are capable of binding to
CC	multidrug-resistant (MDR) human tumour cells. The CDR sequences from both
CC	the heavy and light chains (HCDR1, HCDR2, HCDR3, LCDR1, LCDR2, and LCDR3)
CC	are all used in an expression cassette that can be used in a method for
CC	inducing the production of a polypeptide. The method is useful for
CC	producing recombinant scFv, which can be used for diagnosis or therapy
CC	(e.g. in the form of an immunotoxin) for MDR tumours.
XX	
SQ	Sequence 119 AA;
	Query Match 78.2%; Score 43; DB 19; Length 119;
	Best Local Similarity 70.0%; Pred. No. 6.5;

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:54:45 ; Search time 1.96078 Seconds
(without alignments)
76.811 Million cell updates/sec

Title: US-09-016-061-54
Perfect score: 55
Sequence: 1 WAKVKSGGG 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 97044 seqs, 15060890 residues

Total number of hits satisfying chosen parameters: 97044

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match %	Score	Length	ID	Description
1	50	90.9	117	8	US-08-790-540A-2
2	50	90.9	117	8	US-08-790-540A-6
3	50	90.9	117	8	US-08-791-391A-2
4	50	90.9	117	8	US-08-791-391A-6
5	43	78.2	98	10	US-09-840-459-44
6	43	78.2	140	10	US-09-286-240-4
7	39	70.9	87	10	US-09-840-459-53
8	39	70.9	98	10	US-09-840-459-41
9	38	69.1	88	10	US-09-840-459-51
10	38	69.1	133	12	US-10-006-773-9
11	38	69.1	144	10	US-09-881-823-12
12	37	67.3	89	10	US-09-840-459-49
13	37	67.3	98	10	US-09-905-243-49
14	37	67.3	98	10	US-09-840-459-38
15	37	67.3	98	10	US-09-840-459-39
16	37	67.3	118	9	US-09-423-800-46
17	37	67.3	118	9	US-09-423-800-56
18	37	67.3	123	9	US-09-144-886-61
19	37	67.3	137	9	US-09-423-800-76

Query Match 90.9%; Score 50; DB 8; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.089;

20	37	67.3	137	9	US-09-423-800-77	Sequence 77, Appl
21	37	67.3	140	12	US-10-006-773-4	Sequence 4, Appl1
22	37	67.3	245	9	US-09-956-086-5	Sequence 5, Appl1
23	37	67.3	245	9	US-09-956-087-5	Sequence 5, Appl1
24	37	67.3	265	9	US-09-985-442-5	Sequence 5, Appl1
25	37	67.3	265	10	US-09-983-580-5	Sequence 8, Appl1
26	36	65.5	130	10	US-09-764-304-8	Sequence 18, Appl1
27	36	65.5	130	10	US-09-764-304-18	Sequence 18, Appl1
28	35	63.6	95	10	US-09-864-761-47118	Sequence 47118, A
29	35	63.6	101	10	US-09-864-761-38468	Sequence 38468, A
30	35	63.6	139	12	US-10-006-773-17	Sequence 17, Appl1
31	35	63.6	443	10	US-09-917-410-4	Sequence 4, Appl1
32	34	61.8	76	9	US-10-001-873-39	Sequence 39, Appl1
33	34	61.8	119	10	US-09-736-371B-17	Sequence 17, Appl1
34	34	61.8	119	12	US-10-060-714-17	Sequence 17, Appl1
35	34	61.8	143	12	US-10-062-234-368	Sequence 368, App
36	34	61.8	621	10	US-09-733-300-4	Sequence 4, Appl1
37	33	60.0	98	10	US-09-840-459-45	Sequence 45, Appl1
38	33	60.0	118	9	US-09-144-886-62	Sequence 62, Appl1
39	33	60.0	118	9	US-09-144-886-63	Sequence 63, Appl1
40	33	60.0	118	9	US-09-144-886-64	Sequence 64, Appl1
41	33	60.0	118	9	US-09-144-886-65	Sequence 65, Appl1
42	33	60.0	118	9	US-09-144-886-66	Sequence 66, Appl1
43	33	60.0	118	9	US-09-144-886-67	Sequence 67, Appl1
44	33	60.0	123	9	US-09-144-886-60	Sequence 60, Appl1
45	33	60.0	124	10	US-09-840-459-89	Sequence 89, Appl1

ALIGNMENTS

RESULT 1
US-08-790-540A-2
; Sequence 2, Application US/08790540A
; Patent No. US20010011125A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,540A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-790-540A-2

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Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WVAKVSGG 10
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Db 47 WVAKVSSGG 56

RESULT 2
US-08-790-540A-6
; Sequence 6, Application US/08790540A
; Patent No. US20010011125A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790.540A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-790-540A-6

Query Match 90.9%; Score 50; DB 8; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.089;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WVAKVSGG 10
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Db 47 WVAKVSSGG 56

RESULT 3
US-08-791-391A-2
; Sequence 2, Application US/08791391A
; Patent No. US20010016645A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791.391A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-391A-2

Query Match 90.9%; Score 50; DB 8; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.089;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WVAKVSGG 10
    ||||| ||||
Db 47 WVAKVSSGG 56

RESULT 4
US-08-791-391A-6
; Sequence 6, Application US/08791391A
; Patent No. US20010016645A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791.391A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-391A-6

Query Match 90.9%; Score 50; DB 8; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.089;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791.391A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-391A-2

Query Match 90.9%; Score 50; DB 8; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.089;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WVAKVSGG 10
    ||||| ||||
Db 47 WVAKVSSGG 56

RESULT 4
US-08-791-391A-6
; Sequence 6, Application US/08791391A
; Patent No. US20010016645A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791.391A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-391A-6
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Query Match 90.9%; Score 50; DB 8; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.089;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WVAKVSGG 10
| | | | |
Db 47 WVAKVSGG 56

RESULT 5

US-09-840-459-44
; Sequence 44, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 44
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-840-459-44

Query Match 78.2%; Score 43; DB 10; Length 98;
Best Local Similarity 70.0%; Pred. No. 1;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WVAKVSGG 10
| | | | |
Db 47 WVAKVSGG 56

RESULT 6

US-09-286-240-4
; Sequence 4, Application US/09286240
; Patent No. US20020010320A1
; GENERAL INFORMATION:
; APPLICANT: Fett, James W
; TITLE OF INVENTION: Chimeric and Humanized Antibodies to Angiogenin
; FILE REFERENCE: 10498/74073
; CURRENT APPLICATION NUMBER: US/09/286,240
; CURRENT FILING DATE: 1999-04-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-286-240-4

Query Match 78.2%; Score 43; DB 10; Length 140;
Best Local Similarity 70.0%; Pred. No. 1.5;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WVAKVSGG 10
| | | | |
Db 66 WVAKVSGG 75

RESULT 7

US-09-840-459-53
; Sequence 53, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 53
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-840-459-53

Query Match 70.9%; Score 39; DB 10; Length 87;
Best Local Similarity 60.0%; Pred. No. 4.2;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WVAKVSGG 10
| | | | |
Db 36 WVAKVSGG 45

RESULT 8

US-09-840-459-41
; Sequence 41, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 41

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; LENGTH: 98
; TYPE: PRT
; ORGANISM: Mus musculus
us-09-840-459-41

Query Match      70.9%; Score 39; DB 10; Length 98;
Best Local Similarity 60.0%; Pred. No. 4.7;
Matches 6; Conservative 2; Mismatches 2; Indels 2; Gaps 0;

QY 1 WYAKVKSGG 10
   ||| : |||
Db 47 WYAVISGGG 56

RESULT 9
US-09-840-459-51
; Sequence 51, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 51
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-840-459-51

Query Match      69.1%; Score 38; DB 10; Length 88;
Best Local Similarity 60.7%; Pred. No. 6.2;
Matches 6; Conservative 1; Mismatches 2; Indels 2; Gaps 0;

QY 1 WYAKVKSGG 9
   ||| : |||
Db 38 WYAVISGGG 46

RESULT 10
US-10-006-773-9
; Sequence 9, Application US/10006773
; Patent No. US20020132983A1
; GENERAL INFORMATION:
; APPLICANT: Jungbans, Richard P.
; TITLE OF INVENTION: Antibodies as Chimeric Effector Cell Receptors Against Tumor Anti
; FILE REFERENCE: 003
; CURRENT APPLICATION NUMBER: US/10/006,773
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: 60/250,089
; PRIOR FILING DATE: 2000-11-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Mus sp.

US-10-006-773-9
Query Match      69.1%; Score 38; DB 12; Length 133;
Best Local Similarity 66.7%; Pred. No. 9;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WYAKVKSGG 9
   ||| : |||
Db 66 WYAVISGGG 74

RESULT 11
US-09-881-823-12
; Sequence 12, Application US/09881823
; Patent No. US2002006066A1
; GENERAL INFORMATION:
; APPLICANT: SHI, WENYUAN
; APPLICANT: ANDERSON, MAXWELL
; APPLICANT: MORRISON, SHERIE
; APPLICANT: TRINH, RYAN
; APPLICANT: WIMS, LETITIA
; APPLICANT: CHEN, LI
; TITLE OF INVENTION: Method for the Treatment and Prevention of Dental Caries
; FILE REFERENCE: 22851-032
; CURRENT APPLICATION NUMBER: US/09/881,823
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 07/378,577
; PRIOR FILING DATE: 1999-08-20
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Murine
US-09-881-823-12

Query Match      69.1%; Score 38; DB 10; Length 144;
Best Local Similarity 66.7%; Pred. No. 9.7;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WYAKVKSGG 9
   ||| : |||
Db 66 WYAVISGGG 74

RESULT 12
US-09-840-459-49
; Sequence 49, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 49
; LENGTH: 89
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; TYPE: PRT
; ORGANISM: Mus musculus
US-09-840-459-49

Query Match 67.3%; Score 37; DB 10; Length 89;
Best Local Similarity 66.7%; Pred. No. 9.1;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WVAKVSGG 9
||| : |||
Db 38 WVAATISSGG 46

RESULT 13

US-09-905-243-49
; Sequence 49, Application US/09905243
; Patent No. US20020062009A1
; GENERAL INFORMATION:
; APPLICANT: Taylor, Alexander H
; TITLE OF INVENTION: Monoclonal Antibodies with Reduced
; IMMUNOGENICITY
; FILE REFERENCE: P50770
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: US/09/905,243
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/300,970
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 49
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Macaca cynomolgus
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (31)...(35)
; OTHER INFORMATION: CDR1
; NAME/KEY: DOMAIN
; LOCATION: (50)...(66)
; OTHER INFORMATION: CDR2
US-09-905-243-49

Query Match 67.3%; Score 37; DB 10; Length 98;
Best Local Similarity 60.0%; Pred. No. 10;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 WVAKVSGG 10
| : |||||
Db 47 WIGHVSGG 56

RESULT 14

US-09-840-459-38
; Sequence 38, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781

; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 38
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-840-459-38

Query Match 67.3%; Score 37; DB 10; Length 98;
Best Local Similarity 66.7%; Pred. No. 10;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WVAKVSGG 9
||| : |||
Db 47 WVAATISSGG 55

RESULT 15

US-09-840-459-39
; Sequence 39, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 39
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-840-459-39

Query Match 67.3%; Score 37; DB 10; Length 98;
Best Local Similarity 66.7%; Pred. No. 10;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WVAKVSGG 9
||| : |||
Db 47 WVAATISSGG 55

Search completed: November 18, 2002, 18:45:13
Job time : 1.96078 secs

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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:01 ; Search time 4.2402 Seconds
(without alignments)
69.390 Million cell updates/sec

Title: US-09-016-061-54

Perfect score: 55

Sequence: 1 WVAKVSGGG 10

Scoring table: BLOSUM62

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43	78.2	119	2	US-08-475-000-16
2	43	78.2	119	2	US-08-483-199-16
3	43	78.2	119	2	US-08-484-508-16
4	42	76.4	119	5	PCT-US94-07659-6
5	42	76.4	247	5	PCT-US94-07659-2
6	39	70.9	119	1	US-08-053-171-12
7	39	70.9	119	1	US-08-053-171-13
8	39	70.9	119	1	US-08-053-171-14
9	39	70.9	119	1	US-08-053-171-17
10	39	70.9	119	3	US-08-815-190A-13
11	39	70.9	122	1	US-07-634-278-48
12	39	70.9	122	1	US-07-634-278-49
13	39	70.9	122	1	US-08-477-728-48
14	39	70.9	122	1	US-08-477-728-49
15	39	70.9	122	1	US-08-474-040-48
16	39	70.9	122	1	US-08-474-040-49
17	39	70.9	122	1	US-08-487-200-48
18	39	70.9	122	1	US-08-487-200-49
19	39	70.9	122	4	US-08-484-537-48
20	39	70.9	122	4	US-08-484-537-49
21	39	70.9	125	1	US-08-331-398A-65
22	39	70.9	125	2	US-08-331-397B-65
23	39	70.9	125	2	US-08-759-804A-64
24	39	70.9	138	1	US-08-053-171-7
25	39	70.9	138	1	US-08-053-171-11
26	39	70.9	139	1	US-08-129-930B-96
27	39	70.9	139	4	US-08-134-346A-51

28 39 70.9 139 4 US-08-976-288A-96 Sequence 96, Appl
29 39 70.9 623 1 US-08-332-838-2 Sequence 2, Appl
30 37 67.3 109 2 US-08-733-490-6 Sequence 6, Appl
31 37 67.3 116 2 US-08-888-366-10 Sequence 10, Appl
32 37 67.3 116 2 US-08-888-366-12 Sequence 12, Appl
33 37 67.3 116 3 US-09-184-658-48 Sequence 48, Appl
34 37 67.3 117 4 US-08-752-693A-3 Sequence 3, Appl
35 37 67.3 117 4 US-08-752-693A-4 Sequence 4, Appl
36 37 67.3 119 1 US-08-207-996-18 Sequence 18, Appl
37 37 67.3 119 1 US-08-207-996-19 Sequence 19, Appl
38 37 67.3 119 1 US-08-207-996-20 Sequence 20, Appl
39 37 67.3 119 1 US-08-207-996-21 Sequence 21, Appl
40 37 67.3 119 1 US-08-207-996-22 Sequence 22, Appl
41 37 67.3 119 1 US-08-207-996-27 Sequence 27, Appl
42 37 67.3 119 1 US-08-497-312-20 Sequence 20, Appl
43 37 67.3 119 2 US-08-760-840A-18 Sequence 18, Appl
44 37 67.3 119 2 US-08-760-840A-19 Sequence 19, Appl
45 37 67.3 119 2 US-08-760-840A-20 Sequence 20, Appl

ALIGNMENTS

RESULT 1
US-08-475-000-16
; Sequence 16, Application US/08475000
; Patent No. 5811267
; GENERAL INFORMATION:
; APPLICANT: RING, DAVID B.
; TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
; TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: INTELLECTUAL PROPERTY R440 - P.O. BOX 8097
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,000
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: SAVERIDE, PAUL
; REGISTRATION NUMBER: 36,914
; REFERENCE/DOCKET NUMBER: 0850.007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2585
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-475-000-16

Query Match: 78.2%; Score 43; DB 2; Length 119;
Best Local Similarity 70.0%; Pred. No. 1.8;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WVAKVSGGG 10

||| : ||||

Db 47 WVAATISSGGG 56

RESULT 2

US-08-483-199-16
; Sequence 16, Application US/08483199
; Patent No. 5849877
; GENERAL INFORMATION:
; APPLICANT: RING, DAVID B.
; TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
; TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: INTELLECTUAL PROPERTY - R440, P.O. BOX 8097
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,199
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: SAVEREIDE, PAUL
; REGISTRATION NUMBER: 36,914
; REFERENCE/DOCKET NUMBER: 0850.009
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2585
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-483-199-16

Query Match 78.2%; Score 43; DB 2; Length 119;
Best Local Similarity 70.0%; Pred. No. 1.8;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WVAKVSGGG 10
||| : ||||
Db 47 WVATISSGGG 56

RESULT 3
US-08-484-508-16
; Sequence 16, Application US/08484508
; Patent No. 5948647
; GENERAL INFORMATION:
; APPLICANT: RING, DAVID B.
; TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
; TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: INTELLECTUAL PROPERTY - R440, P.O. BOX 8097
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,508
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:
; NAME: SAVEREIDE, PAUL
; REGISTRATION NUMBER: 36,914
; REFERENCE/DOCKET NUMBER: 0850.008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-585
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-484-508-16

Query Match 78.2%; Score 43; DB 2; Length 119;
Best Local Similarity 70.0%; Pred. No. 1.8;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WVAKVSGGG 10
||| : ||||
Db 47 WVATISSGGG 56

RESULT 4
PCT-US94-07659-6
; Sequence 6, Application PC/TUS9407659
; GENERAL INFORMATION:
; APPLICANT: Young, Peter
; APPLICANT: Gross, Mitchell
; APPLICANT: Jonak, Zdenka L.
; APPLICANT: Theisen, Timothy
; APPLICANT: Hurler, Mark
; APPLICANT: Jackson, Jeffrey R.
; TITLE OF INVENTION: Recombinant and Humanized Il-1 beta
; TITLE OF INVENTION: Antibodies for Treatment of Il-1 Mediated Inflammatory
; TITLE OF INVENTION: Disorders in Man
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation - Corp.
; ADDRESSEE: Intellectual Property
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07659
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER: US 08/090,534
; FILING DATE: 09-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50171-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 270-5024
; TELEFAX: (610) 270-5090
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-07659-6

Query Match 76.4%; Score 42; DB 5; Length 119;
Best Local Similarity 70.0%; Pred. No. 2.6;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WVAKVSGG 10
||| : ||||
Db 47 WWAYISGG 56

RESULT 5
PCT-US94-07659-2
; Sequence 2, Application PC/TUS9407659
; GENERAL INFORMATION:
; APPLICANT: Young, Peter
; APPLICANT: Gross, Mitchell
; APPLICANT: Jonak, Zdenka L.
; APPLICANT: Thelsen, Timochy
; APPLICANT: Hurtle, Mark
; APPLICANT: Jackson, Jeffrey R.
; TITLE OF INVENTION: Recombinant and Humanized IL-1 beta
; TITLE OF INVENTION: Antibodies for Treatment of IL-1 Mediated Inflammatory
; TITLE OF INVENTION: Disorders in Man
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation - Corp.
; ADDRESSEE: Intellectual Property
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07659
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/090,534
; FILING DATE: 09-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50171-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 270-5024
; TELEFAX: (610) 270-5090
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 247 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US94-07659-2

Query Match 76.4%; Score 42; DB 5; Length 247;
Best Local Similarity 70.0%; Pred. No. 5.4;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WVAKVSGG 10
||| : ||||
Db 66 WWAYISGG 75

RESULT 6
US-08-053-171-12
; Sequence 12, Application US/08053171
; Patent No. 5562903
; GENERAL INFORMATION:
; APPLICANT: Co, Loibner

; TITLE OF INVENTION: Antibody Derivatives
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/053,171
; FILING DATE: 22-APR-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-54-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..119
; OTHER INFORMATION: /note= "Sequence of Humanized
; Patent No. 5562903
; OTHER INFORMATION: BR55-2 Antibody, Heavy Chain Variant
; OTHER INFORMATION: H-hu-BR55-2/1"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 31..35
; OTHER INFORMATION: /note= "Complementarity-determining
; OTHER INFORMATION: region"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 50..66
; OTHER INFORMATION: /note= "Complementarity-determining
; OTHER INFORMATION: region"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 99..108
; OTHER INFORMATION: /note= "Complementarity-determining
; OTHER INFORMATION: region"
; US-08-053-171-12

Query Match 70.9%; Score 39; DB 1; Length 119;
Best Local Similarity 60.0%; Pred. No. 8.5;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WVAKVSGG 10
||| : ||||
Db 47 WWAYISGG 56

RESULT 7
US-08-053-171-13
; Sequence 13, Application US/08053171
; Patent No. 5562903
; GENERAL INFORMATION:
; APPLICANT: Co, Loibner
; TITLE OF INVENTION: Antibody Derivatives
; NUMBER OF SEQUENCES: 32

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/053,171
; FILING DATE: 22-APR-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-54-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..119
; OTHER INFORMATION: /note= "Sequence of Humanized
; Patent No. 5562903
; OTHER INFORMATION: BR55-2 Antibody, Heavy Chain Variant H-hu-BR5-2/2"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 31..35
; OTHER INFORMATION: /note= "Complementarity-determining
; OTHER INFORMATION: region"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 50..66
; OTHER INFORMATION: /note= "Complementarity-determining
; OTHER INFORMATION: region"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 99..108
; OTHER INFORMATION: /note= "Complementarity-determining
; OTHER INFORMATION: region"
; US-08-053-171-13
; Query Match 70.9%; Score 39; DB 1; Length 119;
; Best Local Similarity 60.0%; Pred. No. 8.5;
; Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
; QY 1 WVAKVSGGG 10
; ||| : |||
; DB 47 WWAYISNGGG 56
; RESULT 8
; US-08-053-171-14
; Sequence 14, Application US/08053171
; Patent No. 5562903
; GENERAL INFORMATION:
; APPLICANT: Co, Loibner
; TITLE OF INVENTION: Antibody Derivatives
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California

; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/053,171
; FILING DATE: 22-APR-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-54-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..119
; OTHER INFORMATION: /note= "Sequence of Humanized
; Patent No. 5562903
; OTHER INFORMATION: BR55-2 Antibody, Heavy Chain Variant
; FEATURE:
; NAME/KEY: Region
; LOCATION: 31..35
; OTHER INFORMATION: /note= "Complementarity-determining
; OTHER INFORMATION: region"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 50..66
; OTHER INFORMATION: /note= "Complementarity-determining
; OTHER INFORMATION: region"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 99..108
; OTHER INFORMATION: /note= "Complementarity-determining
; OTHER INFORMATION: region"
; US-08-053-171-14
; Query Match 70.9%; Score 39; DB 1; Length 119;
; Best Local Similarity 60.0%; Pred. No. 8.5;
; Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
; QY 1 WVAKVSGGG 10
; ||| : |||
; DB 47 WWAYISNGGG 56
; RESULT 9
; US-08-053-171-17
; Sequence 17, Application US/08053171
; Patent No. 5562903
; GENERAL INFORMATION:
; APPLICANT: Co, Loibner
; TITLE OF INVENTION: Antibody Derivatives
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California

; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/053.171
; FILING DATE: 22-APR-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-54-1
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..119
; OTHER INFORMATION: /note= "Sequence of the heavy chain
; Patent No. 5562903
; OTHER INFORMATION: of humanized BR55-2/3 antibody."
; FEATURE:
; NAME/KEY: Region
; LOCATION: 31..35
; OTHER INFORMATION: /note= "Complementarity-determining
; OTHER INFORMATION: region"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 50..66
; OTHER INFORMATION: /note= "Complementarity-determining
; OTHER INFORMATION: region"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 99..108
; OTHER INFORMATION: /note= "Complementarity-determining
; OTHER INFORMATION: region"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 42
; OTHER INFORMATION: /note= "Residue in the framework
; OTHER INFORMATION: replaced with mouse amino acid in the humanized
; OTHER INFORMATION: antibody."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 44
; OTHER INFORMATION: /note= "Residue replaced with mouse
; OTHER INFORMATION: amino acid in humanized antibody."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 73..75
; OTHER INFORMATION: /note= "Residues replaced with
; OTHER INFORMATION: mouse amino acids in humanized antibody."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 82
; OTHER INFORMATION: /note= "Residue replaced with mouse
; OTHER INFORMATION: amino acids in humanized antibody."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 87
; OTHER INFORMATION: /note= "Residue replaced with mouse
; OTHER INFORMATION: amino acid in humanized antibody."
; FEATURE:

; NAME/KEY: Modified-site
; LOCATION: 109
; OTHER INFORMATION: /note= "Residue replaced with mouse
; OTHER INFORMATION: amino acid in humanized antibody."
; US-08-053-171-17
Query Match 70.9%; Score 39; DB 1; Length 119;
Best Local Similarity 60.0%; Pred. No. 8.5;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 WVAKVSGGG 10
||| : |||
Db 47 WVAYSNGGG 56
RESULT 10
US-08-815-190A-13
; Sequence 13, Application US/08815190A
; Patent No. 6046310
; GENERAL INFORMATION:
; APPLICANT: Queen, Cary L.
; APPLICANT: Schneider, William P.
; APPLICANT: Vasquez, Maximiliano
; TITLE OF INVENTION: Fas Ligand Fusion Proteins and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/815,190A
; FILING DATE: 11-MAR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/614,584
; FILING DATE: 13-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 011823-006710US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..119
; OTHER INFORMATION: /note= "mature heavy chain variable
; OTHER INFORMATION: region of humanized ABL 364 antibody"
; US-08-815-190A-13
Query Match 70.9%; Score 39; DB 3; Length 119;
Best Local Similarity 60.0%; Pred. No. 8.5;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 WVAKVSGGG 10
||| : |||
Db 47 WVAYSNGGG 56

RESULT 11
US-07-634-278-48
; Sequence 48, Application US/07634278
; Patent No. 5530101
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07634,278
; FILING DATE: 19-DEC-1990
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-634-278-48

Query Match 70.9%; Score 39; DB 1; Length 122;
Best Local Similarity 60.0%; Pred. No. 8.7;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WYAKVKGSGG 10
Db 47 WVASIRGGG 56

RESULT 12
US-07-634-278-49
; Sequence 49, Application US/07634278
; Patent No. 5530101
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.

; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/634,278
; FILING DATE: 19-DEC-1990
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-634-278-49

Query Match 70.9%; Score 39; DB 1; Length 122;
Best Local Similarity 60.0%; Pred. No. 8.7;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WYAKVKGSGG 10
Db 47 WVASIRGGG 56

RESULT 13
US-08-477-728-48
; Sequence 48, Application US/08477728
; Patent No. 5585089
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/477,728
;; FILING DATE: 07-JUN-1995
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/634,278
;; FILING DATE: 19-DEC-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/590,274
;; FILING DATE: 28-SEP-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/310,252
;; FILING DATE: 13-FEB-1989
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/290,975
;; FILING DATE: 28-DEC-1988
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Smith, William M
;; REGISTRATION NUMBER: 30,223
;; REFERENCE/DOCKET NUMBER: 11823-002600
;; TELEPHONE: (415) 326-2400
;; TELEFAX: (415) 326-2422
;; INFORMATION FOR SEQ ID NO: 48:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 122 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-08-477-728-48

Query Match 70.9%; Score 39; DB 1; Length 122;
Best Local Similarity 60.0%; Pred. No. 8.7;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 WVAKVSGGG 10
||| : |||
Db 47 WVASIRGGG 56

RESULT 14
US-08-477-728-49
; Sequence 49, Application US/08477728
; Patent No. 5585089
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,728
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278

;; FILING DATE: 19-DEC-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/590,274
;; FILING DATE: 28-SEP-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/310,252
;; FILING DATE: 13-FEB-1989
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/290,975
;; FILING DATE: 28-DEC-1988
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Smith, William M
;; REGISTRATION NUMBER: 30,223
;; REFERENCE/DOCKET NUMBER: 11823-002600
;; TELEPHONE: (415) 326-2400
;; TELEFAX: (415) 326-2422
;; INFORMATION FOR SEQ ID NO: 49:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 122 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-08-477-728-49

Query Match 70.9%; Score 39; DB 1; Length 122;
Best Local Similarity 60.0%; Pred. No. 8.7;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 WVAKVSGGG 10
||| : |||
Db 47 WVASIRGGG 56

RESULT 15
US-08-474-040-48
; Sequence 48, Application US/08474040
; Patent No. 5693761
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourle and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,040
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-474-040-48

Query Match 70.9%; Score 39; DB 1; Length 122;
Best Local Similarity 60.0%; Pred. NO. 8.7;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WVAKVKGSGG 10
||| : |||
Db 47 WVASISRGSGG 56

Search completed: November 18, 2002, 17:43:34
Job time : 5.2402 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:01 ; Search time 4.90196 Seconds
(without alignments)
196.114 Million cell updates/sec

Title: US-09-016-061-56
Perfect score: 56
Sequence: 1 STYYPDTVQG 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	52	92.9	111	2 S51211	Ig heavy chain V r
2	52	92.9	113	2 S02717	Ig heavy chain V r
3	52	92.9	113	2 S26468	Ig heavy chain V r
4	52	92.9	115	2 PH1538	Ig H chain V regio
5	52	92.9	117	1 HVMSRF	Ig heavy chain pre
6	52	92.9	117	1 HVMS84	Ig heavy chain pre
7	52	92.9	117	1 HVMS34	Ig heavy chain pre
8	52	92.9	117	2 PH1552	Ig H chain V regio
9	52	92.9	119	2 PH1548	Ig H chain V regio
10	52	92.9	119	2 PH1549	Ig H chain V regio
11	49	87.5	108	2 PH1006	Ig heavy chain V r
12	49	87.5	118	2 PH1532	Ig H chain V regio
13	49	87.5	118	2 PH1550	Ig H chain V regio
14	49	87.5	119	2 PH1544	Ig H chain V regio
15	49	87.5	119	2 PH1551	Ig H chain V regio
16	49	87.5	119	2 PH1547	Ig H chain V regio
17	49	87.5	119	2 PH1555	Ig H chain V regio
18	49	87.5	119	2 PH1531	Ig H chain V regio
19	49	87.5	119	2 PH1533	Ig H chain V regio
20	49	87.5	120	2 PH1534	Ig H chain V regio
21	49	87.5	122	2 PH1537	Ig H chain V regio
22	48	85.7	70	2 PL0250	Ig heavy chain V r
23	48	85.7	97	1 HVMS91	Ig heavy chain V r
24	48	85.7	108	2 PL0248	Ig heavy chain V r
25	48	85.7	111	2 PH1007	Ig heavy chain V r
26	48	85.7	112	2 S26327	Ig heavy chain V r
27	48	85.7	117	2 PH1535	Ig H chain V regio
28	48	85.7	117	2 PH1553	Ig H chain V regio
29	48	85.7	117	2 PH1542	Ig H chain V regio

RESULT 1
S51211
Ig heavy chain V region (AC7) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 01-Aug-1995 #sequence_revision 01-Dec-1995 #text_change 30-May-1997
C:Accession: S51211; S58929
R:Jarrin, A.; Andrieux, A.; Chapel, A.; Buchou, T.; Marguerie, G.
FEBS Lett. 354, 169-172, 1994
A:Title: A synthetic peptide with anti-platelet activity derived from a CDR of an ant
A:Reference number: S51210; MUID:95046326; PMID:7957919
A:Accession: S51211
A:Molecule type: mRNA
A:Residues: 9-111 <JAR>
A:Accession: S58929
A:Molecule type: protein
A:Residues: 1-20 <JAR>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 92.9%; Score 52; DB 2; Length 111;
Best Local Similarity 90.0%; Pred. No. 0.024;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 STYYPDTVQG 10
Db 57 STYYPDTVKG 66

RESULT 2
S02717
Ig heavy chain V region (clone PH62) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000
C:Accession: S02717
R:Sollazzo, M.; Hasemann, C.A.; Meek, K.D.; Glotz, D.; Capra, J.D.; Zanetti, M.
submitted to the EMBL Data Library, February 1989
A:Reference number: S02717
A:Accession: S02717
A:Molecule type: DNA
A:Residues: 1-113 <SOL>
A:Cross-references: EMBL:Y00744; NID:G52472; PIDN:CAA68713.1; PID:gl334095
A:Note: this sequence was determined from the differentiated gene
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 92.9%; Score 52; DB 2; Length 113;
Best Local Similarity 90.0%; Pred. No. 0.024;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 STYYPDTVQG 10

Db 57 STYYPDTVKG 66
|||||||:|

RESULT 3

S26468

Ig heavy chain V region - mouse

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C:Accession: S26468

R:Kavaler, J.

submitted to the EMBL Data Library, April 1991

A:Reference number: S26459

A:Accession: S26468

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-113 <KAV>

A:Cross-references: EMBL:X59107; NID:g51944; PIDN:CAA41833.1; PID:g51945

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:11-94/Domain: immunoglobulin homology <IMM>

Query Match 92.9%; Score 52; DB 2; Length 113;

Best Local Similarity 90.0%; Pred. No. 0.024;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDTVQG 10

|||||||:|

Db 53 STYYPDTVKG 62

RESULT 4

PH1538

Ig H chain V region (clone 13G12) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 21-Jan-2000

C:Accession: PH1538

R:Mukherjee, J.; Casadevall, A.; Scharff, M.D.

J. Exp. Med. 177, 1105-1116, 1993

A:Title: Molecular characterization of the humoral responses to *Cryptococcus neoformans*

A:Reference number: PH1528; MUID:93210465; PMID:8459205

A:Accession: PH1538

A:Molecule type: mRNA

A:Residues: 1-115 <MUK>

A:Note: the stop codons X appear in residues 82, 85 and 106

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

F:14-99/Domain: immunoglobulin homology <IMM>

Query Match 92.9%; Score 52; DB 2; Length 115;

Best Local Similarity 90.0%; Pred. No. 0.025;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDTVQG 10

|||||||:|

Db 56 STYYPDTVKG 65

RESULT 5

HVM58F

Ig heavy chain precursor V region (RF) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 31-Mar-1997

C:Accession: JT0503

R:Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.

J. Exp. Med. 169, 2007-2019, 1989

A:Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary

A:Reference number: JT0501; MUID:89279149; PMID:2499654

A:Accession: JT0503

A>Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-117 <LEV>

A:Experimental source: strain BALB/cJ

A:Note: this sequence belongs to the VH7183 subfamily
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; hybridoma; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-117/Product: Ig heavy chain V region (RF) #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>
F:41-115/Disulfide bonds: #status predicted

Query Match 92.9%; Score 52; DB 1; Length 117;

Best Local Similarity 90.0%; Pred. No. 0.025;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDTVQG 10

|||||||:|

Db 76 STYYPDTVKG 85

RESULT 6

HVM584

Ig heavy chain precursor V region (5-84) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 31-Mar-1997

C:Accession: JT0505

R:Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.

J. Exp. Med. 169, 2007-2019, 1989

A:Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary

A:Reference number: JT0501; MUID:89279149; PMID:2499654

A:Accession: JT0505

A>Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-117 <LEV>

A:Experimental source: strain BALB/cJ

A:Note: this sequence belongs to the VH7183 subfamily

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-117/Product: Ig heavy chain V region (5-84) #status predicted <MAT>

F:34-117/Domain: immunoglobulin homology <IMM>

F:41-115/Disulfide bonds: #status predicted

Query Match 92.9%; Score 52; DB 1; Length 117;

Best Local Similarity 90.0%; Pred. No. 0.025;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDTVQG 10

|||||||:|

Db 76 STYYPDTVKG 85

RESULT 7

HVM534

Ig heavy chain precursor V region (345) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 31-Mar-1997

C:Accession: JT0502

R:Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.

J. Exp. Med. 169, 2007-2019, 1989

A:Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary

A:Reference number: JT0501; MUID:89279149; PMID:2499654

A:Accession: JT0502

A>Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-117 <LEV>

A:Experimental source: strain BALB/cJ

A:Note: this sequence belongs to the VH7183 subfamily

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-117/Product: Ig heavy chain V region (345) #status predicted <MAT>

F:34-117/Domain: immunoglobulin homology <IMM>

F:41-115/Disulfide bonds: #status predicted

Query Match 92.9%; Score 52; DB 1; Length 117;

Best Local Similarity 90.0%; Pred. No. 0.025; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 1;

QY 1 STYYPDTVQG 10

|||||||:|

Db 76 STYYPDTVKG 85

RESULT 8

PHI552

Ig H chain V region (clone 16E4) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 21-Jan-2000

C:Accession: PH1552

R:Mukherjee, J.; Casadevall, A.; Scharff, M.D.

J. Exp. Med. 177, 1105-1116, 1993

A:Title: Molecular characterization of the humoral responses to Cryptococcus neoformans

A:Reference number: PH1528; MUID:93210465; PMID:8459205

A:Accession: PH1552

A:Molecule type: mRNA

A:Residues: 1-117 <MUK>

A:Note: the stop codon X appears in residue 87

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

F:15-97/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 92.9%; Score 52; DB 2; Length 117;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDTVQG 10

|||||||:|

Db 57 STYYPDTVKG 66

RESULT 9

PHI548

Ig H chain V region (clone 12F4) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 17-Mar-1999

C:Accession: PH1548

R:Mukherjee, J.; Casadevall, A.; Scharff, M.D.

J. Exp. Med. 177, 1105-1116, 1993

A:Title: Molecular characterization of the humoral responses to Cryptococcus neoformans

A:Reference number: PH1528; MUID:93210465; PMID:8459205

A:Accession: PH1548

A:Molecule type: mRNA

A:Residues: 1-119 <MUK>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 92.9%; Score 52; DB 2; Length 119;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDTVQG 10

|||||||:|

Db 57 STYYPDTVKG 66

RESULT 10

PHI549

Ig H chain V region (clone 13F1) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 17-Mar-1999

C:Accession: PH1549

R:Mukherjee, J.; Casadevall, A.; Scharff, M.D.

J. Exp. Med. 177, 1105-1116, 1993

A:Title: Molecular characterization of the humoral responses to Cryptococcus neoformans

A:Reference number: PH1528; MUID:93210465; PMID:8459205

A:Accession: PH1549

A:Molecule type: mRNA

A:Residues: 1-119 <MUK>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

A:Residues: 1-119 <MUK>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 92.9%; Score 52; DB 2; Length 119;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDTVQG 10

|||||||:|

Db 57 STYYPDTVKG 66

RESULT 11

PHI006

Ig heavy chain V region (clone 202.33) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C:Accession: PH1006

R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective

A:Reference number: PH0971; MUID:92381444; PMID:1512540

A:Accession: PH1006

A>Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-108 <TIG>

A:Experimental source: B cell, strain [N2B x NZW]F1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:10-93/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 87.5%; Score 49; DB 2; Length 108;

Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDTVQG 10

|||||||:|

Db 52 NTYYPDTVKG 61

RESULT 12

PHI532

Ig H chain V region (clone 4D4) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 17-Mar-1999

C:Accession: PH1532

R:Mukherjee, J.; Casadevall, A.; Scharff, M.D.

J. Exp. Med. 177, 1105-1116, 1993

A:Title: Molecular characterization of the humoral responses to Cryptococcus neoforma

A:Reference number: PH1528; MUID:93210465; PMID:8459205

A:Accession: PH1532

A:Molecule type: mRNA

A:Residues: 1-118 <MUK>

A:Note: the stop codons X appear in residues 82 and 85

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

Query Match

Best Local Similarity 87.5%; Score 49; DB 2; Length 118;

Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDTVQG 10

|||||||:|

Db 56 NTYYPDTVKG 65

RESULT 13

PHI550

Ig H chain V region (clone 14E1) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 17-Mar-1999

Search completed: November 18, 2002, 17:47:01
Job time : 5.90196 secs

C:Accession: PH1550
R:Mukherjee, J.; Casadevall, A.; Scharff, M.D.
J. Exp. Med. 177, 1105-1116, 1993
A:Title: Molecular characterization of the humoral responses to Cryptococcus neoformans
A:Reference number: PH1528; MUID:93210465; PMID:8459205
A:Accession: PH1550
A:Molecule type: mRNA
A:Residues: 1-118 <MUK>
A:Note: the stop codon X appears in residue 30
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin

Query Match 87.5%; Score 49; DB 2; Length 118;
Best Local Similarity 80.0%; Pred. No. 0.09;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDTVQG 10
:|||||:
DB 56 NTYYPDTVKG 65

RESULT 14
PH1544
Ig H chain V region (clone 9E11) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 17-Mar-1999
C:Accession: PH1544
R:Mukherjee, J.; Casadevall, A.; Scharff, M.D.
J. Exp. Med. 177, 1105-1116, 1993
A:Title: Molecular characterization of the humoral responses to Cryptococcus neoformans
A:Reference number: PH1528; MUID:93210465; PMID:8459205
A:Accession: PH1544
A:Molecule type: mRNA
A:Residues: 1-119 <MUK>
A:Note: the stop codons X appear in residues 83, 86 and 107
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin

Query Match 87.5%; Score 49; DB 2; Length 119;
Best Local Similarity 80.0%; Pred. No. 0.09;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDTVQG 10
:|||||:
DB 57 NTYYPDTVKG 66

RESULT 15
PH1551
Ig H chain V region (clone 15E8) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 21-Jan-2000
C:Accession: PH1551
R:Mukherjee, J.; Casadevall, A.; Scharff, M.D.
J. Exp. Med. 177, 1105-1116, 1993
A:Title: Molecular characterization of the humoral responses to Cryptococcus neoformans
A:Reference number: PH1528; MUID:93210465; PMID:8459205
A:Accession: PH1551
A:Molecule type: mRNA
A:Residues: 1-119 <MUK>
A:Note: the stop codons X appear in residues 88, 100 and 107
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 87.5%; Score 49; DB 2; Length 119;
Best Local Similarity 80.0%; Pred. No. 0.09;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDTVQG 10
:|||||:
DB 57 NTYYPDTVKG 66

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:00 ; Search time 2.45098 Seconds
(without alignments)
169.223 Million cell updates/sec

Title: US-09-016-061-56
Perfect score: 56
Sequence: 1 STYYPDTVQC 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	92.9	117	1 HV53_MOUSE	P18524 mus musculus
2	52	92.9	117	1 HV54_MOUSE	P18525 mus musculus
3	52	92.9	117	1 HV55_MOUSE	P18526 mus musculus
4	48	85.7	97	1 HV56_MOUSE	P18527 mus musculus
5	44	78.6	98	1 HV57_MOUSE	P18528 mus musculus
6	44	78.6	117	1 HV58_MOUSE	P18529 mus musculus
7	44	78.6	117	1 HV59_MOUSE	P18530 mus musculus
8	40	71.4	116	1 HV05_CARAU	P19181 carassius a
9	39	69.6	117	1 HV3C_HUMAN	P01764 homo sapien
10	39	69.6	501	1 ADCA_STRPN	O05703 streptococc
11	39	69.6	706	1 HDAL_YEAST	P53973 saccharomyc
12	38	67.9	3460	1 RELN_HUMAN	P78509 homo sapien
13	37	66.1	115	1 HV3F_HUMAN	P01767 homo sapien
14	37	66.1	426	1 GUNZ_ERWCH	P07103 erwinia chr
15	37	66.1	517	1 FGR_MOUSE	P14234 mus musculus
16	37	66.1	3209	1 RELN_CHICK	O93574 gallus gall
17	37	66.1	3433	1 POLG_KUNJM	P14335 k genome po
18	37	66.1	3461	1 RELN_MOUSE	O60841 mus musculus
19	37	66.1	3462	1 RELN_RAT	P38751 rattus norv
20	36	64.3	119	1 HV3L_HUMAN	P01773 homo sapien
21	36	64.3	329	1 YP22_CAEEL	O09201 caenorhabdi
22	36	64.3	352	1 LICH_PSEWI	O05938 pseudomonas
23	36	64.3	624	1 YE70_METJA	O58865 methanococc
24	36	64.3	889	1 IREB_CHICK	O30875 gallus gall
25	35	62.5	117	1 HV02_CANFA	P01785 canis fami
26	35	62.5	121	1 HV3J_HUMAN	P01771 homo sapien
27	35	62.5	519	1 ACH4_DROME	P25162 drosophila
28	35	62.5	807	1 PTNM_HUMAN	O9y2r2 homo sapien
29	35	62.5	3097	1 CADN_DROME	O15943 drosophila
30	34.5	61.6	507	1 VLL_HPV09	Q02480 human papil
31	34	60.7	352	1 GBAI_COPCO	P30675 coprinus co
32	34	60.7	358	1 COQ2_SCHPO	Q10252 schizosacch
33	34	60.7	566	1 Y397_MYCCE	P47637 mycoplasma

ALIGNMENTS

RESULT 1

HV53_MOUSE

ID HV53_MOUSE

AC P18524;

DT 01-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig heavy chain V region RF precursor.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BA1B/CJ;

RX MEDLINE=89279149; PubMed=2499654;

RA Levy N.S., Malipiero U.V., Lebecqec S.G., Gearhart P.J.;

RT "Early onset of somatic mutation in immunoglobulin VH genes during

RT the primary immune response.";

RL J. Exp. Med. 169:2007-2019(1989).

CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.

DR PIR: J70503; HVMSRF.

DR HSSP: P01810; 2FBJ.

DR InterPro: IPR003006; Ig_MHC.

DR InterPro: IPR003596; Ig_V.

DR Pfam: PF00047; Ig: 1.

DR SMART: SM00406; IGV: 1.

KW Immunoglobulin V region; Hybridoma; Signal.

FT SIGNAL 1 19.

FT CHAIN 20 117

FT DOMAIN 20 49

FT DOMAIN 50 54

FT DOMAIN 55 68

FT DOMAIN 69 85

FT DOMAIN 86 117

FT DISULFID 41 115

FT NON_TER 117 117

SQ SEQUENCE 117 AA; 12866 MW; 2CE3295F390F725B CRC64;

Query Match 92.9%; Score 52; DB 1; Length 117;

Best Local Similarity 90.0%; Pred. NO. 0.0038; 0; Indels 0; Gaps 0;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDTVQC 10

Db 76 STYYPDTVKG 85

|||||||:|

RESULT 2

HV54_MOUSE

ID HV54_MOUSE

AC P18525;

DT 01-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig heavy chain V region 5-84 precursor.

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OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; JT0505; HVMS84.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 5-84.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12872 MW; 234055CB6A469861 CRC64;

Query Match 92.9%; Score 52; DB 1; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.0038;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDPTVQV 10
DB 76 STYYPDPTVKG 85

RESULT 3
HV55_MOUSE STANDARD; PRT; 117 AA.
AC P18526;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 345 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; JT0502; HVMS34.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 345.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.

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FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 49380E4627ACA99A CRC64;

Query Match 92.9%; Score 52; DB 1; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.0038;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDPTVQV 10
DB 76 STYYPDPTVKG 85

RESULT 4
HV56_MOUSE STANDARD; PRT; 97 AA.
AC P18527;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 914.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; JT0504; HVMS91.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
KW Immunoglobulin V region.
FT NON_TER 97 97
SQ SEQUENCE 97 AA; 10661 MW; C23CB33FF55DA893 CRC64;

Query Match 85.7%; Score 48; DB 1; Length 97;
Best Local Similarity 80.0%; Pred. No. 0.018;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDPTVQV 10
DB 56 STYYPDSVKG 65

RESULT 5
HV57_MOUSE STANDARD; PRT; 98 AA.
AC P18528;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 6.96.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during

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RT the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR: JT0501; HVMS96.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT NON_TER 98
SQ SEQUENCE 98 AA; 11007 MW; B8644F7F92FBF95B CRC64;

Query Match 78.6%; Score 44; DB 1; Length 98;
Best Local Similarity 77.8%; Pred. No. 0.13;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 TYTPDVTQVG 10
   |||||:|:|
Db 58 TYYPDSVKG 66

RESULT 6
HV58_MOUSE
ID HV58_MOUSE STANDARD; PRT; 117 AA.
AC P18529;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 5-76 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SQ SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR: JT0507; HVMS39.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 5-76.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117
SQ SEQUENCE 117 AA; 12991 MW; 93A04782B78B8FA0 CRC64;

Query Match 78.6%; Score 44; DB 1; Length 117;
Best Local Similarity 77.8%; Pred. No. 0.13;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 TYTPDVTQVG 10
   |||||:|:|
Db 77 TYYPDSVKG 85

RESULT 7
HV59_MOUSE
ID HV59_MOUSE STANDARD; PRT; 117 AA.

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AC P18530;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 7-39 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SQ SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR: JT0507; HVMS39.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 7-39.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117
SQ SEQUENCE 117 AA; 12972 MW; D5CA4167D0F1774F CRC64;

Query Match 78.6%; Score 44; DB 1; Length 117;
Best Local Similarity 77.8%; Pred. No. 0.13;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 TYTPDVTQVG 10
   |||||:|:|
Db 77 TYYPDSVKG 85

RESULT 8
HV05_CARAU
ID HV05_CARAU STANDARD; PRT; 116 AA.
AC P19181;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 5A precursor.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
SQ SEQUENCE FROM N.A.
RC MEDLINE=88144476; PubMed=3125551;
RA Wilson M.R., Middleton D., Warr G.W.;
RT "Immunoglobulin heavy chain variable region gene evolution: structure
and family relationships of two genes and a pseudogene in a teleost
fish.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:1566-1570(1988).
DR PIR; B28966; B28966.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.

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FT SIGNAL          1 19
FT CHAIN           20 116 IG HEAVY CHAIN V REGION 5A.
FT DOMAIN          20 49 FRAMEWORK-1.
FT DOMAIN          50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN          55 68 FRAMEWORK-2.
FT DOMAIN          69 84 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN          85 116 FRAMEWORK-3.
FT DISULFID        41 114 BY SIMILARITY.
FT NON_TER         116 116
SQ SEQUENCE        116 AA; 12808 MW; 9C2279E2DF199B12 CRC64;

Query Match          71.4%; Score 40; DB 1; Length 116;
Best Local Similarity 70.0%; Pred. No. 0.76;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 STYYPDVTQVG 10
    ||||| I:I:I
Db 75 STYYADSVKG 84

RESULT 9
HV3C_HUMAN STANDARD; PRT; 117 AA.
AC P01764;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-III region VH26 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81101090; PubMed=6450418;
RA Mathysens G., Rabbitts T.H.;
RT "Structure and multiplicity of genes for the human immunoglobulin
RL heavy chain variable region.";
RC Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).
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DR EMBL; J00236; AAA53516.1; -
DR EMBL; M35415; AAA58735.1; -
DR PIR; A02047; H3HU26.
DR HSP; P01772; 2FB4.
DR Genew; HGNC:5545; IGHV6.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin V region; Signal.
FT SIGNAL          1 19
FT CHAIN           20 117 IG HEAVY CHAIN V-III REGION VH26.
FT NON_TER         117 117
SQ SEQUENCE        117 AA; 12582 MW; E826733F1A3CB0F1 CRC64;

Query Match          69.68%; Score 39; DB 1; Length 117;
Best Local Similarity 70.0%; Pred. No. 1.2;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 STYYPDVTQVG 10
    ||||| I:I:I
Db 76 STYYGDSVKG 85

RESULT 10

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ADCA_STRPN
ID ADCA_STRPN STANDARD; PRT; 501 AA.
AC 005703; Q97N86;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Zinc-binding lipoprotein adca precursor.
GN ADCA OR SP2169.
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TIGR4;
RX MEDLINE=21357209; PubMed=11463916;
RA Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
RA Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,
RA Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
RA Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,
RA McDonald L.A., Feldblyum T.V., Angluoli S., Dickinson T., Hickey E.K.,
RA Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
RT "Complete genome sequence of a virulent isolate of Streptococcus
RL pneumoniae.";
RL Science 293:498-506(2001).
RN [2]
RP SEQUENCE OF 1-423 FROM N.A.
RC STRAIN=R6;
RX MEDLINE=98438930; PubMed=9765793;
RA Dintilhac A., Claverys J.-P.;
RT "The adc locus, which affects competence for genetic transformation in
RT Streptococcus pneumoniae, encodes an ABC transporter with a putative
RL lipoprotein homologous to a family of streptococcal adhesins.";
RL Res. Microbiol. 148:119-131(1997).
RN [3]
RP REVISIONS.
RA Claverys J.-P.;
RT "Reevaluation of the size of the Zn-binding lipoprotein Adca and
RL evidence for two domains.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP FUNCTION.
RX MEDLINE=98025470; PubMed=9379902;
RA Dintilhac A., Allioing G., Granadel C., Claverys J.-P.;
RT "Competence and virulence of Streptococcus pneumoniae: Adc and Psaa
RT mutants exhibit a requirement for Zn and Mn resulting from
RT inactivation of putative ABC metal permeases.";
RL Mol. Microbiol. 25:727-739(1997).
CC -!- FUNCTION: PART OF THE ATP-DRIVEN TRANSPORT SYSTEM ADCABC FOR ZINC.
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
CC (Probable).
CC -!- SIMILARITY: BELONGS TO THE BACTERIAL SOLUTE-BINDING PROTEIN FAMILY
CC 9.
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CC -----
DR EMBL; AE007505; AAK76223.1; -
DR EMBL; Z71552; CAA96185.1; -
DR TIGR; SP2169; -
DR InterPro; IPR001987; Lipoprotein_4.
DR Pfam; PF01297; SBP_bac.9; 1.
DR PRINTS; PR00690; ADHESNFAMILY.
KW Transport; Zinc transport; Membrane; Lipoprotein; Signal;
KW Complete proteome.
FT SIGNAL          1 18 PROBABLE.

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FT CHAIN 19 501 ZINC-BINDING LIPOPROTEIN ADCA.
 FT LIPID 19 19 N-ACYL DIGLYCERIDE (PROBABLE).
 FT CONFLICT 158 158 S -> T (IN REF. 2).
 FT CONFLICT 183 183 A -> S (IN REF. 2).
 FT CONFLICT 197 197 Q -> E (IN REF. 2).
 FT CONFLICT 387 387 H -> Q (IN REF. 2).
 SQ SEQUENCE 501 AA; 56221 MW; 95FC60B509DC242C CRC64;

Query Match 69.6%; Score 39; DB 1; Length 501;
 Best Local Similarity 66.7%; Pred. No. 6.1;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 TYPDVTVOG 10
 ||||| : |
 DB 483 TYPDNLGS 491

RESULT 11
 HDAL_YEAST STANDARD; PRT; 706 AA.
 AC P53973;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Histone deacetylase HDAL.
 GN HDAL OR YNL021W OR N2819.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Andre B., Iraqui Housaini I., Urrestarazu L.A., Vissers S.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP CHARACTERIZATION.
 RA Rundlett S.E., Carmen A.A., Kobayashi R., Bavykin S., Turner B.M.,
 RA Grunstein M.;
 RT "HDAL and RPD3 are members of distinct yeast histone deacetylase
 RT complexes that regulate silencing and transcription.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:14503-14508(1996).
 CC -1- FUNCTION: RESPONSIBLE FOR THE DEACETYLATION OF LYSINE RESIDUES ON
 CC THE N-TERMINAL PART OF THE CORE HISTONES (H2A, H2B, H3 AND H4).
 CC HISTONE DEACETYLATION PLAYS AN IMPORTANT ROLE IN TRANSCRIPTIONAL
 CC REGULATION AND CELL CYCLE PROGRESSION.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- SIMILARITY: BELONGS TO THE HISTONE DEACETYLASE / ACUC / APHA
 CC FAMILY. HD SUBFAMILY 2.

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DR EMBL: 271297; CAA05883.1; -;
 DR TRANSFAC: T04600; -;
 DR SGD: S0004986; HDAL.
 DR InterPro: IPR000286; Hist_deacetylase.
 DR Pfam: PF00850; Hist_deacetyl; 1.
 DR PRINTS: PR01270; HDASUPER.
 KW Hydrolase; Nuclear protein.
 SQ SEQUENCE 706 AA; 80069 MW; 4E7069E56D03264D CRC64;

Query Match 69.6%; Score 39; DB 1; Length 706;
 Best Local Similarity 75.0%; Pred. No. 8.9;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 YPDTVOG 10
 ||||| : |

DB 275 YYPGTIQG 282
 RESULT 12
 RELN_HUMAN STANDARD; PRT; 3460 AA.
 AC P78509; Q9UDQ2;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Reelin precursor (EC 3.4.21.-).
 GN RELN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=97202106; PubMed=9049633;
 RA Desilva U., D'Arcangelo G., Braden V.V., Chen J., Miao G.G.,
 RA Curran T., Green E.D.;
 RT "The human reelin gene: isolation, sequencing, and mapping on
 RT chromosome 7.";
 RL Genome Res. 7:157-164(1997).
 RN [2]
 RP SEQUENCE OF 194-2556 FROM N.A.
 RA Lamar B., Wamsley P., Gibson A., Maas J., Bauer C., Sapetti L.;
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP ALTERNATIVE SPLICING.
 RX MEDLINE=99263436; PubMed=10328932;
 RA Lambert de Rouvroit C., Bernier B., Royaux I., de Bergeyck V.,
 RA Goffinet A.M.;
 RT "Evolutionarily conserved, alternative splicing of reelin during brain
 RT development.";
 RL Exp. Neurol. 156:229-238(1999).
 RN [4]
 RP DISEASE, AND TISSUE SPECIFICITY.
 RX MEDLINE=99080080; PubMed=9861036;
 RA Impagnatiello F., Guidotti A.R., Pesold C., Dwivedi Y., Caruncho H.,
 RA Pisu M.G., Uzunov D.P., Smalheiser N.R., Davis J.M., Pandey G.N.,
 RA Pappas G.D., Tuetting P., Sharma R.P., Costa E.;
 RT "A decrease of reelin expression as a putative vulnerability factor in
 RT schizophrenia.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:15718-15723(1998).
 RN [5]
 RP DISEASE.
 RX MEDLINE=20428190; PubMed=10973257;
 RA Hong S.E., Shugart Y.Y., Huang D.T., Shahwan S.A., Grant P.E.,
 RA Hourihane J.O.B., Martin N.D.T., Walsh C.A.;
 RT "Autosomal recessive lissencephaly with cerebellar hypoplasia is
 RT associated with human RELN mutations.";
 RL Nat. Genet. 26:93-96(2000).
 RN [6]
 RP ERRATUM.
 RA Hong S.E., Shugart Y.Y., Huang D.T., Shahwan S.A., Grant P.E.,
 RA Hourihane J.O.B., Martin N.D.T., Walsh C.A.;
 RL Nat. Genet. 27:225-225(2001).
 RN [7]
 RP DISEASE.
 RX MEDLINE=21217116; PubMed=11317216;
 RA Persico A.M., D'Agruma L., Maiorano N., Totaro A., Militeri R.,
 RA Bravaccio C., Wassink T.H., Schneider C., Melmed R., Trillo S.,
 RA Montecchi F., Palermo M., Pascucci T., Puglisi-Allegra S.,
 RA Reichelt K.-L., Conciatori M., Marino R., Quattrocchi C.C., Baldi A.,
 RA Zelante L., Gasparini P., Keller F.;
 RT "Reelin gene alleles and haplotypes as a factor predisposing to
 RT autistic disorder.";
 RL Mol. Psych. 6:150-159(2001).
 CC -1- FUNCTION: Extracellular matrix serine protease that plays a role
 CC in layering of neurons in the cerebral cortex and cerebellum.
 CC Regulates microtubule function in neurons and neuronal migration.
 CC Affects migration of sympathetic preganglionic neurons in the

spinal cord, where it seems to act as a barrier to neuronal migration. Enzymatic activity is important for the modulation of cell adhesion. Binding to the extracellular domains of lipoprotein receptors VLDLR and ApoER2 induces tyrosine phosphorylation of Dab1 and modulation of Tau phosphorylation (By similarity).

-1- SUBUNIT: Binds to the ectodomains of VLDLR and ApoER2 (By similarity).

-1- SUBCELLULAR LOCATION: Secreted (By similarity).

-1- ALTERNATIVE PRODUCTS: 3 isoforms; 1 (shown here), 2 and 3; are produced by alternative splicing.

-1- TISSUE SPECIFICITY: Abundantly produced during brain ontogenesis by the Cajal-Retzius cells and other pioneer neurons located in the telencephalic marginal zone and by granule cells of the external granular layer of the cerebellum. In adult brain, preferentially expressed in GABAergic interneurons of prefrontal cortices, temporal cortex, hippocampus and glutamatergic granule cells of cerebellum. Also expressed in fetal and adult liver.

-1- DEVELOPMENTAL STAGE: Expressed in fetal and postnatal brain and liver. Expression in postnatal human brain is high in the cerebellum.

-1- DOMAIN: The basic C-terminal region is essential for secretion (By similarity).

-1- DISEASE: Defects in RELN are the cause of autosomal recessive lissencephaly with cerebellar hypoplasia (Also known as Norman-Roberts syndrome). Some patients also displayed persistent lymphedema neonatally, and one showed accumulation of chylous (i.e., fatty) ascites fluid.

-1- DISEASE: Defects in RELN may contribute to susceptibility to schizophrenia. Expression of the protein is reduced (about 50%) in patients with schizophrenia.

-1- DISEASE: Defects in RELN may predispose to autistic disorder. A polymorphic GGC triplet repeat located in the 5'UTR region of RELN (8 to 10 repeats) in the normal population is significantly increased in autistic patients (4 to 23 additional repeats).

-1- SIMILARITY: BELONGS TO THE REELIN FAMILY.

-1- SIMILARITY: CONTAINS 8 EGF-LIKE DOMAINS.

-1- SIMILARITY: CONTAINS 15 BNR REPEATS.

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EMBL; U79716; AAC51105.1; ...
EMBL; AC000121; AAB46357.1; ...
EMBL; AC006316; AAD29127.1; ...
HSP; P05106; LJV2.
Genew; HGNC:9957; RELN.
MIM; 600514; ...
MIM; 257320; ...
InterPro; IPR000561; EGF-like.
InterPro; IPR002860; GH_BNR.
InterPro; IPR002861; Reeler.
Pfam; PF000008; EGF; 4
Pfam; PF02012; BNR; 15.
Pfam; PF02014; Reeler; 1.
SMART; SM00181; EGF; 5.
PROSITE; PS00022; EGF_1; 7.
PROSITE; PS01186; EGF_2; 6.
Hydrolase; Serine protease; Developmental protein; Matrix protein;
Cell adhesion; EGF-like domain; Glycoprotein; Repeat; Signal;
Alternative splicing; Lissencephaly.
SIGNAL 1 25 POTENTIAL.
CHAIN 26 3460 REELIN.
DOMAIN 39 171 REELIN.
DOMAIN 670 701 EGF-LIKE 1.
DOMAIN 1029 1060 EGF-LIKE 2.
DOMAIN 1408 1441 EGF-LIKE 3.
DOMAIN 1764 1795 EGF-LIKE 4.
DOMAIN 2128 2160 EGF-LIKE 5.

FT	DOMAIN	2477	2508	EGF-LIKE 6.
FT	DOMAIN	2852	2883	EGF-LIKE 7.
FT	DOMAIN	3227	3259	EGF-LIKE 8.
FT	REPEAT	592	603	BNR 1.
FT	REPEAT	798	809	BNR 2.
FT	REPEAT	951	962	BNR 3.
FT	REPEAT	1156	1167	BNR 4.
FT	REPEAT	1322	1333	BNR 5.
FT	REPEAT	1534	1545	BNR 6.
FT	REPEAT	1685	1696	BNR 7.
FT	REPEAT	1883	1894	BNR 8.
FT	REPEAT	2042	2053	BNR 9.
FT	REPEAT	2249	2260	BNR 10.
FT	REPEAT	2398	2409	BNR 11.
FT	REPEAT	2597	2608	BNR 12.
FT	REPEAT	2777	2788	BNR 13.
FT	REPEAT	2978	2989	BNR 14.
FT	REPEAT	3362	3373	BNR 15.
FT	DOMAIN	3431	3460	ARG-RICH (BASIC).
FT	CARBOHYD	140	140	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	257	257	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	289	289	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	305	305	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	628	628	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	1266	1266	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	1599	1599	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	1749	1749	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	1920	1920	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	2144	2144	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	2268	2268	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	2316	2316	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	2568	2568	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	2961	2961	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	3015	3015	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	3072	3072	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	3184	3184	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	3411	3411	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	3438	3438	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	VARSPLIC	3428	3429	MISSING (IN ISOFORM 2).
FT	VARSPLIC	3428	3460	MISSING (IN ISOFORM 3).
FT	CONFLICT	752	752	E -> D (IN REF. 2).
SQ	SEQUENCE	3460 AA;	388399 MW;	BB2C0BA415AB93C1 CRC64;

Query Match 67.9%; Score 38; DB 1; Length 3460;
Best Local Similarity 70.0%; Pred No; 80;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY	1	STYYPDTVQG 10	
		I:	
Db	2077	STYYAGTMQG 2086	

RESULT 13
HV3F_HUMAN
ID HV3F_HUMAN STANDARD; PRT; 115 AA.
AC P01767;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-III region BUT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=78137069; PubMed=416441;
RA Torano A., Putnam F.W.;
RT "Complete amino acid sequence of the alpha 2 heavy chain of a human
IgA2 immunoglobulin of the A2m (2) allotype.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:966-969(1978).
CC -1- MISCELLANEOUS: THE SEQUENCE OF THE ALPHA-2, A2M(2) ALLOTYPIC, C
REGION OF THIS MYELOMA PROTEIN IS ALSO GIVEN.


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DR PIR: A02050; A2HUBU.
DR HSSP: P01789; IMCP.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR Immunoglobulin V region.
KW NON_TER 115
SQ SEQUENCE 115 AA; 12379 MW; 208876A7DF52DCF4 CRC64;

Query Match 66.1%; Score 37; DB 1; Length 115;
Best Local Similarity 60.0%; Pred. No. 2.9;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 STYYPDTVQG 10
Db 56 TTYADSVKG 65

RESULT 14
GUNZ_ERWCH STANDARD; PRT; 426 AA.
AC P07103;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Endoglucanase Z precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase Z)
DE (Cellulase Z) (EGZ).
GN CELZ OR CEL5.
OS Erwinia chrysanthemi.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Pectobacterium.
OX NCBI_TaxID=556;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3937;
RX MEDLINE=88216177; PubMed=2835589;
RA Guiseppe A., Cami B., Aymeric J.-L., Ball G., Creuzet N.;
RT "Homology between endoglucanase Z of Erwinia chrysanthemi and
RT endoglucanases of Bacillus subtilis and alkalophilic Bacillus."
RL Mol. Microbiol. 2:159-164(1988).
RN [2]
RP REVISIONS, AND DISULFIDE BOND.
RC STRAIN=3937;
RX MEDLINE=94203057; PubMed=8152378;
RA Bortoli-German I., Brun E., Py B., Chippaux M., Barras F.;
RT "Periplasmic disulphide bond formation is essential for cellulase
RT secretion by the plant pathogen Erwinia chrysanthemi."
RL Mol. Microbiol. 11:545-553(1994).
RN [3]
RP MUTAGENESIS, AND DOMAINS.
RX MEDLINE=91312880; PubMed=1677466;
RA Py B., Bortoli-German I., Halech J., Chippaux M., Barras F.;
RT "Cellulase EGZ of Erwinia chrysanthemi: structural organization and
RT importance of His98 and Glu133 residues for catalysis."
RL Protein Eng. 4:323-333(1991).
RN [4]
RP STEREOCHEMISTRY OF THE REACTION.
RX MEDLINE=92225124; PubMed=1563515;
RA Barras F., Bortoli-German I., Bauzan M., Rouvier J., Gey C.,
RA Heyraud A., Henrissat B.;
RT "Stereochemistry of the hydrolysis reaction catalyzed by
RT endoglucanase Z from Erwinia chrysanthemi."
RL FEBS Lett. 300:145-148(1992).
RN [5]
RP STRUCTURE BY NMR OF 365-426.
RX MEDLINE=98070232; PubMed=9405041;
RA Brun E., Moriaud F., Gans P., Blackledge M.J., Barras F., Marion D.;
RT "Solution structure of the cellulose-binding domain of the
RT endoglucanase Z secreted by Erwinia chrysanthemi."
RL Biochemistry 36:16074-16086(1997).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.30 ANGSTROMS) OF 44-335.

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RX MEDLINE=21392910; PubMed=11501995;
RA Chapon V., Czjzek M., El Hassouni M., Py B., Juy M., Barras F.;
RT "Type II protein secretion in Gram-negative pathogenic bacteria: the
RT study of the structure/secretion relationships of the cellulase Cel5
RT (formerly EGZ) from Erwinia chrysanthemi."
RL J. Mol. Biol. 310:1055-1066(2001).
CC -!- FUNCTION: REPRESENTS 97% OF THE GLOBAL CELLULOSE ACTIVITY.
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic
CC linkages in cellulose.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO CELLULOSE FAMILY A (FAMILY 5 OF GLYCOSYL
CC HYDROLASES).
CC -----
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CC -----
DR EMBL: Y00540; CAA68604.1; -.
DR PIR: S03767; S03767.
DR PDB: 1AIW; 06-MAY-98.
DR PDB: 1EGZ; 26-MAR-99.
DR InterPro: IPR003610; CBM_5_12.
DR InterPro: IPR001547; GH_5.
DR Pfam: PF00150; cellulase; 1.
DR Pfam: PF02839; CBM_5_12; 1.
DR SMART: SM00495; ChtBD3; 1.
DR PROSITE: PS00659; GLYCOSYL_HYDROL_F5; 1.
DR Cellulose degradation; Hydrolase; Glycosidase; Signal; 3D-structure.
KW SIGNAL
FT CHAIN 1 43
FT DOMAIN 44 426
FT CATALYTIC LINKER.
FT DOMAIN 333 366
FT DOMAIN 367 426
FT ACT_SITE 176 176
FT ACT_SITE 263 263
FT DISULFID 368 425
FT MUTAGEN 141 141
FT MUTAGEN 176 176
FT CONFLICT 293 295
FT CONFLICT 350 364
FT CONFLICT 388 426
FT THNEAGQSVYKGNLYTANWYTASVPGSDSSWTVQGSNC
FT -> LITQANSSSTKATCIPQTGTTPHPRAAIPPCRRLLV
FT AVTN (IN REF. 1).
SQ SEQUENCE 426 AA; 46418 MW; E78F2EE021FCA5DA CRC64;

Query Match 66.1%; Score 37; DB 1; Length 426;
Best Local Similarity 85.7%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STYYPDT 7
Db 307 STYYPDS 313

RESULT 15
FGR_MOUSE STANDARD; PRT; 517 AA.
AC P14234; 061404;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Proto-oncogene tyrosine-protein kinase FGR (EC 2.7.1.112) (P55-FGR)
DE (C-FGR).
GN FGR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

```

[1]
SEQUENCE FROM N.A.
RC STRAIN=DBA/2J;
RA MEDLINE=89385605; PubMed=2674853;
Yi T.L., Willman C.L.;
"Cloning of the murine c-fgr proto-oncogene cDNA and induction of
RT c-fgr expression by proliferation and activation factors in normal
RT bone marrow-derived monocytic cells.";
RL Oncogene 4:1081-1087(1989).
[2]
SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Monocytic leukemia;
RX MEDLINE=90191719; PubMed=2179817;
King F.J., Cole M.D.;
RA "Molecular cloning and sequencing of the murine c-fgr gene.";
RL Oncogene 5:337-344(1990).
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein
CC tyrosine phosphate.
CC -!- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
CC SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
CC -----
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CC -----
DR EMBL: X16440; CAA34463.1; -
DR EMBL: X52191; CAA36437.1; -
DR PIR: A33127; A33127.
DR PIR: S10072; S10072.
DR HSSP: P00523; 2PTK.
DR MGD; MGI:95527; Fgr.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR000980; SH2.
DR InterPro: IPR001452; SH3.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00017; SH2; 1.
DR Pfam: PF00018; SH3; 1.
DR Pfam: PF00069; pkinase; 1.
DR PRINTS: PR00401; SH2DOMAIN.
DR PRINTS: PR00452; SH3DOMAIN.
DR PRINTS: PR00109; TYRKINASE.
DR ProDom: PD000001; Euk_pkinase; 1.
DR ProDom: PD000066; SH3; 1.
DR ProDom: PD000093; SH2; 1.
DR SMART: SM00252; SH2; 1.
DR SMART: SM00326; SH3; 1.
DR SMART: SM00219; TyrKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS50001; SH2; 1.
DR PROSITE: PS50002; SH3; 1.
KW Transferase; Tyrosine-protein kinase; Proto-oncogene; ATP-binding;
KW Phosphorylation; SH2 domain; SH3 domain.
FT DOMAIN 65 126
FT DOMAIN 132 229 SH2.
FT DOMAIN 251 504 PROTEIN KINASE.
FT NP_BIND 257 265 ATP (BY SIMILARITY).
FT BINDING 279 279 ATP (BY SIMILARITY).
FT ACT_SITE 370 370 BY SIMILARITY.
FT MOD_RES 400 400 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT CONFLICT 41 41 N -> T (IN REF. 2).
FT CONFLICT 212 212 Q -> R (IN REF. 2).
FT SEQUENCE 517 AA; 58867 MW; F655BDB4510F3076 CRC64;
Query Match - 66.1%; Score 37; DB 1; Length 517;
Best Local Similarity 75.0%; Pred. No. 15;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 3 YYPDTVQG 10
||| |
Db 32 YYPDTQG 39
Search completed: November 18, 2002, 17:33:21
Job time : 3.45098 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:01 ; Search time 10.4412 Seconds
(without alignments)
197.341 Million cell updates/sec

Title: us-09-016-061-56
Perfect score: 56
Sequence: 1 STYPTDVQV 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL21.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp Vertebrate.*
14: sp Unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	44	78.6	119	11 Q920E7	Q920E7 mus musculus
2	44	78.6	486	11 Q91Z07	Q91Z07 mus musculus
3	43	76.8	487	11 Q99KA4	Q99KA4 mus musculus
4	41	73.2	179	16 Q8YNG8	Q8YNG8 anabaena sp
5	40	71.4	121	4 Q9UL71	Q9UL71 homo sapien
6	40	71.4	426	2 Q9REW0	Q9REW0 erwinia chr
7	40	71.4	597	4 Q96BB9	Q96BB9 homo sapien
8	40	71.4	1151	11 Q9QVN5	Q9QVN5 rattus sp.
9	40	71.4	1174	11 Q91Z60	Q91Z60 rattus norv
10	39	69.6	337	16 Q8RCF2	Q8RCF2 thermoaer
11	39	69.6	594	8 Q9T3A0	Q9T3A0 nephroselmi
12	39	69.6	4065	3 Q9P4Z1	Q9P4Z1 neurospora
13	38	67.9	411	16 Q929F1	Q929F1 listeria in
14	38	67.9	479	11 Q91WP5	Q91WP5 mus musculus
15	38	67.9	529	5 Q961H6	Q961H6 drosophila
16	38	67.9	534	5 Q9VM10	Q9VM10 drosophila

17	37	66.1	262	13 Q9PWM6	Q9PWM6 brachydanio
18	37	66.1	316	16 Q97P62	Q97P62 streptococc
19	37	66.1	411	16 Q8Y554	Q8Y554 listeria mo
20	37	66.1	480	11 Q91XEL	Q91XEL mus musculu
21	37	66.1	517	11 Q63206	Q63206 rattus norv
22	37	66.1	522	12 Q91FV8	Q91FV8 chilo iride
23	37	66.1	622	5 Q9NBC7	Q9NBC7 helisoma tr
24	37	66.1	962	12 Q89443	Q89443 african swi
25	37	66.1	963	12 Q8V9U2	Q8V9U2 african swi
26	37	66.1	3433	12 Q9Q6P4	Q9Q6P4 west nile v
27	37	66.1	3433	12 Q9Q519	Q9Q519 west nile v
28	37	66.1	3433	12 Q9EMB6	Q9EMB6 west nile v
29	37	66.1	3433	12 Q9EMB5	Q9EMB5 west nile v
30	37	66.1	3433	12 Q9EA21	Q9EA21 west nile v
31	37	66.1	3433	12 Q99D37	Q99D37 west nile v
32	37	66.1	3433	12 Q9Q3G9	Q9Q3G9 west nile v
33	37	66.1	3433	12 Q8QRN6	Q8QRN6 west nile v
34	36	64.3	116	12 Q91R73	Q91R73 eupatorium
35	36	64.3	116	12 Q5JH40	Q5JH40 tobacco lea
36	36	64.3	118	4 Q9UL72	Q9UL72 homo sapien
37	36	64.3	194	5 Q16565	Q16565 caenorhabdi
38	36	64.3	211	11 Q9D8R6	Q9D8R6 mus musculu
39	36	64.3	304	2 Q93QX6	Q93QX6 corynebacte
40	36	64.3	316	4 Q9H342	Q9H342 homo sapien
41	36	64.3	349	5 Q17863	Q17863 caenorhabdi
42	36	64.3	370	5 Q8SXE4	Q8SXE4 drosophila
43	36	64.3	380	10 Q9FJX7	Q9FJX7 arabidopsis
44	36	64.3	384	17 Q9HLZ3	Q9HLZ3 thermoplasma
45	36	64.3	534	16 Q9K996	Q9K996 bacillus ha

ALIGNMENTS

RESULT 1

Q920E7 PRELIMINARY; PRT; 119 AA.
AC Q920E7;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Pterin-mimicking anti-idiotope heavy chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Atkin J.D., Tape A., Jennings I.G., Horaitis O., Cotton R.G.H.;
RT "Definition of the idiotope of pterin-Mimicking Antibodies Expressed
in Mammalian Cells."
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307937; AAL09421.1; -;
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
FT NON_TER 1
FT NON_TER 119
SQ SEQUENCE 119 AA; 13025 MW; F6E904044381CA7C CRC64;

Query Match 78.6%; Score 44; DB 11; Length 119;
Best Local Similarity 77.8%; Pred. NO. 0.89;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 TYPTDVQV 10
|||||:
Db 58 TYPTDSVKG 66

RESULT 2

Q91Z07 PRELIMINARY; PRT; 486 AA.
AC Q91Z07;

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DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical 52.7 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC010324; AAI10324.1; -.
DR InterPro; IPR003598; Ig_G2.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00408; Igc2; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein; Immunoglobulin domain.
SQ SEQUENCE 486 AA; 52682 MW; 4FEF835125DA870B CRC64;

Query Match 78.6%; Score 44; DB 11; Length 486;
Best Local Similarity 70.0%; Pred. No. 4.2;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYPDTVQG 10
Db 75 NTYYPDNVKG 84

RESULT 3
Q99KA4
ID Q99KA4 PRELIMINARY; PRT; 487 AA.
AC Q99KA4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical 52.6 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC004786; AAH04786.1; -.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; IG; 3.
DR SMART; SM00407; Igc1; 3.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS00410; IG_like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 487 AA; 52554 MW; 7DC8E95DB333077B CRC64;

Query Match 76.8%; Score 43; DB 11; Length 487;
Best Local Similarity 77.8%; Pred. No. 6.5;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 TYYPDTVQG 10
Db 77 TYYPDNVKG 85

RESULT 4
Q8YMG8
ID Q8YMG8 PRELIMINARY; PRT; 179 AA.
AC Q8YMG8;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein Alr4965.
GN ALR4965.
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriiguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain PCC 7120.";
RL DNA Res. 8:205-213(2001).
DR EMBL; AP003598; BAB76664.1; -.
DR Hypothetical protein; Complete proteome.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 179 AA; 20400 MW; B52955D50F2D432D CRC64;

Query Match 73.2%; Score 41; DB 16; Length 179;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDT 7
Db 15 STYYPDT 21

RESULT 5
Q9UL71
ID Q9UL71 PRELIMINARY; PRT; 121 AA.
AC Q9UL71;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035043; AAD56279.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
DR NON_TER 1
FT NON_TER 121 121
SQ SEQUENCE 121 AA; 13154 MW; 2F045CCFA5D50736 CRC64;

Query Match 71.4%; Score 40; DB 4; Length 121;
Best Local Similarity 70.0%; Pred. No. 5.3;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYPDTVQG 10
Db 57 STYVADSVKG 66

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RESULT 6

Q9REW0 PRELIMINARY; PRT; 426 AA.
ID Q9REW0
AC Q9REW0
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Endo-1,4-beta-glucanase (EC 3.2.1.4).
GN CEL5Z.
OS Erwinia chrysanthemi.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Pectobacterium.
OX NCBI_TaxID=556;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PY35;
RX MEDLINE=20145449; PubMed=10679220;
RA Park S.R., Kim M.K., Kim J.O., Bae D.W., Cho S.J., Cho Y.U., Yun H.D.;
RT "Characterization of Erwinia chrysanthemi PY35 cel and pel gene
existing in tandem and rapid identification of their gene products.";
RL Biochem. Biophys. Res. Commun. 268:420-425(2000).
DR EMBL: AF208495; AAF18152.1; -;
DR HSSP: P07103; 1EGZ.
DR InterPro: IPR003610; CBM_5_12.
DR InterPro: IPR001547; GH_5.
DR Pfam: PF02839; CBM_5_12; 1.
DR Pfam: PF00150; cellulase; 1.
DR SMART: SM00495; ChtBD3; 1.
DR PROSITE: PS00659; GLYCOSYL_HYDROL_F5; UNKNOWN_1.
KW Glycosidase; Hydrolase.
SQ SEQUENCE 426 AA; 46502 MW; 60217A1C6C05FE16 CRC64;

Query Match 71.4%; Score 40; DB 2; Length 426;
Best Local Similarity 75.0%; Pred. No. 21;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDRV 8

|||||
Db 307 STYYPDSI 314

RESULT 7

Q96BB9 PRELIMINARY; PRT; 597 AA.
ID Q96BB9
AC Q96BB9
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical 65.0 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B-CELL;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC015760; AALH5760.1; -;
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig; 5.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_3.
KW Hypothetical protein.
SQ SEQUENCE 597 AA; 65039 MW; 4FCA3AD8CE263D9 CRC64;

Query Match 71.4%; Score 40; DB 4; Length 597;
Best Local Similarity 70.0%; Pred. No. 30;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYPDRV 10

|||||
Db 76 STYYPDSI 85

RESULT 8

Q9QVN5 PRELIMINARY; PRT; 1151 AA.
ID Q9QVN5
AC Q9QVN5
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE NEUROFASCIN isoform.
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97103184; PubMed=8947556;
RA Davis J.O., Lambert S., Bennett V.;
RT "Molecular composition of the node of Ranvier: identification of
ankyrin-binding cell adhesion molecules neurofascin (mucin+/third
FNIII domain-) and NrCAM at nodal axon segments.";
RL J. Cell Biol. 135:1355-1367(1996).
DR HSSP: P20241; 1CPB.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003598; Ig_C2.
DR InterPro: IPR003600; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00041; fn3; 4.
DR Pfam: PF00047; Ig; 6.
DR SMART: SM00060; FN3; 4.
DR SMART: SM00408; IGC2; 4.
DR SMART: SM00410; IG_Like; 2.
KW Immunoglobulin domain.
SQ SEQUENCE 1151 AA; 129732 MW; 770BD492C4A4ECC5 CRC64;

Query Match 71.4%; Score 40; DB 11; Length 1151;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YPDTVQG 10

|||||
Db 823 YPDTVQG 829

RESULT 9

Q91Z60 PRELIMINARY; PRT; 1174 AA.
ID Q91Z60
AC Q91Z60
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Neurofascin 155 kDa isoform.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WISTAR;
RX MEDLINE=98220650; PubMed=9562181;
RA Collinson J.M., Marshall D., Gillespie C.S., Brophy P.J.;
RT "Transient expression of neurofascin by oligodendrocytes at the onset
of myelogenesis: implications for mechanisms of axon-glia
interaction";
RL Glia 23:11-23(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=WISTAR;
RX MEDLINE=203191985; PubMed=10931875;
RA Tait S., Gunn-Moore F., Collinson J.M., Huang J., Lubetzki C.,
Pedraza L., Sherman D.L., Colman D.R., Brophy P.J.;
RT "An oligodendrocyte cell adhesion molecule at the site of assembly of
the paranodal axo-glia junction.";

RL J. Cell Biol. 150:657-666(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=WISTAR;
 RA Tait S., Collinson J.M., Brophy P.J.;
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY061639; AAL27854.1; -;
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR003006; Iq_MHC.
 DR Pfam; PF00041; fn3; 4.
 DR Pfam; PF00047; ig; 6.
 SQ SEQUENCE 1174 AA; 13227 MW; B9FF8D9A2C20F30 CRC64;

Query Match 71.4%; Score 40; DB 11; Length 1174;
 Best Local Similarity 100.0%; Pred. No. 64;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YPDTVQG 10
 :|||||
 Db 846 YPDTVQG 852

RESULT 10
 Q8RCF2 PRELIMINARY; PRT; 337 AA.
 AC Q8RCF2;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Transcriptional regulator.
 GN PURR4 OR TTE0480.
 OS Thermoanaerobacter tengcongensis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
 OC Thermoanaerobacteriales; Thermoanaerobacteriaceae; Thermoanaerobacter.
 OX NCBI_TaxID=119072;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MB4T / JCM11007;
 RX MEDLINE=21992816; PubMed=11997336;
 RA Bao O., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
 RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
 RA Tan H., Chen R., Wang J., Yu J., Yang H.;
 RT "A complete sequence of T. tengcongensis genome.";
 RL Genome Res. 12:689-700(2002).
 DR EMBL; AE013019; AAM23760.1; -;
 KW Complete proteome.
 SQ SEQUENCE 337 AA; 37548 MW; 1A81A6B7A914088C CRC64;

Query Match 69.6%; Score 39; DB 16; Length 337;
 Best Local Similarity 60.0%; Pred. No. 25;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYPTDVQG 10
 :|:|:|:|:
 Db 72 STYPEVVRG 81

RESULT 11
 Q9T3A0 PRELIMINARY; PRT; 594 AA.
 AC Q9T3A0;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Hypothetical 67.7 kDa protein.
 OS Nephroselmis olivacea.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Chlorophyta; Prasinophyceae;
 OC Chlorodendreales; Chlorodendraceae; Nephroselmis.
 OX NCBI_TaxID=31312;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99398694; PubMed=10468594;

RA Turmel M., Otis C., Lemieux C.;
 RT "The complete chloroplast DNA sequence of the green alga Nephroselmis
 RT olivacea: Insights into the architecture of ancestral chloroplast
 RT genomes";
 RL Proc. Natl. Acad. Sci. U.S.A. 96:10248-10253(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Turmel M., Otis C., Lemieux C.;
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF137379; AAD54924.1; -;
 DR EMBL; AF137379; AAD54865.1; -;
 KW Chloroplast; Hypothetical protein.
 SQ SEQUENCE 594 AA; 67671 MW; C6AD240A53F19231 CRC64;

Query Match 69.6%; Score 39; DB 8; Length 594;
 Best Local Similarity 70.0%; Pred. No. 47;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 STYPTDVQG 10
 :|:|:|:|:
 Db 223 SSXPDTVHG 232

RESULT 12
 Q9P4Z1 PRELIMINARY; PRT; 4065 AA.
 AC Q9P4Z1;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Related to TOM1 protein.
 GN B11B22.010.
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariales; Sordariaceae; Neurospora.
 OX NCBI_TaxID=5141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R.,
 RA Nyakatura G., Mewes H.W., Mannhaupt G.;
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA German Neurospora genome project;
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL356834; CAB92704.2; -;
 DR InterPro; IPR000569; HECT_domain.
 DR Pfam; PF00632; HECT; 2.
 DR SMART; SM00119; HECTc; 2.
 DR PROSITE; PS50237; HECT; 2.
 SQ SEQUENCE 4065 AA; 452568 MW; F74683CEC36F9350 CRC64;

Query Match 69.6%; Score 39; DB 3; Length 4065;
 Best Local Similarity 66.7%; Pred. No. 3.8e+02;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 TYYPDTVQG 10
 :|:|:|:|:
 Db 286 SYYPDTTNG 294

RESULT 13
 Q929F1 PRELIMINARY; PRT; 411 AA.
 AC Q929F1;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Hypothetical protein lin2325.
 GN Lin2325.
 OS Listeria innocua.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Listeriaceae; Listeria.

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OX NCBI_faxID=1642;
RN [1];
RP SEQUENCE FROM N.A.
RC STRAIN=CLIP 11262 / SEROVAR 6A;
RX PubMed=11679669;
RA Glaser P., Frangeule P., Buchrieser C., Rusniok C., Amend A.,
RA Baquero F., Bange P., Bloeker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
RA Gauthier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Krefit J., Kuhn M., Kunst F., Kutapkat G.,
RA Madaeno E., Maitounam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordsiek G., Novella S., de Pablo S., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
DR EMBL: AL596171; CAC97853.1; -.
DR ListList; LIN02325; -.
DR InterPro; IPR004843; M-peptase.
DR InterPro; IPR004844; S/T_phosphatase.
DR Pfam; PF00149; Metallophos; 1.
DR KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 411 AA; 46889 MW; 210BD00F9FA59762 CRC64;

Query Match 67.9%; Score 38; DB 16; Length 411;
Best Local Similarity 60.0%; Pred. No. 49;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 STYYPDVTQVG 10
Db 211 SVYYPGNIQ 220
| | | | | | | | | |

RESULT 14
Q91WP5 ID Q91WP5 PRELIMINARY; PRT; 479 AA.
AC Q91WP5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical 51.6 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1];
RP SEQUENCE FROM N.A.
RC TISSUE=COLON;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC013656; AAH13656.1; -.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
DR KW Hypothetical protein; Immunoglobulin domain.
SQ SEQUENCE 479 AA; 51603 MW; ECB2D0877748584F CRC64;

Query Match 67.9%; Score 38; DB 11; Length 479;
Best Local Similarity 60.0%; Pred. No. 58;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYPDVTQVG 10
Db 76 NTYYSDTMKG 85
| | | | | | | | | |

RESULT 15
Q961H6 ID Q961H6 PRELIMINARY; PRT; 529 AA.

```

```

AC Q961H6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE CH23019p.
GN BEST:CK01577 OR CG12789.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1];
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY051582; AAK93006.1; -.
DR FlyBase; FBgn0025697; BEST:CK01577.
DR InterPro; IPR002159; CD36.
DR Pfam; PF01130; CD36; 1.
DR PRINTS; PR01610; CD36ANTIGEN.
DR PRINTS; PR01609; CD36FAMILY.
DR SEQUENCE 529 AA; 59222 MW; 4F884D06E7AFC5B1 CRC64;

Query Match 67.9%; Score 38; DB 5; Length 529;
Best Local Similarity 75.0%; Pred. No. 64;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 YYPDVTQVG 10
Db 333 YYPDQVEG 340
| | | | | | | | | |

Search completed: November 18, 2002, 17:40:39
Job time : 12.4912 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:21:57 ; Search time 13.8235 Seconds
(without alignments)
96.394 Million cell updates/sec

Title: US-09-016-061-56
Perfect score: 56
Sequence: 1 STYPTVQV 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_101002:*
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2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
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23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	56	100.0	10	19	AAW76018
2	56	100.0	10	22	AAW76018
3	56	100.0	17	22	AAW76018
4	52	92.9	17	18	AAW76018
5	52	92.9	17	22	AAW76018
6	52	92.9	87	22	AAW76018
7	52	92.9	98	22	AAW76018
8	52	92.9	112	22	AAW76018
9	52	92.9	117	16	AAW76018
10	52	92.9	117	18	AAW76018

11	52	92.9	117	18	AAW76018	Heavy chain variab
12	52	92.9	117	18	AAW76018	Heavy chain variab
13	52	92.9	118	16	AAW76018	Human IgE receptor
14	52	92.9	120	17	AAW00240	EGF receptor chime
15	52	92.9	125	22	AAW48937	Anti-TrkA murine m
16	52	92.9	139	18	AAW21652	Humanised reshaped
17	52	92.9	139	18	AAW21656	Chimeric MAb 15 PC
18	52	92.9	140	18	AAW21654	Mouse MAb 15 heavy
19	52	92.9	158	18	AAW19577	Mouse anti-idiotyp
20	52	92.9	158	18	AAW19577	Mouse anti-idiotyp
21	52	92.9	239	20	AAW73874	Human antiFc epsil
22	52	92.9	242	20	AAW73876	Human antiFc epsil
23	52	92.9	260	16	AAW7617	Anti-C5 MAb N19/8
24	52	92.9	295	22	AAW48934	Anti-TrkA single c
25	52	92.9	461	22	AAU07745	Humanised monoclon
26	50	89.3	117	16	AAW79157	Human IgE receptor
27	49	87.5	98	14	AAW36526	Heavy chain VH 718
28	49	87.5	123	19	AAW6099	Anti-CD22 monoclon
29	49	87.5	136	11	AAW06251	Variable region of
30	48	85.7	88	22	AAE06988	Mouse germline hea
31	48	85.7	89	22	AAE06985	Mouse germline hea
32	48	85.7	119	16	AAW11919	Humanised MAB SK48
33	48	85.7	121	15	AAW60526	ME1-14 heavy chain
34	48	85.7	121	18	AAW22951	Monoclonal antibod
35	48	85.7	121	18	AAW16648	Anti-cancer specif
36	48	85.7	121	20	AAW86124	Protein sequence o
37	48	85.7	121	20	AAW86125	Protein sequence o
38	48	85.7	121	20	AAW86122	Protein sequence o
39	48	85.7	121	20	AAW86120	Protein sequence o
40	48	85.7	121	20	AAW86118	Murine 340 Vh amin
41	48	85.7	121	23	AAE15703	Mouse monoclonal a
42	48	85.7	121	23	AAE15706	Mouse monoclonal a
43	48	85.7	121	23	AAE15707	Mouse monoclonal a
44	48	85.7	121	23	AAE15708	Mouse monoclonal a
45	48	85.7	121	23	AAE15709	Mouse monoclonal a

ALIGNMENTS

RESULT 1
AAW76018
ID AAW76018 standard; Protein; 10 AA.
AC AAW76018;
XX
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR2 protein fragment #4.
XX
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
XX
OS Mus sp.
XX
PN WO9833919-A2.
XX
PD 06-AUG-1998.
XX
PF 30-JAN-1998; 98WO-US01826.
XX
PR 30-JAN-1997; 97US-0791391.
XX
PA (IXSY-) IXSYS INC.
XX
PI Glaser SM, Huse WD;
XX
WP 1998-437472/37.
DR N-PSDB; AAW49855.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
PS Claim 61; Page 41; 129pp; English.
XX
CC AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
CC antibodies contain non-murine framework regions so are suitable for use
CC in humans. Enhanced types of LM609 have affinity more than 90 times
CC greater than that of parent the parent antibody.
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 56; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00043;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDTVQG 10
|||||
Db 1 STYYPDTVQG 10

RESULT 2

AAB61376
ID AAB61376 standard; peptide; 10 AA.

AC AAB61376;

DT 03-APR-2001 (first entry)

XX Mutant VH CDR2 peptide #2.

XX LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
KW inflammatory; cancer; retina; restenosis; osteoporosis.
XX

OS Unidentified.

XX WO200078815-A1.

XX 28-DEC-2000.

XX 23-JUN-2000; 2000WO-US17454.

XX 24-JUN-1999; 99US-0339922.

XX (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX Huse WD, Wu H;

XX WPI; 2001-050110/06.

XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
PT osteoporosis -
XX

PS Disclosure; Page 41; 132pp; English.

XX The present invention relates to enhanced LM609 grafted antibodies
CC exhibiting selective binding affinity to alphavbeta_3 integrin or
CC their functional fragments. The antibodies or their functional
CC fragments can be used in the diagnosis and treatment of
CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory

CC diseases (such as psoriasis and chronic articular rheumatism),
CC disorders associated with inappropriate or inopportune invasion of
CC vessels (such as diabetic retinopathy, neovascular glaucoma and
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
CC diseases (such as macular degeneration), restenosis and
CC osteoporosis.
XX

SQ Sequence 10 AA;

Query Match 100.0%; Score 56; DB 22; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.00043;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDTVQG 10
|||||
Db 1 STYYPDTVQG 10

RESULT 3

AAB61400

ID AAB61400 standard; peptide; 17 AA.

AC AAB61400;

DT 03-APR-2001 (first entry)

XX Enhanced LM609 VH CDR2 peptide.

XX LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
KW inflammatory; cancer; retina; restenosis; osteoporosis.
XX

OS Unidentified.

XX WO200078815-A1.

XX 28-DEC-2000.

XX 23-JUN-2000; 2000WO-US17454.

XX 24-JUN-1999; 99US-0339922.

XX (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX Huse WD, Wu H;

XX WPI; 2001-050110/06.

XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
PT osteoporosis -
XX

PS Claim 1; Page 45; 132pp; English.

XX The present invention relates to enhanced LM609 grafted antibodies
CC exhibiting selective binding affinity to alphavbeta_3 integrin or
CC their functional fragments. The antibodies or their functional
CC fragments can be used in the diagnosis and treatment of
CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
CC diseases (such as psoriasis and chronic articular rheumatism),
CC disorders associated with inappropriate or inopportune invasion of
CC vessels (such as diabetic retinopathy, neovascular glaucoma and
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
CC diseases (such as macular degeneration), restenosis and
CC osteoporosis.
XX

SQ Sequence 17 AA;

Query Match 100.0%; Score 56; DB 22; Length 17;

Best Local Similarity 100.0%; Pred. No. 0.00077;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDTVQG 10

Db
 8 STYYPDTVQG 17
 |||

RESULT 4

AAW27342
 ID AAW27342 standard; peptide; 17 AA.
 XX
 AC AAW27342;
 XX
 DT 12-DEC-1997 (first entry)
 XX
 DE CDR2 from murine anti-human IgE receptor antibody heavy chain.
 XX
 KW Complementarity determining region; CDR2; murine; mouse; human;
 KW high affinity; immunoglobulin E; receptor; monoclonal antibody;
 KW IgE; MAb; heavy chain; variable region; humanised; semi-chimeric;
 KW chimeric; treatment; prevention; disease; allergy.
 XX
 OS Mus spp.
 XX
 PN JF09191886-A.
 XX
 XX 29-JUL-1997.
 XX
 PF 19-JAN-1996; 96JP-0024816.
 XX
 PR 19-JAN-1996; 96JP-0024816.
 XX
 PA (ASAK) ASAKI BREWERIES LTD.
 PA (NIKK-) NIKKA WHISKEY KK.
 PA (TORI) TORII YAKUHIIN KK.
 PA (TSUR/) TSURA T.
 XX
 DR WPI; 1997-429186/40.
 XX
 PT Humanised, semi-chimeric and chimeric antibodies against human
 PT high-affinity IgE receptor - useful medicinally and have low
 PT antigenicity in humans
 XX
 PS Claim 1; Page 12; 26pp; Japanese.
 XX
 CC The present complementarity determining region 2 (CDR2), which is
 CC from a murine, anti-human high affinity immunoglobulin E (IgE)
 CC receptor, monoclonal antibody (MAB) heavy chain variable region,
 CC can be used in the preparation of humanised or semi-chimeric
 CC anti-human high affinity IgE receptor MAB. The MAB can be used to
 CC treat or prevent diseases, specifically allergies, associated with
 CC the receptor. The humanised, semi-chimeric or chimeric MAB have
 CC very low antigenicity in humans.
 XX
 SQ Sequence 17 AA;

Query Match 92.9%; Score 52; DB 18; Length 17;
 Best Local Similarity 90.0%; Pred. No. 0.0044;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 STYYPDTVQG 10
 |||
 Db 8 STYYPDTVKG 17

RESULT 5

AAU07738
 ID AAU07738 standard; peptide; 17 AA.
 XX
 AC AAU07738;
 XX
 DT 04-DEC-2001 (first entry)
 XX
 DE Human heavy chain complementarity determining region, CDR2.
 XX
 KW Complementarity determining region; CDR2; Hu266; nootropic;

KW neuroprotective; Abeta peptide; Alzheimer's disease; Down's syndrome;
 KW cerebral amyloid angiopathy; antibody; gene therapy.
 XX

OS Homo sapiens.
 OS Synthetic.
 XX

PN WO200162801-A2.
 XX

PD 30-AUG-2001.
 XX

PF 26-FEB-2001; 2001WO-US06191.
 XX

PR 24-FEB-2000; 2000US-0184601.
 XX

PR 08-DEC-2000; 2000US-0254465.
 XX

PR 08-DEC-2000; 2000US-0254498.
 XX

PA (UNIW) UNIV WASHINGTON.
 PA (ELIL) LILLY & CO ELI.
 XX

PI Holtzman DM, Demattos R, Bales KR, Paul SM, Tsurushita N;
 PI Vasquez M;
 XX

DR WPI; 2001-550087/61.
 XX

XX
 PT New humanised antibody for the treatment of Alzheimer's comprises the
 PT inhibition and reduction of the formation of amyloid plaques -
 XX

PS Claim 14; Page 45; 63pp; English.
 XX

CC The invention relates a humanised antibody that specifically binds
 CC an epitope contained within positions 13-28 of amyloid beta peptide,
 CC Abeta. The antibody is useful to inhibit and reduce the formation of
 CC amyloid plaques or the effects of toxic soluble Abeta species in humans
 CC their fragments are used for the manufacture of a medicament. This includes
 CC the prolonged expression of recombinant sequences of them in human
 CC tissues for the treatment of clinical/pre-clinical Alzheimer's disease,
 CC Down's syndrome or pre-clinical cerebral amyloid angiopathy.
 CC Specifically, the antibody is used to sequester Abeta into plasma, brain
 CC or cerebrospinal fluid to prevent/reverse accumulation of the Abeta
 CC peptide within the brain thereby improving cognition. The present
 CC sequence is human heavy chain CDR2 (complementarity determining region 2)
 CC used to humanise the mouse monoclonal antibody 266 to produce Hu266.
 XX

SQ Sequence 17 AA;

Query Match 92.9%; Score 52; DB 22; Length 17;
 Best Local Similarity 90.0%; Pred. No. 0.0044;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDTVQG 10
 |||
 Db 8 STYYPDTVKG 17

RESULT 6
 AAEO6990
 ID AAEO6990 standard; Protein; 87 AA.
 XX
 AC AAEO6990;
 XX

DT 16-OCT-2001 (first entry)
 XX

DE Mouse germline heavy chain variable (VH) region, VH7183.13.
 XX

KW Mouse; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;
 KW neuroprotective; immunosuppressive; human immunodeficiency virus;
 KW HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;
 KW inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;
 KW multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma;
 KW anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;
 KW fibrotic disease; angioplasty; acquired immune deficiency syndrome;
 KW AIDS; inflammatory glomerulopathy; vascular intervention;
 KW neointimal hyperplasia; VH; heavy chain variable region.

XX Mus sp.
OS WO200157226-A1.
XX 09-AUG-2001.
XX 02-FEB-2001; 2001WO-US03537.
XX 03-FEB-2000; 2000US-0497625.
XX (MILL-) MILLENNIUM PHARM INC.
XX Larosa GJ, Horvath C, Newman W, Jones ST, O'Brien S, O'Keefe T;
XX WPI; 2001-488888/53.
XX Humanized immunoglobulin for treating a CC-chemokine receptor
PT 2-mediated disorder in a patient, comprises a binding specificity for
PT CCR2, and a non-human antigen binding region and human immunoglobulin
PT -
XX Disclosure; Page 159; 183pp; English.
XX The patent discloses a humanised antibody or its antigen-binding
XX fragment, having binding specificity for CC-chemokine receptor 2
XX (CCR2), comprising an antigen binding region of non-human origin
XX and at least a portion of an immunoglobulin of human origin. The
XX humanised antibodies are useful for inhibiting the interaction of
XX a cell expressing CCR2. They are useful for inhibiting or treating
XX HIV infection. The proteins of the invention are useful for inhibiting
XX leukocyte trafficking, for treating CCR2-mediated disorders such as
XX inflammatory disorder, autoimmune disorders such as rheumatoid
XX arthritis and multiple sclerosis, atherogenesis and atherosclerosis,
XX and for inhibiting restenosis. They are useful in therapy or diagnosis,
XX and in the manufacture of a medicament for treating CCR2 mediated
XX disease. They are also useful for treating allergy, anaphylaxis,
XX malignancy, chronic and acute inflammation, histamine and IgE-
XX mediated allergic reaction, shock, stenosis, allograft rejection,
XX fibrotic disease, asthma, inflammatory glomerulopathies, acquired
XX immune deficiency syndrome (AIDS), restenosis associated with vascular
XX intervention, including angioplasty and/or stent placement in a mammal.
XX Humanised antibodies are also useful for inhibiting narrowing of the
XX lumen of a vessel in a mammal, and inhibiting neointimal hyperplasia of
XX a vessel in a mammal, preferably associated with vascular intervention.
XX The present sequence is mouse germline heavy chain variable (VH)
XX region, VH183.13.
XX SQ Sequence 87 AA;
Query Match 92.9%; Score 52; DB 22; Length 87;
Best Local Similarity 90.0%; Pred. No. 0.027; Indels 0; Gaps 0;
Matches 9; Conservative 1; Mismatches 0;
QY 1 STYYPDTVQG 10
DQ 46 STYYPDTVKG 55
RESULT 7
AAE06978
ID AAE06978 standard; Protein; 98 AA.
XX AAE06978;
XX 16-OCT-2001 (first entry)
XX Mouse germline heavy chain variable (VH) region, V(H) 50.1.
XX Mous^g; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;
KW neuroprotective; immunosuppressive; human immunodeficiency virus;
KW HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;
KW inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;

KW multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma;
KW anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;
KW fibrotic disease; angioplasty; acquired immune deficiency syndrome;
KW AIDS; inflammatory glomerulopathy; vascular intervention;
KW neointimal hyperplasia; VH; heavy chain variable region.
XX
OS Mus sp.
XX WO200157226-A1.
XX 09-AUG-2001.
XX 02-FEB-2001; 2001WO-US03537.
XX 03-FEB-2000; 2000US-0497625.
XX (MILL-) MILLENNIUM PHARM INC.
XX Larosa GJ, Horvath C, Newman W, Jones ST, O'Brien S, O'Keefe T;
XX WPI; 2001-488888/53.
XX Humanized immunoglobulin for treating a CC-chemokine receptor
PT 2-mediated disorder in a patient, comprises a binding specificity for
PT CCR2, and a non-human antigen binding region and human immunoglobulin
PT -
XX Disclosure; Page 154-155; 183pp; English.
XX The patent discloses a humanised antibody or its antigen-binding
XX fragment, having binding specificity for CC-chemokine receptor 2
XX (CCR2), comprising an antigen binding region of non-human origin
XX and at least a portion of an immunoglobulin of human origin. The
XX humanised antibodies are useful for inhibiting the interaction of
XX a cell expressing CCR2. They are useful for inhibiting or treating
XX HIV infection. The proteins of the invention are useful for inhibiting
XX leukocyte trafficking, for treating CCR2-mediated disorders such as
XX inflammatory disorder, autoimmune disorders such as rheumatoid
XX arthritis and multiple sclerosis, atherogenesis and atherosclerosis,
XX and for inhibiting restenosis. They are useful in therapy or diagnosis,
XX and in the manufacture of a medicament for treating CCR2 mediated
XX disease. They are also useful for treating allergy, anaphylaxis,
XX malignancy, chronic and acute inflammation, histamine and IgE-
XX mediated allergic reaction, shock, stenosis, allograft rejection,
XX fibrotic disease, asthma, inflammatory glomerulopathies, acquired
XX immune deficiency syndrome (AIDS), restenosis associated with vascular
XX intervention, including angioplasty and/or stent placement in a mammal.
XX Humanised antibodies are also useful for inhibiting narrowing of the
XX lumen of a vessel in a mammal, and inhibiting neointimal hyperplasia of
XX a vessel in a mammal, preferably associated with vascular intervention.
XX The present sequence is mouse germline heavy chain variable (VH)
XX region, V(H)50.1.
XX SQ Sequence 98 AA;
Query Match 92.9%; Score 52; DB 22; Length 98;
Best Local Similarity 90.0%; Pred. No. 0.031;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 STYYPDTVQG 10
DQ 57 STYYPDTVKG 66
RESULT 8
AAU07743
ID AAU07743 standard; peptide; 112 AA.
XX AAU07743;
XX AAU07743;
XX 04-DEC-2001 (first entry)
XX Human heavy chain variable region derived from DP53/LH4 #2.

XX Light chain variable region: DPK18; Jkl; Hu266; nootropic;
 KW neuroprotective; Abeta peptide; Alzheimer's disease; Down's syndrome;
 KW cerebral amyloid angiopathy; antibody; gene therapy.
 XX
 OS Homo sapiens.
 OS Synthetic.
 PN WO200162801-A2.
 XX
 PD 30-AUG-2001.
 XX
 XX 26-FEB-2001; 2001WO-US06191.
 XX
 XX 24-FEB-2000; 2000US-0184601.
 PR 08-DEC-2000; 2000US-0254465.
 PR 08-DEC-2000; 2000US-0254498.
 XX
 XX (UNIV) UNIV WASHINGTON.
 PA (ELIL) LILLY & CO ELI.
 XX
 XX Holtzman DM, Demattos R, Bales KR, Paul SM, Tsurushita N;
 PI Vasquez M;
 XX
 XX WPI; 2001-550087/61.
 DR
 XX
 PT New humanised antibody for the treatment of Alzheimer's comprises the
 PT inhibition and reduction of the formation of amyloid plaques -
 XX
 XX Claim 16; Page 15-16; 63pp; English.
 PS
 XX
 CC The invention relates a humanised antibody that specifically binds
 CC an epitope contained within positions 13-28 of amyloid beta peptide,
 CC Abeta. The antibody is useful to inhibit and reduce the formation of
 CC amyloid plaques or the effects of toxic soluble Abeta species in humans
 CC their fragments are used for the manufacture of a medicant. This includes
 CC the prolonged expression of recombinant sequences of them in human
 CC tissues for the treatment of clinical/pre-clinical Alzheimer's disease,
 CC Down's syndrome or pre clinical cerebral amyloid angiopathy.
 CC Specifically, the antibody is used to sequester Abeta into plasma, brain
 CC or cerebrospinal fluid to prevent/reverse accumulation of the Abeta
 CC peptide within the brain thereby improving cognition. The present
 CC sequence is a humanised heavy chain variable region originating
 CC from germline VH segment Dp53 and J segment JH4, with several amino
 CC acid substitutions to reduce antigenicity.
 XX
 SQ Sequence 112 AA;
 Query Match 92.9%; Score 52; DB 22; Length 112;
 Best Local Similarity 90.0%; Pred. No. 0.035;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 STYYPDTVQG 10
 Db |||||:|
 57 STYYPDTVKG 66
 RESULT 9
 AAR79155
 ID AAR79155 standard; peptide; 117 AA.
 XX
 AC AAR79155;
 XX
 XX 04-MAR-1996 (first entry)
 DT
 XX
 DE Human IgE receptor-binding antibody-related peptide heavy chain.
 XX
 KW Immunoglobulin E; antibody; receptor; monoclonal; detection;
 KW complementarity determining region.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers

FT Region 31..35
 /label= CDR1H
 /note= "all CDR regions are claimed"
 FT 50..86
 /label= CDR2H
 /note= "all CDR regions are claimed"
 FT 99..106
 /label= CDR3H
 /note= "all CDR regions are claimed"
 XX
 PN JP07165799-A.
 XX
 XX 27-JUN-1995.
 PD
 XX 22-OCT-1993; 93JP-0264792.
 PF
 XX 22-OCT-1993; 93JP-0264792.
 PR
 XX (ASAK) ASahi BREWERIES LTD.
 PA (NIKK-) NIKKA WHISKEY KK.
 PA (TORI) TORII YAHUKIN KK.
 PA (TSUR/) TSURA T.
 XX
 DR WPI; 1995-261292/34.
 DR N-PSDB; AAQ96282.
 XX
 PT Novel monoclonal antibody against human high-affinity IgE receptor -
 PT and DNA fragment encoding the MAb, for the specific identification
 of human Fc-epsilon RI
 PT
 XX Claim 3; Page 13; 20pp; Japanese.
 PS
 XX Polypeptides which specifically recognise human IgE receptor (Fc-
 CC epsilon-RI) have been isolated and sequenced. The new peptides are
 CC related to a monoclonal antibody against Fc-epsilon-RI and are
 CC either heavy or light chain molecules. The heavy chain molecules
 CC have the general formula FRI-CDRIH-FR2-CDR2H-FR3-CDR3H-FR4 (corresp.
 CC to AAR79155, AAR79157, AAR79159 and AAR79161) and are encoded
 CC by AAQ96280, AAQ96282, AAQ96284, AAQ96286 and AAQ96288. FRI is a
 CC polypeptide having 29-36 amino acids (aa), FR2 is a 10-16 aa polypeptide,
 CC FR3 is a 33-35 aa polypeptide and FR4 is a 12-14 aa polypeptide.
 CC Similarly the light chains have the general formula
 CC FR5-CDRL1-FR6-CDRL2-FR7-CDR3L-FR8, (corresp. to AAR79154, AAR79156,
 CC AAR79158, AAR79160 and AAR79162) and are encoded by AAQ96281, AAQ96283,
 CC AAQ96285, AAQ96287 and AAQ96289. FR5 is a 23-28 aa polypeptide, FR6 is a
 CC 14-16 aa polypeptide, FR7 is a 30-34 aa polypeptide and FR8 is a 9-11 aa
 CC polypeptide. All the peptides are derived from mouse hybridoma cells and
 CC are useful in the detection of the human Fc-epsilon-RI or for the
 CC elucidation of an antigen recognising region of a monoclonal antibody
 CC against human Fc-epsilon-RI.
 XX
 SQ Sequence 117 AA;
 Query Match 92.9%; Score 52; DB 16; Length 117;
 Best Local Similarity 90.0%; Pred. No. 0.037;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 STYYPDTVQG 10
 Db |||||:|
 57 STYYPDTVKG 66
 RESULT 10
 AAW27357
 ID AAW27357 standard; Protein; 117 AA.
 XX
 AC AAW27357;
 XX
 DT 16-DEC-1997 (first entry)
 XX
 DE Heavy chain variable region of chimeric human CRA2 antibody.
 XX
 KW Complementarity determining region; CDR; murine; mouse; human;

region of the human antibody (Ab) CRA2, was used in the preparation of a humanised or semi-chimeric monoclonal Ab (MAB), comprising complementarity determining regions (CDR) from a murine, anti-human high affinity immunoglobulin E (IgE) receptor, MAB. The humanised, semi-chimeric or chimeric MAB can be used to treat or prevent diseases, specifically allergies, associated with the receptor, and has very low antigenicity in humans.

XX Sequence 117 AA;

Query Match 92.9%; Score 52; DB 18; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.037;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDTVQG 10
| | | | | | | | | |
DB 57 STYYPDTVKG 66

RESULT 13

AAR79161
ID AAR79161 standard; peptide: 118 AA.

AC AAR79161;

XX 04-MAR-1996 (first entry)

XX Human IgE receptor-binding antibody-related peptide heavy chain.

DE Immunoglobulin E; antibody; receptor; monoclonal; detection;

KW complementarity determining region.

XX Mus sp.

XX Key Location/Qualifiers

FT Region 29..33

FT /label= CDR1H

FT /note= "all CDR regions are claimed"

FT Region 48..64

FT /label= CDR2H

FT /note= "all CDR regions are claimed"

FT Region 97..107

FT /label= CDR3H

FT /note= "all CDR regions are claimed"

XX JP07165799-A.

XX 27-JUN-1995.

XX 22-OCT-1993; 93JP-0264792.

XX 22-OCT-1993; 93JP-0264792.

XX (ASAK) ASAKI BREWERIES LTD.

XX (NIKK-) NIKKA WHISKEY KK.

XX (TORI) TORII YAHUKIN KK.

XX (TSUR/) TSURA T.

XX WPI; 1995-261292/34.

XX N-PSDB; AAQ96288.

XX Novel monoclonal antibody against human high-affinity IgE receptor -

XX and DNA fragment encoding the MAB, for the specific identification

XX of human Fc-epsilon RI

XX Claim 9; Page 16; 20pp; Japanese.

XX Polypeptides which specifically recognise human IgE receptor (Fc-

XX epsilon-RI) have been isolated and sequenced. The new peptides are

XX related to a monoclonal antibody against Fc-epsilon-RI and are

XX either heavy or light chain molecules. The heavy chain molecules

XX have the general formula FR1-CDRIH-FR2-CDR2H-FR3-CDR3H-FR4 (corresp.

XX to AAR79153, AAR79155, AAR79157, AAR79159 and AAR79161), and are encoded

CC by AAQ96280, AAQ96282, AAQ96284, AAQ96286 and AAQ96288. FR1 is a

CC polypeptide having 29-36 amino acids (aa), FR2 is a 10-16 aa polypeptide,

CC FR3 is a 33-35 aa polypeptide and FR4 is a 12-14 aa polypeptide.

CC Similarly the light chains have the general formula

CC FR5-CDRIH-FR6-CDR2L-FR7- CDR3L-FR8, (corresp. to AAR79154, AAR79156,

CC AAR79158, AAR79160 and AAR79162) and are encoded by AAQ96281, AAQ96283,

CC AAQ96285, AAQ96287 and AAQ96289. FR5 is a 23-28 aa polypeptide, FR6 is a

CC 14-16 aa polypeptide, FR7 is a 30-34 aa polypeptide and FR8 is a 9-11 aa

CC polypeptide. All the peptides are derived from mouse hybridoma cells and

CC are useful in the detection of the human Fc-epsilon-RI or for the

CC elucidation of an antigen recognising region of a monoclonal antibody

CC against human Fc-epsilon-RI.

XX Sequence 118 AA;

Query Match 92.9%; Score 52; DB 16; Length 118;

Best Local Similarity 90.0%; Pred. No. 0.038;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDTVQG 10
| | | | | | | | | |

DB 55 STYYPDTVKG 64

RESULT 14

AAW00240

ID AAW00240 standard; Protein; 120 AA.

XX AC AAW00240;

XX 22-NOV-1996 (first entry)

XX EGF receptor chimeric MAB chMint5 VH chain.

XX Mouse-human chimeric antibody; monoclonal antibody; chMint5;

XX epidermal growth factor receptor; EGF-R; diagnosis; therapy;

XX Immunotoxin; immunocytokine; tumour; cancer.

XX Mus musculus.

XX Key Location/Qualifiers

FT Region 31..35

FT /label= CDR1

FT Region 51..66

FT /label= CDR2

FT Region 99..109

FT /label= CDR3

XX WO9627010-A1.

XX 06-SEP-1996.

XX 01-MAR-1996; 96WO-EP00805.

XX 01-MAR-1995; 95IT-0FI0036.

XX (ITUY-) ITAL MIN UNIV RICERCA SCI & TECNOLOGICA.

XX Anastasi AM, Colnaghi MI, De Santis R, Di Massimo AM;

XX Ferrer Marsal C, Mele A;

XX WPI; 1996-412776/41.

XX N-PSDB; AAT33445.

XX Murine/human chimeric monoclonal antibody, chMint5 specific for

XX EGF-R - shows a lower immunogenicity when administered to humans

XX Claim 7; Page 15; 28pp; English.

XX The amino acid sequence (AAW00240) of the heavy chain variable region

XX (VH) of the epidermal growth factor receptor (EGF-R)-specific mouse-

XX human chimeric antibody chMint5 was deduced from a cDNA clone

XX (AAT33445) obt'd. by PCR amplification of murine Mint5 hybridoma DSM

CC ACC2150 cDNA. chMint5 comprises Mint5 VH and VL regions fused
CC to human C-gamma1 and CK regions. Constructs were expressed in
CC CHO cell transfectants. chMint5 shows lower immunogenicity than
CC Mint5 when administered to humans. It can be used in diagnostic
CC assays or used to produce immunotoxins or immunocytokines useful
CC for tumour therapy.
XX
SQ Sequence 120 AA;

Query Match 92.9%; Score 52; DB 17; Length 120;
Best Local Similarity 90.0%; Pred. NO. 0.038;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDTVQG 10
|||||||:|
Db 57 STYYPDVTVGK 66

RESULT 15
AAB48937
ID AAB48937 standard; Protein: 125 AA.
XX AC
XX AAB48937;
XX
XX 16-MAR-2001 (first entry)
XX
XX Anti-TrkA murine monoclonal antibody MNAC13 light chain variable region.
XX
XX Murine monoclonal antibody MNAC13; heavy chain variable region; VH;
XX human TrkA antagonist; NGF receptor; nerve growth factor;
XX neurological pathology; acute pain; chronic pain; analgesic; neuroma;
XX cancer; TrkA-expressing tumour; gene therapy; in vivo imaging;
XX diagnosis.
XX
XX Mus sp.
XX
XX WO200073344-A2.
XX
XX 07-DEC-2000.
XX
XX 26-MAY-2000; 2000WO-IT00218.
XX
XX 26-MAY-1999; 99IT-RM00333.
XX
XX (SIRS-) SIRS SOC ITAL RICERCA SCI SRL.
XX
XX Novak MM;
XX
XX WPI; 2001-061515/07.
XX
XX N-PSDB; AAC87642.
XX
XX Monoclonal antibody and its derivatives specific to high affinity
XX tyrosine kinase receptor of nerve growth factor useful for treating and
XX diagnosing neuropathological disorders such as pain, neuromas, TrkA
XX expressing neoplastic tumors -
XX
XX Claim 3; Page -: 33pp; English.

CC The invention relates to a murine monoclonal antibody, MNAC13, which
CC recognises the human nerve growth factor (NGF) receptor tyrosine
CC kinase, TrkA, and acts as an antagonist of NGF/TrkA binding. MNAC13
CC has a light chain variable region (VL) as given in AAB48936, and a heavy
CC chain variable region (VH) as given in AAB48937. The invention also
CC encompasses synthetic derivatives of monoclonal antibody MNAC13, such as
CC the single chain antibody, scFvMNAC13 (AAB48934), which comprises the
CC VL and VH regions of MNAC13 in one polypeptide chain. The invention
CC additionally relates to pharmaceutical compositions comprising the
CC antibody or antibody derivatives of the invention, engineered eukaryotic
CC cells able to express the MNAC13 antibody or its derivatives, and a
CC diagnostic composition comprising the antibody or its derivatives for in
CC vivo imaging. NGF antagonist (inhibitor of binding of NGF to TrkA
CC receptor The MNAC13 monoclonal antibody and its derivatives are useful
CC for treating neurological pathologies such as acute or chronic pain,

CC neuromas, and TrkA-expressing neoplastic tumours. A composition
CC comprising MNAC13 or its derivatives with a diagnostically acceptable
CC carrier is useful for in vivo imaging diagnostics. The present
CC murine monoclonal antibody MNAC13.
CC Note: The present sequence is derived from that of the single chain
CC antibody scFvMNAC13 shown on pages 32-33 and the information given in
CC claim 3.
XX
SQ Sequence 125 AA;

Query Match 92.9%; Score 52; DB 22; Length 125;
Best Local Similarity 90.0%; Pred. NO. 0.04;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDTVQG 10
|||||||:|
Db 56 STYYPDVTVGK 65

Search completed: November 18, 2002, 17:31:35
Job time : 13.8235 secs

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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:54:45 ; Search time 1.96078 Seconds
(without alignments)
76.811 Million cell updates/sec

Title: US-09-016-061-56
Perfect score: 56
Sequence: 1 STYYPDTVQG 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 97044 seqs, 15060890 residues

Total number of hits satisfying chosen parameters: 97044

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB pep.*
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14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	52	92.9	87	10	US-09-840-459-53
2	52	92.9	98	10	US-09-840-459-41
3	48	85.7	88	10	US-09-840-459-51
4	48	85.7	89	10	US-09-840-459-48
5	48	85.7	443	10	US-09-917-410-4
6	46	82.1	117	8	US-09-790-540A-2
7	46	82.1	117	8	US-08-790-540A-6
8	46	82.1	117	8	US-08-791-391A-2
9	46	82.1	117	8	US-08-791-391A-6
10	45	80.4	17	10	US-09-286-240-21
11	45	80.4	98	10	US-09-840-459-44
12	45	80.4	120	10	US-09-229-200A-6
13	45	80.4	120	10	US-09-229-200A-24
14	45	80.4	120	10	US-09-229-200A-25
15	45	80.4	120	10	US-09-229-200A-27
16	45	80.4	120	10	US-09-229-200A-28
17	45	80.4	140	10	US-09-286-240-4
18	44	78.6	32	9	US-09-956-206A-35
19	44	78.6	89	10	US-09-840-459-49

20	44	78.6	98	10	US-09-840-459-38	Sequence 38, Appl
21	44	78.6	98	10	US-09-840-459-39	Sequence 39, Appl
22	44	78.6	98	10	US-09-840-459-45	Sequence 45, Appl
23	44	78.6	118	9	US-09-144-886-62	Sequence 62, Appl
24	44	78.6	118	9	US-09-144-886-63	Sequence 63, Appl
25	44	78.6	118	9	US-09-423-800-46	Sequence 46, Appl
26	44	78.6	118	9	US-09-423-800-56	Sequence 56, Appl
27	44	78.6	123	9	US-09-144-886-60	Sequence 60, Appl
28	44	78.6	137	9	US-09-423-800-76	Sequence 76, Appl
29	44	78.6	137	9	US-09-423-800-77	Sequence 77, Appl
30	44	78.6	140	12	US-10-006-773-4	Sequence 4, Appl
31	44	78.6	144	10	US-09-881-823-12	Sequence 12, Appl
32	41	73.2	124	10	US-09-840-459-81	Sequence 81, Appl
33	40	71.4	17	9	US-09-968-561A-14	Sequence 14, Appl
34	40	71.4	17	9	US-09-968-561A-38	Sequence 38, Appl
35	40	71.4	17	9	US-09-968-561A-68	Sequence 68, Appl
36	40	71.4	17	9	US-09-968-561A-74	Sequence 74, Appl
37	40	71.4	17	9	US-09-968-561A-80	Sequence 80, Appl
38	40	71.4	17	9	US-09-968-561A-86	Sequence 86, Appl
39	40	71.4	17	9	US-09-968-561A-92	Sequence 92, Appl
40	40	71.4	17	9	US-09-968-561A-122	Sequence 122, App
41	40	71.4	17	9	US-09-968-561A-128	Sequence 128, App
42	40	71.4	17	9	US-09-968-561A-134	Sequence 134, App
43	40	71.4	17	9	US-09-968-561A-140	Sequence 140, App
44	40	71.4	17	9	US-09-968-561A-146	Sequence 146, App
45	40	71.4	17	9	US-09-968-561A-188	Sequence 188, App

ALIGNMENTS

RESULT 1
US-09-840-459-53
; Sequence 53, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 53
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-840-459-53

Query Match 92.9%; Score 52; DB 10; Length 87;
Best Local Similarity 90.0%; Pred. No. 0.0065;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STYYPDTVQG 10

Db 46 STYYPDTVKG 55

RESULT 2

US-09-840-459-41
; Sequence 41, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840.459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 41
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-840-459-41

Query Match 92.9%; Score 52; DB 10; Length 98;
Best Local Similarity 90.0%; Pred. No. 0.0073;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STYYPDVTVOG 10
Db 57 STYYPDVTVKG 66

RESULT 3
US-09-840-459-51
; Sequence 51, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840.459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 51
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-840-459-51

Query Match * 85.7%; Score 48; DB 10; Length 88;

Best Local Similarity 80.0%; Pred. No. 0.034;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 STYYPDVTVOG 10
Db 47 STYYPDSVKG 56
RESULT 4
US-09-840-459-48
; Sequence 48, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840.459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 48
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-840-459-48

Query Match 85.7%; Score 48; DB 10; Length 89;
Best Local Similarity 80.0%; Pred. No. 0.035;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STYYPDVTVOG 10
Db 48 STYYPDSVKG 57

RESULT 5
US-09-917-410-4
; Sequence 4, Application US/09917410
; Patent No. US20020098183A1
; GENERAL INFORMATION:
; APPLICANT: MARTIN, Ulrich; HASELBECK, Anton; SCHUMACHER, Guenther;
; CO., Man S.
; TITLE OF INVENTION: ANTI-L-SELECTIN ANTIBODIES FOR PREVENTION OF
; MULTIPLE ORGAN FAILURE AFTER POLYTRAUMA AND FOR
; PREVENTION OF ACUTE ORGAN DAMAGE AFTER
; EXTRACORPOREAL BLOOD CIRCULATION
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Computer Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII, WordPerfect 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/917,410
FILING DATE: 26-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/578,953
FILING DATE: <Unknown>
APPLICATION NUMBER: EP 95 114 969.9
FILING DATE: 19-Sep-95
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. US20020098183Alman D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: BOER 1059-PFF/NDH/SLH
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 443
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-917-410-4

Query Match 85.7%; Score 48; DB 10; Length 443;
Best Local Similarity 80.0%; Pred. No. 0.19;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDVTQVG 10
|||||:|:|

Db 56 STYYPSVKG 65

RESULT 6
US-08-790-540A-2
; Sequence 2, Application US/08790540A
; Patent No. US2001001125A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,540A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-790-540A-2

Query Match 82.1%; Score 46; DB 8; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYPDVTQVG 10
|||||:|:|

Db 57 STYYLDTVQG 66

RESULT 7
US-08-790-540A-6
; Sequence 6, Application US/08790540A
; Patent No. US2001001125A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,540A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-790-540A-6

Query Match 82.1%; Score 46; DB 8; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYPDVTQVG 10
|||||:|:|

Db 57 STYYLDTVQG 66

RESULT 8
US-08-791-391A-2
; Sequence 2, Application US/08791391A
; Patent No. US20010016645A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700

```
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791.391A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-391A-2

Query Match      82.1%; Score 46; DB 8; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 STYYPDVTQV 10
Db 57 STYILDVTQV 66

RESULT 9
US-08-791-391A-6
; Sequence 6, Application US/08791391A
; Patent No. US20010016645A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791.391A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-391A-6

Query Match      82.1%; Score 46; DB 8; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 STYYPDVTQV 10
Db 57 STYILDVTQV 66

RESULT 10
US-09-286-240-21
; Sequence 21, Application US/09286240
; Patent No. US20020010320A1
; GENERAL INFORMATION:
; APPLICANT: Fett, James W
; TITLE OF INVENTION: Chimeric and Humanized Antibodies to Angiogenin
; FILE REFERENCE: 10498/74073
; CURRENT APPLICATION NUMBER: US/09/286,240
; CURRENT FILING DATE: 1999-04-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
US-09-286-240-21

Query Match      80.4%; Score 45; DB 10; Length 17;
Best Local Similarity 70.0%; Pred. No. 0.021;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STYYPDVTQV 10
Db 8 NTYYPDSVKG 17

RESULT 11
US-09-840-459-44
; Sequence 44, Application US/09840459
; Patent No. US20020150376A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 44
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-840-459-44
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Query Match 80.4%; Score 45; DB 10; Length 98;
Best Local Similarity 70.0%; Pred. No. 0.16;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDVTQV 10
Db :||||:|
57 NTYYPDSVK 66

RESULT 12

US-09-229-200A-6
; Sequence 6, Application US/09229200A
; Patent No. US20020099179A1
; GENERAL INFORMATION:
; APPLICANT: Jolliffe et al.
; TITLE OF INVENTION: CD4 Specific Recombinant Antibody
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Johnson & Johnson
; STREET: One Johnson & Johnson Plaza
; CITY: New Brunswick
; STATE: NJ
; COUNTRY: USA
; ZIP: 08933-7003

COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: <Unknown>

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/229,200A
FILING DATE: 13-Jan-1999
CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: John W. Wallen, III
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: ORT-948

TELECOMMUNICATION INFORMATION:
TELEPHONE: (858) 784-3239
TELEFAX: (908) 524-2808
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 120
TYPE: amino acid
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Query Match 80.4%; Score 45; DB 10; Length 120;
Best Local Similarity 70.0%; Pred. No. 0.16;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDVTQV 10
Db :||||:|
57 NTYYPDSVK 66

RESULT 13

US-09-229-200A-24
; Sequence 24, Application US/09229200A
; Patent No. US20020099179A1
; GENERAL INFORMATION:
; APPLICANT: Jolliffe et al.
; TITLE OF INVENTION: CD4 Specific Recombinant Antibody
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Johnson & Johnson
; STREET: One Johnson & Johnson Plaza
; CITY: New Brunswick
; STATE: NJ
; COUNTRY: USA
; ZIP: 08933-7003

COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: <Unknown>

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/229,200A
FILING DATE: 13-Jan-1999
CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: John W. Wallen, III
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: ORT-948

TELECOMMUNICATION INFORMATION:
TELEPHONE: (858) 784-3239
TELEFAX: (908) 524-2808

INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 120
TYPE: amino acid
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 24:

US-09-229-200A-24

Query Match 80.4%; Score 45; DB 10; Length 120;
Best Local Similarity 70.0%; Pred. No. 0.16;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDVTQV 10
Db :||||:|
57 NTYYPDSVK 66

RESULT 14

US-09-229-200A-25
; Sequence 25, Application US/09229200A
; Patent No. US20020099179A1
; GENERAL INFORMATION:

APPLICANT: Jolliffe et al.
TITLE OF INVENTION: CD4 Specific Recombinant Antibody
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:

ADDRESSEE: Johnson & Johnson
STREET: One Johnson & Johnson Plaza
CITY: New Brunswick
STATE: NJ
COUNTRY: USA
ZIP: 08933-7003

COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: <Unknown>

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/229,200A
FILING DATE: 13-Jan-1999
CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: John W. Wallen, III
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: ORT-948

TELECOMMUNICATION INFORMATION:
TELEPHONE: (858) 784-3239
TELEFAX: (908) 524-2808

INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 120
TYPE: amino acid
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 25:

US-09-229-200A-25

Query Match 80.4%; Score 45; DB 10; Length 120;

Best Local Similarity 70.0%; Pred. No. 0.16;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDVQ 10
:||||:|
Db 57 NTYYPSVK 66

RESULT 15

US-09-229-200A-27
; Sequence 27, Application US/09229200A
; Patent No. US20020099179A1
; GENERAL INFORMATION:
; APPLICANT: Jolliffe et al.
; TITLE OF INVENTION: CD4 Specific Recombinant Antibody
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Johnson & Johnson
; STREET: One Johnson & Johnson Plaza
; CITY: New Brunswick
; STATE: NJ
; COUNTRY: USA
; ZIP: 08933-7003
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/229, 200A
; FILING DATE: 13-Jan-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: John W. Wallen, III
; REGISTRATION NUMBER: 35,403
; REFERENCE/DOCKET NUMBER: ORT-948
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (858) 784-3239
; TELEFAX: (908) 524-2808
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-09-229-200A-27

Query Match 80.4%; Score 45; DB 10; Length 120;
Best Local Similarity 70.0%; Pred. No. 0.16;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDVQ 10
:||||:|
Db 57 NTYYPSVK 66

Search completed: November 18, 2002, 18:45:14
Job time : 2.96078 secs

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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:01 ; Search time 4.2402 Seconds
(without alignments)
69.390 Million cell updates/sec

Title: US-09-016-061-56

Perfect score: 56

Sequence: 1 STYPPDTVQC 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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- 2: /cgn2_6/ptodata/1/iaa/5B-COMB.pep:*
- 3: /cgn2_6/ptodata/1/iaa/6A-COMB.pep:*
- 4: /cgn2_6/ptodata/1/iaa/6B-COMB.pep:*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS-COMB.pep:*
- 6: /cgn2_6/ptodata/1/iaa/backfiles.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	92.9	125	1	US-08-331-398A-65
2	52	92.9	125	2	US-08-331-397B-65
3	52	92.9	125	2	US-08-759-804A-64
4	52	92.9	158	2	US-08-653-402B-6
5	52	92.9	158	2	US-08-653-402B-10
6	48	85.7	119	5	PCT-US94-07659-6
7	48	85.7	121	1	US-08-339-582-2
8	48	85.7	130	1	US-08-398-613A-22
9	48	85.7	130	1	US-08-398-612A-22
10	48	85.7	130	1	US-08-398-611A-22
11	48	85.7	130	2	US-08-491-334A-22
12	48	85.7	130	3	US-09-027-449-19
13	48	85.7	130	3	US-08-804-444A-19
14	48	85.7	130	4	US-09-026-985-19
15	48	85.7	130	4	US-09-121-952A-19
16	48	85.7	130	4	US-09-234-340A-19
17	48	85.7	135	4	US-08-579-378A-16
18	48	85.7	135	4	US-08-579-378A-20
19	48	85.7	138	2	US-08-379-057-14
20	48	85.7	247	5	PCT-US94-07659-2
21	48	85.7	251	1	US-08-398-612A-30
22	48	85.7	251	1	US-08-398-611A-30
23	48	85.7	251	2	US-08-491-334A-30
24	48	85.7	251	3	US-09-027-449-27
25	48	85.7	251	3	US-08-804-444A-27
26	48	85.7	251	4	US-09-026-985-27
27	48	85.7	251	4	US-09-121-952A-27

28	48	85.7	251	4	US-09-234-340A-27	Sequence 27, Appl
29	48	85.7	252	1	US-08-398-613A-30	Sequence 30, Appl
30	48	85.7	443	5	PCT-US96-13152-4	Sequence 4, Appl
31	46	82.1	17	5	PCT-US93-08435-18	Sequence 18, Appl
32	46	82.1	118	5	PCT-US93-08435-10	Sequence 10, Appl
33	46	82.1	122	5	PCT-US93-08435-12	Sequence 12, Appl
34	46	82.1	122	5	PCT-US93-08435-14	Sequence 14, Appl
35	46	82.1	122	5	PCT-US93-08435-43	Sequence 43, Appl
36	45	80.4	119	2	US-08-475-000-16	Sequence 16, Appl
37	45	80.4	119	2	US-08-483-199-16	Sequence 16, Appl
38	45	80.4	119	2	US-08-484-508-16	Sequence 16, Appl
39	45	80.4	467	1	US-08-704-744-81	Sequence 81, Appl
40	44	78.6	16	4	US-09-170-769A-11	Sequence 11, Appl
41	44	78.6	30	4	US-09-336-093-4	Sequence 4, Appl
42	44	78.6	32	4	US-08-525-539A-35	Sequence 35, Appl
43	44	78.6	109	2	US-08-793-490-6	Sequence 6, Appl
44	44	78.6	113	1	US-07-789-344A-10	Sequence 10, Appl
45	44	78.6	116	2	US-08-888-366-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-08-331-398A-65
; Sequence 65, Application US/08331398A
; Patent No. 5608039
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Willingham, Mark
; APPLICANT: Fitzgerald, David
; APPLICANT: Brinkmann, Ulrich
; APPLICANT: Pai, Lee
; TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins
; TITLE OF INVENTION: and Their Uses (as amended)
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,398A
FILING DATE: 28-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 015280-1261100S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 125 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:

NAME/KEY: Region
LOCATION: 1..125
OTHER INFORMATION: /note= "Mouse monoclonal antibody B5 Fv
OTHER INFORMATION: Heavy chain region"
US-08-331-398A-65

Query Match 92.9%; Score 52; DB 1; Length 125;
Best Local Similarity 90.0%; Pred. No. 0.039;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STYYPDTVQG 10
|||||||:|
Db 57 STYYPDTVKG 66

RESULT 2

US-08-331-397B-65
; Sequence 65, Application US/08331397B
; Patent No. 5981726
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Benhar, Itai
; TITLE OF INVENTION: Chimeric and Mutationally Stabilized Tumor-
; TITLE OF INVENTION: Specific Antibody Fragments, Fusion Proteins, and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,397B
; FILING DATE: 28-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA: US 07/596,289
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 015280-126120US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 125 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..125
; OTHER INFORMATION: /note= "Mouse monoclonal antibody B5 Fv
; OTHER INFORMATION: Heavy chain region"
US-08-331-397B-65

Query Match 92.9%; Score 52; DB 2; Length 125;
Best Local Similarity 90.0%; Pred. No. 0.039;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STYYPDTVQG 10
|||||||:|
Db 57 STYYPDTVKG 66

RESULT 3
US-08-759-804A-64
; Sequence 64, Application US/08759804A
; Patent No. 5990296
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Willingham, Mark
; APPLICANT: Fitzgerald, David J.
; APPLICANT: Brinkmann, Ulrich
; APPLICANT: Pai, Lee
; TITLE OF INVENTION: Tumor-Specific Antibody Fragments,
; TITLE OF INVENTION: Fusion Proteins, and Uses Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/759,804A
; FILING DATE: 03-DEC-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/331,398
; FILING DATE: 28-OCT-1994
; PRIOR APPLICATION DATA: US 07/767,331
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA: US 07/596,289
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen L. 32,762
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 015280-126140US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 125 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..125
; OTHER INFORMATION: /note= "Mouse monoclonal antibody B5 Fv
; OTHER INFORMATION: Heavy chain region"
US-08-759-804A-64

Query Match 92.9%; Score 52; DB 2; Length 125;
Best Local Similarity 90.0%; Pred. No. 0.039;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STYYPDTVQG 10
|||||||:|
Db 57 STYYPDTVKG 66

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RESULT 4
US-08-653-402B-6
; Sequence 6, Application US/08653402B
; Patent No. 5969107
; GENERAL INFORMATION:
; APPLICANT: CARCELLER, Ana
; APPLICANT: ROSELL, Elisabeth
; APPLICANT: GOMEZ, Alicia
; APPLICANT: ADEN, Jaume
; APPLICANT: PIULATS, Jaume
; TITLE OF INVENTION: Anti-idiotypic antibodies which induce an
; immune response against epidermal growth factor receptor.
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
; STREET: 2200 Clarendon Boulevard, Suite 1400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/653,402B
; FILING DATE: 24-MAY-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95107967.2
; FILING DATE: 26-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lebovitz, Richard M.
; REGISTRATION NUMBER: 37,067
; REFERENCE/DOCKET NUMBER: MERCK 1781
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-243-6410
; TELEFAX: 703-243-6410
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 158 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-653-402B-6

Query Match 92.9%; Score 52; DB 2; Length 158;
Best Local Similarity 90.0%; Pred. No. 0.049;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDTVQG 10
Db 76 STYYPDTVKG 85

RESULT 5
US-08-653-402B-10
; Sequence 10, Application US/08653402B
; Patent No. 5969107
; GENERAL INFORMATION:
; APPLICANT: CARCELLER, Ana
; APPLICANT: ROSELL, Elisabeth
; APPLICANT: GOMEZ, Alicia
; APPLICANT: ADEN, Jaume
; APPLICANT: PIULATS, Jaume
; TITLE OF INVENTION: Anti-idiotypic antibodies which induce an
; immune response against epidermal growth factor receptor.
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
; STREET: 2200 Clarendon Boulevard, Suite 1400
; CITY: Arlington

Query Match 92.9%; Score 52; DB 2; Length 158;
Best Local Similarity 90.0%; Pred. No. 0.049;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDTVQG 10
Db 76 STYYPDTVKG 85

RESULT 6
PCT-US94-07659-6
; Sequence 6, Application PC/TUS9407659
; GENERAL INFORMATION:
; APPLICANT: Young, Peter
; APPLICANT: Gross, Mitchell
; APPLICANT: Jonak, Zdenka L.
; APPLICANT: Theisen, Timothy
; APPLICANT: Hurie, Mark
; APPLICANT: Jackson, Jeffrey R.
; TITLE OF INVENTION: Recombinant and Humanized Il-1 beta
; Antibodies for Treatment of Il-1 Mediated Inflammatory
; Disorders in Man
; TITLE OF INVENTION: Disorders in Man
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation - Corp.
; ADDRESSEE: Intellectual Property
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07659
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 158 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-653-402B-6

Query Match 92.9%; Score 52; DB 2; Length 158;
Best Local Similarity 90.0%; Pred. No. 0.049;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDTVQG 10
Db 76 STYYPDTVKG 85
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ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50171-1
TELEPHONE: (610) 270-5024
TELEFAX: (610) 270-5090
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
MOLECULE TYPE: protein
PCT-US94-07659-6

Query Match 85.7%; Score 48; DB 5; Length 119;
Best Local Similarity 88.9%; Pred. No. 0.18;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 TYPDPTVQG 10
Db 58 TYPDPTVKG 66

RESULT 7
US-08-339-582-2
Sequence 2, Application US/08339582
Patent No. 5558852
GENERAL INFORMATION:
APPLICANT: Bigner, Dorell D.
APPLICANT: Zalutsky, Michael R.
APPLICANT: Carrel, Stefan
TITLE OF INVENTION: METHOD OF TREATMENT
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenneth D. Sibley
STREET: P.O. Drawer 34009
CITY: Charlotte
STATE: No. 5558852th Carolina
COUNTRY: USA
ZIP: 28234

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/339,582
FILING DATE:

CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/033,864
FILING DATE: 19-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5405-89
TELEPHONE: 919-420-2200
TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: amino acid
MOLECULE TYPE: protein

US-08-339-582-2
Query Match 85.7%; Score 48; DB 1; Length 121;
Best Local Similarity 80.0%; Pred. No. 0.18;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDPTVQG 10

Db 60 STYYPDPSVKG 69

RESULT 8

US-08-398-613A-22
Sequence 22, Application US/08398613A
Patent No. 5677426
GENERAL INFORMATION:
APPLICANT: Fong, Sherman
APPLICANT: Hebert, Caroline Alice
APPLICANT: Kim, Kyung Jin
APPLICANT: Leong, Steven R.
TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for Treatment of Inflammatory Disorders
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/398,613A
FILING DATE: 01-MAR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/205864
FILING DATE: 03-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 874P1-3
TELEPHONE: 415/225-1489
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
TOPOLOGY: linear

US-08-398-613A-22
Query Match 85.7%; Score 48; DB 1; Length 130;
Best Local Similarity 80.0%; Pred. No. 0.2;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDPTVQG 10
Db 57 STYYPDPSVKG 66

RESULT 9

US-08-398-612A-22
Sequence 22, Application US/08398612A
Patent No. 5686070
GENERAL INFORMATION:
APPLICANT: Doershuk, Claire M.
APPLICANT: Fong, Sherman
APPLICANT: Hebert, Caroline Alice
APPLICANT: Kim, Kyung Jin
APPLICANT: Leong, Steven R.
TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for Treatment of Inflammatory Disorders
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/398,612A
FILING DATE: 01-MAR-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/398611
FILING DATE: 01-MAR-1995
APPLICATION NUMBER: 08/205864
FILING DATE: 03-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P0874P1
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-398-612A-22

Query Match 85.7%; Score 48; DB 1; Length 130;
Best Local Similarity 80.0%; Pred. No. 0.2;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STYYPDTVQG 10
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Db 57 STYYPDSVKG 66

RESULT 10
US-08-398-611A-22
Sequence 22, Application US/08398611A
Patent No. 5702946
GENERAL INFORMATION:
APPLICANT: Doershuk, Claire M.
APPLICANT: Fong, Sherman
APPLICANT: Hebert, Caroline Alice
APPLICANT: Kim, Kyung Jin
APPLICANT: Leong, Steven R.
TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for Treatment
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/398,611A
FILING DATE: 01-MAR-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/205864
FILING DATE: 03-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P0874P1
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-398-611A-22

Query Match 85.7%; Score 48; DB 1; Length 130;
Best Local Similarity 80.0%; Pred. No. 0.2;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STYYPDTVQG 10
|||||:|:
Db 57 STYYPDSVKG 66

RESULT 11
US-08-491-334A-22
Sequence 22, Application US/08491334A
Patent No. 5874080
GENERAL INFORMATION:
APPLICANT: Hebert, Caroline A.
APPLICANT: Kabakoff, Rhona C.
APPLICANT: Moore, Mark W.
TITLE OF INVENTION: IL-8 Antagonists for Treatment of Inflammatory
Disorders and Asthma
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/491,334A
FILING DATE: 27-Jun-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/398611
FILING DATE: 01-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/205864
FILING DATE: 03-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P0874P2
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-491-334A-22

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Query Match      85.7%; Score 48; DB 2; Length 130;
Best Local Similarity 80.0%; Pred. No. 0.2;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDTRVQG 10
   |||||:|:|
Db 57 STYYPDSVKG 66

RESULT 12
US-09-027-449-19
; Sequence 19, Application US/09027449
; Patent No. 6025158
; GENERAL INFORMATION:
; APPLICANT: Gonzalez, Tania R.
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA: US/09/027,449
; APPLICATION NUMBER: 60/074,330
; FILING DATE: 20-Feb-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/074,330
; FILING DATE: 22-Jan-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/038,664
; FILING DATE: 21-Feb-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: PI085R3-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 130 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-027-449-19

Query Match      85.7%; Score 48; DB 3; Length 130;
Best Local Similarity 80.0%; Pred. No. 0.2;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDTRVQG 10
   |||||:|:|
Db 57 STYYPDSVKG 66

RESULT 13
US-08-804-444A-19
; Sequence 19, Application US/0880444A
; Patent No. 6117980
; GENERAL INFORMATION:
; APPLICANT: Gonzalez, Tania N
; APPLICANT: Leong, Steven R.

```

```

; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA: US/08/804,444A
; APPLICATION NUMBER: US/08/804,444A
; FILING DATE: 21-Feb-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: PI085
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 130 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-804-444A-19

Query Match      85.7%; Score 48; DB 3; Length 130;
Best Local Similarity 80.0%; Pred. No. 0.2;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDTRVQG 10
   |||||:|:|
Db 57 STYYPDSVKG 66

RESULT 14
US-09-026-985-19
; Sequence 19, Application US/09026985
; Patent No. 6133426
; GENERAL INFORMATION:
; APPLICANT: Gonzalez, Tania R.
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/026,985
; FILING DATE: 20-Feb-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: PI085R3-1

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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-026-985-19

Query Match 85.7%; Score 48; DB 4; Length 130;
Best Local Similarity 80.0%; Pred. No. 0.2;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STYYPDVVG 10
Db 57 STYYPDSVKG 66

RESULT 15

US-09-121-952A-19
Sequence 19, Application US/09121952A
Patent No. 6458355
GENERAL INFORMATION:
APPLICANT: Genentech, Inc., Hsei, Vanessa
APPLICANT: Koumenis, Iphigenia
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
APPLICANT: Shahrokh, Zahra
APPLICANT: Zapata, Gerardo A.
TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/121,952A
FILING DATE: 24-Jul-1998
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/074330
FILING DATE: 22-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/075467
FILING DATE: 20-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-121-952A-19

Query Match 85.7%; Score 48; DB 4; Length 130;
Best Local Similarity 80.0%; Pred. No. 0.2;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STYYPDVVG 10
Db 57 STYYPDSVKG 66

Search completed: November 18, 2002, 17:43:34
Job time : 4.2402 secs

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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:01 ; Search time 4.90196 Seconds
(without alignments)
196.114 Million cell updates/sec

Title: US-09-016-061-58
Perfect score: 53
Sequence: 1 STYYLDTVEG 10

Scoring table: BLOSUM62
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Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

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Listing first 45 summaries

Database :

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- 3: PIR3:*
- 4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	43	81.1	83	2 S21593	Ig heavy chain V r
2	42	79.2	111	2 S51211	Ig heavy chain V r
3	42	79.2	113	2 S02717	Ig heavy chain V r
4	42	79.2	113	2 S26468	Ig heavy chain V r
5	42	79.2	115	2 PH1538	Ig H chain V regio
6	42	79.2	117	1 HVMSRF	Ig heavy chain pre
7	42	79.2	117	1 HVMS84	Ig heavy chain pre
8	42	79.2	117	1 HVMS34	Ig heavy chain pre
9	42	79.2	117	2 PH1552	Ig H chain V regio
10	42	79.2	119	2 PH1548	Ig H chain V regio
11	42	79.2	119	2 PH1549	Ig H chain V regio
12	41	77.4	92	2 S56009	Ig heavy chain var
13	41	77.4	150	2 I47200	Ig heavy chain var
14	40	75.5	90	2 S24248	Ig heavy chain V r
15	40	75.5	97	2 S26935	Ig heavy chain V r
16	40	75.5	97	2 S46462	Ig heavy chain V r
17	40	75.5	98	2 S26929	Ig heavy chain V r
18	40	75.5	98	2 S26889	Ig heavy chain V r
19	40	75.5	98	2 S54856	Ig heavy chain V r
20	40	75.5	99	2 S24259	Ig heavy chain V r
21	40	75.5	100	2 S24258	Ig heavy chain V r
22	40	75.5	101	2 S24257	Ig heavy chain V r
23	40	75.5	102	2 S24260	Ig heavy chain V r
24	40	75.5	104	2 S24255	Ig heavy chain V r
25	40	75.5	105	2 S24249	Ig heavy chain V r
26	40	75.5	106	2 S24256	Ig heavy chain V r
27	40	75.5	108	2 PH1648	Ig heavy chain V r
28	40	75.5	109	2 PH1649	Ig heavy chain V r
29	40	75.5	109	2 S24254	Ig heavy chain V r

30	40	75.5	109	2 S24253	Ig heavy chain V r
31	40	75.5	110	2 S24250	Ig heavy chain V r
32	40	75.5	112	2 PH1647	Ig heavy chain V r
33	40	75.5	113	2 S24247	Ig heavy chain V r
34	40	75.5	115	2 S09382	Ig heavy chain - c
35	40	75.5	116	2 B28966	Ig heavy chain pre
36	40	75.5	116	2 S31110	Ig heavy chain - h
37	40	75.5	117	2 A45953	Ig heavy chain pre
38	40	75.5	117	2 A34964	Ig heavy chain pre
39	40	75.5	118	2 S00700	Ig heavy chain V r
40	40	75.5	118	2 S31121	Ig heavy chain - h
41	40	75.5	119	2 C36005	Ig heavy chain V r
42	40	75.5	119	2 D36005	Ig heavy chain V r
43	40	75.5	119	2 S31107	Ig heavy chain - h
44	40	75.5	119	2 S31108	Ig heavy chain - h
45	40	75.5	120	2 S48798	Ig heavy chain V r

ALIGNMENTS

RESULT 1

S21593
Ig heavy chain V region (10C5) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C:Accession: S21593
R:Kaartinen, M.
submitted to the EMBL Data Library, May 1992
A:Reference number: S21591
A:Accession: S21593
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-83 <KAA>
A:Cross-references: EMBL:X66457; NID:g51598; PIDN:CAA47072.1; PID:g51599
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 81.1%; Score 43; DB 2; Length 83;
Best Local Similarity 80.0%; Pred. No. 0.42;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 STYYLDTVEG 10
||||| :|||:
Db 27 STYVSQTVKG 36

RESULT 2

S51211
Ig heavy chain V region (AC7) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 01-Aug-1995 #sequence_revision 01-Dec-1995 #text_change 30-May-1997
C:Accession: S51211; S58929
R:Jarrin, A.; Andrieux, A.; Chapel, A.; Buchou, T.; Marguerie, G.
FEBS Lett. 354, 169-172, 1994
A:Title: A synthetic peptide with anti-platelet activity derived from a CDR of an ant
A:Reference number: S51210; MUID:95046326; PMID:7957919
A:Accession: S51211
A:Molecule type: mRNA
A:Residues: 9-111 <JAR>
A:Accession: S58929
A:Molecule type: protein
A:Residues: 1-20 <JAR2>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 79.2%; Score 42; DB 2; Length 111;
Best Local Similarity 80.0%; Pred. No. 0.88;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 STYYLDTVEG 10
||||| :|||:
Db 27 STYVSQTVKG 36

```
Db 57 STYYPDTVKG 66

RESULT 3
Ig heavy chain V region (clone pH62) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000
C:Accession: S02717
R:Sollazzo, M.; Hasemann, C.A.; Meek, K.D.; Glotz, D.; Capra, J.D.; Zanetti, M.
submitted to the EMBL Data Library, February 1989
A:Reference number: S02717
A:Accession: S02717
A:Molecule type: DNA
A:Residues: 1-113 <SOL>
A:Cross-references: EMBL:X00744; NID:g52472; PIDN:CAA68713.1; PID:g1334095
A:Note: this sequence was determined from the differentiated gene
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 79.2%; Score 42; DB 2; Length 113;
Best Local Similarity 80.0%; Pred. No. 0.9;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYLDTVEG 10
|||||
Db 57 STYYPDTVKG 66

RESULT 4
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S26468
R:Kavaler, J.
submitted to the EMBL Data Library, April 1991
A:Reference number: S26459
A:Accession: S26468
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-113 <KAV>
A:Cross-references: EMBL:X59107; NID:g51944; PIDN:CAA41833.1; PID:g51945
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:11-94/Domain: immunoglobulin homology <IMM>

Query Match 79.2%; Score 42; DB 2; Length 113;
Best Local Similarity 80.0%; Pred. No. 0.9;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYLDTVEG 10
|||||
Db 53 STYYPDTVKG 62

RESULT 5
Ig H chain V region (clone 13G12) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 21-Jan-2000
C:Accession: PH1538
R:Mukherjee, J.; Casadevall, A.; Scharff, M.D.
J. Exp. Med. 177, 1105-1116, 1993
A:Title: Molecular characterization of the humoral responses to Cryptococcus neoformans
A:Reference number: PH1528; MUID:93210465; PMID:8459205
A:Accession: PH1538
A:Molecule type: mRNA
A:Residues: 1-115 <MUK>
A:Note: the stop codons X appear in residues 82, 85 and 106
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
```

```
F:14-99/Domain: immunoglobulin homology <IMM>

Query Match 79.2%; Score 42; DB 2; Length 115;
Best Local Similarity 80.0%; Pred. No. 0.92;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYLDTVEG 10
|||||
Db 56 STYYPDTVKG 65

RESULT 6
HMSRF
Ig heavy chain precursor V region (RF) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 31-Mar-1997
C:Accession: JT0503
R:Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.
J. Exp. Med. 169, 2007-2019, 1989
A:Title: Early onset of somatic mutation in immunoglobulin VH genes during the primar
A:Reference number: JT0501; MUID:89279149; PMID:2499654
A:Accession: JT0503
A>Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-117 <LEV>
A:Experimental source: strain BALB/cJ
A:Note: this sequence belongs to the VH7183 subfamily
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; hybridoma; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <Sig>
F:20-117/Product: Ig heavy chain V region (RF) #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>
F:41-115/Disulfide bonds: #status predicted

Query Match 79.2%; Score 42; DB 1; Length 117;
Best Local Similarity 80.0%; Pred. No. 0.93;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYLDTVEG 10
|||||
Db 76 STYYPDTVKG 85

RESULT 7
HMS84
Ig heavy chain precursor V region (5-84) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 31-Mar-1997
C:Accession: JT0505
R:Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.
J. Exp. Med. 169, 2007-2019, 1989
A:Title: Early onset of somatic mutation in immunoglobulin VH genes during the primar
A:Reference number: JT0501; MUID:89279149; PMID:2499654
A:Accession: JT0505
A>Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-117 <LEV>
A:Experimental source: strain BALB/cJ
A:Note: this sequence belongs to the VH7183 subfamily
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <Sig>
F:20-117/Product: Ig heavy chain V region (5-84) #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>
F:41-115/Disulfide bonds: #status predicted

Query Match 79.2%; Score 42; DB 1; Length 117;
Best Local Similarity 80.0%; Pred. No. 0.93;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYLDTVEG 10
|||||
Db 76 STYYPDTVKG 85
```

RESULT 8

HVMS34
Ig heavy chain precursor V region (345) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 31-Mar-1997
C:Accession: J0502
R;Levy, N.S.; Maipietro, U.V.; Lebecque, S.G.; Gearhart, P.J.
J. Exp. Med. 169, 2007-2019, 1989
A:Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary
A:Reference number: J0501; MUID:89279149; PMID:2499654
A:Accession: J0502
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-117 <LEV>
A:Experimental source: strain BALB/cJ
A:Note: this sequence belongs to the VH7183 subfamily
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-117/Product: Ig heavy chain V region (345) #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>
F:41-115/Disulfide bonds: #status predicted

Query Match 79.2%; Score 42; DB 1; Length 117;
Best Local Similarity 80.0%; Pred. No. 0.93;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 STYYLDTVEG 10

||||| |||:|

Db 76 STYYPDTVKG 85

RESULT 9

PH1552
Ig H chain V region (clone 16E4) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 21-Jan-2000
C:Accession: PH1552
R;Mukherjee, J.; Casadevall, A.; Scharff, M.D.
J. Exp. Med. 177, 1105-1116, 1993
A:Title: Molecular characterization of the humoral responses to Cryptococcus neoformans
A:Reference number: PH1528; MUID:93210465; PMID:8459205
A:Accession: PH1552
A:Molecule type: mRNA
A:Residues: 1-117 <MUK>
A:Note: the stop codon X appears in residue 87
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:15-97/Domain: immunoglobulin homology <IMM>

Query Match 79.2%; Score 42; DB 2; Length 117;
Best Local Similarity 80.0%; Pred. No. 0.93;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 STYYLDTVEG 10

||||| |||:|

Db 57 STYYPDTVKG 66

RESULT 10

PH1548
Ig H chain V region (clone 12F4) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 17-Mar-1999
C:Accession: PH1548
R;Mukherjee, J.; Casadevall, A.; Scharff, M.D.
J. Exp. Med. 177, 1105-1116, 1993
A:Title: Molecular characterization of the humoral responses to Cryptococcus neoformans
A:Reference number: PH1528; MUID:93210465; PMID:8459205
A:Accession: PH1548
A:Molecule type: mRNA

A:Residues: 1-119 <MUK>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 79.2%; Score 42; DB 2; Length 119;
Best Local Similarity 80.0%; Pred. No. 0.95;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 STYYLDTVEG 10

||||| |||:|

Db 57 STYYPDTVKG 66

RESULT 11

PH1549
Ig H chain V region (clone 13F1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 17-Mar-1999
C:Accession: PH1549
R;Mukherjee, J.; Casadevall, A.; Scharff, M.D.
J. Exp. Med. 177, 1105-1116, 1993
A:Title: Molecular characterization of the humoral responses to Cryptococcus neoformans
A:Reference number: PH1528; MUID:93210465; PMID:8459205
A:Accession: PH1549
A:Molecule type: mRNA
A:Residues: 1-119 <MUK>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 79.2%; Score 42; DB 2; Length 119;
Best Local Similarity 80.0%; Pred. No. 0.95;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 STYYLDTVEG 10

||||| |||:|

Db 57 STYYPDTVKG 66

RESULT 12

S56009
Ig heavy chain variable region against dystrophin - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 07-May-1999
C:Accession: S56009
R;Morris, G.E.; Nguyen, C.; Man, N.T.
Biochem. J. 309, 355-359, 1995
A:Title: Specificity and V(H) sequence of two monoclonal antibodies against the N-ter
A:Reference number: S56008; MUID:95344393; PMID:7619079
A:Accession: S56009
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-92 <MOR>
A:Cross-references: EMBL:Z46661
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:6-86/Domain: immunoglobulin homology <IMM>

Query Match 77.4%; Score 41; DB 2; Length 92;
Best Local Similarity 77.8%; Pred. No. 1.1;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TYYLDTVEG 10

||||| |||:|

Db 48 TYILDSVKG 56

RESULT 13

147200
Ig heavy chain variable VDJ region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000

```
C:Accession: I47200
R:Sun, J.; Kacsokovics, I.; Brown, W.R.; Butler, J.E.
J. Immunol. 153, 5618-5627, 1994
A:Title: Expressed swine VH genes belong to a small VH gene family homologous to human V
A:Reference number: I47177; MUID:95081609; PMID:7989761
A:Accession: I47200
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-150 <SUN>
A:Cross-references: EMBL:U15459; NID:g571404; PIDN:AAA67025.1; PID:g571405
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:34-119/Domain: immunoglobulin homology <IMM>

Query Match          77.4%; Score 41; DB 2; Length 150;
Best Local Similarity 77.8%; Pred. No. 1.9;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 TYVLDIVTEG 10
Db 79 TYVLDIVTEG 87
|||||:|:|

RESULT 14
S24248
Ig heavy chain V region (VH26) - human
C:Species: Homo sapiens (man)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S24248
R:Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.
submitted to the EMBL Data Library, June 1992
A:Description: A single VH gene predominates in the rearranged and expressed human B cell
A:Reference number: S24247
A:Accession: S24248
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-90 <STE>
A:Cross-references: EMBL:X67069; NID:g38395; PIDN:CAA7454.1; PID:g38396
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin

Query Match          75.5%; Score 40; DB 2; Length 90;
Best Local Similarity 70.0%; Pred. No. 1.7;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYVLDIVTEG 10
Db 56 STYVLDIVTEG 65
|||||:|:|

RESULT 15
S26935
Ig heavy chain V region (DP-42) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S26935
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A:Reference number: S26885; MUID:93021117; PMID:1404388
A:Accession: S26935
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-97 <TOM>
A:Cross-references: EMBL:Z12342; NID:g32905; PIDN:CAA78212.1; PID:g32906
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:15-97/Domain: immunoglobulin homology <IMM>

Query Match          75.5%; Score 40; DB 2; Length 97;
Best Local Similarity 70.0%; Pred. No. 1.8;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYVLDIVTEG 10
```

```
Db 56 STYVLDIVTEG 65
|||||:|:|
```

```
Search completed: November 18, 2002, 17:47:01
Job time : 4.90196 secs
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:00 ; Search time 2.45098 Seconds
(without alignments)
169.223 Million cell updates/sec

Title: US-09-016-061-58
Perfect score: 53
Sequence: 1 STYLLDTVEG 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
1	42	79.2	117	1	HV53_MOUSE	P18524 mus musculus
2	42	79.2	117	1	HV54_MOUSE	P18525 mus musculus
3	42	79.2	117	1	HV55_MOUSE	P18526 mus musculus
4	40	75.5	116	1	HV05_CARAU	P19181 carassius a
5	38	71.7	97	1	HV56_MOUSE	P18527 mus musculus
6	37	69.8	115	1	HV3F_HUMAN	P01767 homo sapien
7	37	69.8	117	1	HV3C_HUMAN	P01764 homo sapien
8	37	69.8	470	1	GLNA_FREDI	P33035 fremyella d
9	37	69.8	473	1	GLNA_SYNP2	P28605 synecococc
10	37	69.8	755	1	PK61_DROME	Q9w0v1 drosophila
11	36	67.9	473	1	GLNA_ANASP	P00964 anabaena sp
12	36	67.9	523	1	YB34_YEAST	P38299 saccharomyc
13	35	66.0	117	1	HV02_CANFA	P01785 canis famil
14	35	66.0	119	1	HV3L_HUMAN	P01773 homo sapien
15	35	66.0	364	1	YK27_AQAE	O67821 aquifex aeo
16	35	66.0	508	1	YBCK_ECOLI	P77698 escherichia
17	35	66.0	1062	1	CERU_MOUSE	Q61147 mus musculus
18	35	66.0	1162	1	CARB_AGR75	Q8ude9 agrobacteri
19	35	66.0	3460	1	RELN_HUMAN	P78509 homo sapien
20	34	64.2	98	1	HV57_MOUSE	P18528 mus musculus
21	34	64.2	117	1	HV58_MOUSE	P18529 mus musculus
22	34	64.2	117	1	HV59_MOUSE	P18530 mus musculus
23	34	64.2	324	1	Y518_CHLPN	Q92834 chlamydia p
24	34	64.2	329	1	Y429_CHLTR	O84436 chlamydia t
25	34	64.2	353	1	GBQ_LYNST	P38411 lymanaea sta
26	34	64.2	710	1	IGAA_SALTI	P38721 salmonella
27	34	64.2	710	1	IGAA_SALTY	Q9acp0 salmonella
28	34	64.2	711	1	IGAA_ECO57	P58720 escherichia
29	34	64.2	711	1	IGAA_ECOLI	P45800 escherichia
30	34	64.2	3209	1	RELN_CHICK	Q93574 gallus gall
31	34	64.2	3461	1	RELN_MOUSE	Q60841 mus musculus
32	34	64.2	3462	1	RELN_RAT	P38751 rattus norv
33	34	64.2	4488	1	RRPA_CVMJH	P19751 murine coro

ALIGNMENTS

RESULT 1									
ID	HV53_MOUSE	STANDARD;	PRT;	117	AA.				
AC	P18524;								
DT	01-NOV-1990 (Rel. 16, Created)								
DT	01-NOV-1990 (Rel. 16, Last sequence update)								
DT	15-JUL-1999 (Rel. 38, Last annotation update)								
DE	Ig heavy chain V region RF precursor.								
OS	Mus musculus (Mouse).								
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.								
OX	NCBI_TaxID=10090;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RC	STRAIN=BALB/CJ;								
RX	MEDLINE=89279149; PubMed=2499654;								
RA	Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;								
RT	"Early onset of somatic mutation in immunoglobulin VH genes during the primary immune response.";								
RL	J. Exp. Med. 169:2007-2019(1989).								
CC	-I- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.								
DR	PIR: JTO503; HVMSRF.								
DR	HSSP: P01810; 2FBU.								
DR	InterPro: IPR003006; Ig_MHC.								
DR	InterPro: IPR003596; Ig_V.								
DR	Pfam: PF00047; Ig; 1.								
DR	SMART: SM00406; IgV; 1.								
KW	Immunoglobulin V region; Hybridoma; Signal.								
FT	SIGNAL 1 19								
FT	CHAIN 20 117								
FT	DOMAIN 20 49								
FT	DOMAIN 50 54								
FT	DOMAIN 55 68								
FT	DOMAIN 69 85								
FT	DOMAIN 86 117								
FT	DISULFID 41 115								
FT	NON_TER 117 117								
SQ	SEQUENCE 117 AA; 12866 MW; 2CE3295F390F725B CRC64;								
Query Match 79.2%; Score 42; DB 1; Length 117;									
Best Local Similarity 80.0%; Pred. No. 0.24;									
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;									
QY	1 STYLLDTVEG 10								
DB	76 STYYPDTVKG 85								
RESULT 2									
ID	HV54_MOUSE	STANDARD;	PRT;	117	AA.				
AC	P18525;								
DT	01-NOV-1990 (Rel. 16, Created)								
DT	01-NOV-1990 (Rel. 16, Last sequence update)								
DT	15-JUL-1999 (Rel. 38, Last annotation update)								
DE	Ig heavy chain V region 5-84 precursor.								

```

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RT the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; JT0505; HVMS84.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin v region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 5-84.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 59 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12872 MW; 234055CB6A469861 CRC64;

Query Match 79.2%; Score 42; DB 1; Length 117;
Best Local Similarity 80.0%; Pred. No. 0.24;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYLDTVG 10
DB 76 STYPTVKG 85

RESULT 3
HV55_MOUSE
ID HV55_MOUSE STANDARD; PRT; 117 AA.
AC P18526;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain v region 345 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RT the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; JT0502; HVMS34.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin v region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 345.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RT the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; JT0502; HVMS34.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin v region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 345.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.

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FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12902 MW; 49380E4627ACA99A CRC64;

Query Match 79.2%; Score 42; DB 1; Length 117;
Best Local Similarity 80.0%; Pred. No. 0.24;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYLDTVG 10
DB 76 STYPTVKG 85

RESULT 4
HV05_CARAU
ID HV05_CARAU STANDARD; PRT; 116 AA.
AC P19181;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain v region 5A precursor.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88144476; PubMed=3125551;
RA Willson M.R., Middleton D., Warr G.W.;
RT "Immunoglobulin heavy chain variable region gene evolution: structure
RT and family relationships of two genes and a pseudogene in a teleost
RT fish.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:1566-1570(1988).
DR PIR; B28966; B28966.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin v region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 116 IG HEAVY CHAIN V REGION 5A.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 59 84 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 85 116 FRAMEWORK-3.
FT DISULFID 41 114 BY SIMILARITY.
FT NON_TER 116 116
SQ SEQUENCE 116 AA; 12808 MW; 9C2279E2DF199B12 CRC64;

Query Match 75.5%; Score 40; DB 1; Length 116;
Best Local Similarity 70.0%; Pred. No. 0.59;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYLDTVG 10
DB 75 STYADSVKG 84

RESULT 5
HV56_MOUSE
ID HV56_MOUSE STANDARD; PRT; 97 AA.
AC P18527;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain v region 914.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RA MEDLINE=89279149; PubMed=2499654;
RX Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RL the primary immune response.";
RJ J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; JTO504; HVMS91.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region.
FT NON_TER 97
SQ SEQUENCE 97 AA; 10661 MW; C23CB33FF55DA893 CRC64;

Query Match 71.7%; Score 38; DB 1; Length 97;
Best Local Similarity 70.0%; Pred. No. 1.2;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYLDTVEG 10
DB 56 STYYPDSVKG 65

RESULT 6
HV3F_HUMAN STANDARD; PRT; 115 AA.
AC P01767;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DR Ig heavy chain V-III region BUT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=78137069; PubMed=416441;
RA Torano A., Putnam F.W.;
RT "Complete amino acid sequence of the alpha 2 heavy chain of a human
RL IgA2 immunoglobulin of the A2m (2) allotype.";
RJ Proc. Natl. Acad. Sci. U.S.A. 75:966-969(1978).
CC -!- MISCELLANEOUS: THE SEQUENCE OF THE ALPHA-2, A2M(2) ALLOTYPE, C
CC REGION OF THIS MYELOMA PROTEIN IS ALSO GIVEN.
DR PIR; A02050; A2HUBU.
DR HSSP; P01789; 1MCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region.
FT NON_TER 115
SQ SEQUENCE 115 AA; 13379 MW; 208876A7DF52DCF4 CRC64;

Query Match 69.8%; Score 37; DB 1; Length 115;
Best Local Similarity 60.0%; Pred. No. 2.3;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYLDTVEG 10
DB 56 TTYVADSVKG 65

RESULT 7
HV3C_HUMAN STANDARD; PRT; 117 AA.
ID HV3C_HUMAN

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AC P01764;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-III region VH26 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81101090; PubMed=6450418;
RA Matthysens G., Rabbitts T.H.;
RT "Structure and multiplicity of genes for the human immunoglobulin
RL heavy chain variable region.";
RJ Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).
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CC -----
DR EMBL; J00236; AAA53516.1; -
DR EMBL; M35415; AAA58735.1; -
DR PIR; A02047; H3HU26.
DR HSSP; P01772; 2FB4.
DR Genew; HGNC:5545; IGHV@.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V-III REGION VH26.
FT NON_TER 117
SQ SEQUENCE 117 AA; 12582 MW; E826733F1A3CB0F1 CRC64;

Query Match 69.8%; Score 37; DB 1; Length 117;
Best Local Similarity 70.0%; Pred. No. 2.3;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYLDTVEG 10
DB 76 STYYGDSVKG 85

RESULT 8
GLNA_FREDI STANDARD; PRT; 470 AA.
ID GLNA_FREDI
AC P33035;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Glutamine synthetase (EC 6.3.1.2) (Glutamate--ammonia ligase).
GN GLNA.
OS Fremyella diplosiphon (Calothrix PCC 7601).
OC Bacteria; Cyanobacteria; Nostocales; Rivulariaceae; Fremyella.
OX NCBI_TaxID=1197;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93129187; PubMed=1362348;
RA Elmorjani K., Liotenberg S., Houmard J., de Marsac N.T.;
RT "Molecular characterization of the gene encoding glutamine synthetase
RL in the cyanobacterium Calothrix sp. PCC 7601.";
RJ Biochem. Biophys. Res. Commun. 189:1296-1302(1992).
CC -!- CATALYTIC ACTIVITY: ATP + L-glutamate + NH(3) -> ADP + phosphate +
CC L-glutamine.
CC -!- SUBUNIT: OLIGOMER OF 12 SUBUNITS ARRANGED IN THE FORM OF TWO
CC HEXAGONS.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.

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CC -1- SIMILARITY: BELONGS TO THE GLUTAMINE SYNTHETASE FAMILY.
CC -----
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CC -----
CC EMBL; L05609; AAA23288.1; -.
CC PIR; JC1403; JC1403.
CC HSP; P06201; ILGR.
CC InterPro; IPR001691; GLN_synth.
CC InterPro; IPR004809; GlnA.
CC Pfam; PF001637; GlnA_adenyltn.
CC ProDom; PD001057; GlnA_adenyltn; 1.
CC TIGRFAMS; TIGR00653; GlnA; 1.
CC PROSITE; PS00180; GLNA_1; 1.
CC PROSITE; PS00181; GLNA_ATP; 1.
CC PROSITE; PS00182; GLNA_ADENYLATION; 1.
CC KW Ligase.
CC FT INIT_MET 0 0 BY SIMILARITY.
CC SQ SEQUENCE 470 AA; 52919 MW; ADD7849A7789E832 CRC64;

Query Match 69.8%; Score 37; DB 1; Length 470;
Best Local Similarity 75.0%; Pred. No. 11;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 YYLDTVEG 10
Db 150 YYVDSVEG 157
||:|||||

RESULT 9
GLNA_SYN2 ID GLNA_SYN2 STANDARD; PRT; 473 AA.
AC P28605;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Glutamine synthetase (EC 6.3.1.2) (Glutamate--ammonia ligase).
GN GLNA.
OS Synechococcus sp. (strain PCC 7002) (Agmenellum quadruplicatum).
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX NCBI_TaxID=32049;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PR-6;
RX MEDLINE=93139025; PubMed=7678591;
RA Wagner S.J., Thomas S.P., Kaufman R.I., Nixon B.T., Stevens S.E. Jr.;
RT "The glnA gene of the cyanobacterium Agmenellum quadruplicatum PR-6
RL is nonessential for ammonium assimilation."
RL J. Bacteriol. 175:604-612(1993).
CC -1- CATALYTIC ACTIVITY: ATP + L-glutamate + NH(3) = ADP + phosphate +
CC L-glutamine.
CC -1- SUBUNIT: OLIGOMER OF 12 SUBUNITS ARRANGED IN THE FORM OF TWO
CC HEXAGONS.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE GLUTAMINE SYNTHETASE FAMILY.
CC -----
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CC -----
CC EMBL; Z13965; CAA78366.1; -.
CC PIR; S23852; S23852.
CC PIR; A47050; A47050.

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DR HSP; P06201; ILGR.
DR InterPro; IPR001691; GLN_synth.
DR InterPro; IPR004809; GlnA.
DR InterPro; IPR001637; GlnA_adenyltn.
DR Pfam; PF00120; gln-synt; 1.
DR ProDom; PD001057; GlnA_adenyltn; 1.
DR TIGRFAMS; TIGR00653; GlnA; 1.
DR PROSITE; PS00180; GLNA_1; 1.
DR PROSITE; PS00181; GLNA_ATP; 1.
DR KW Ligase.
DR SQ SEQUENCE 473 AA; 53030 MW; 495C6C7A1EDBC576 CRC64;

Query Match 69.8%; Score 37; DB 1; Length 473;
Best Local Similarity 75.0%; Pred. No. 11;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 YYLDTVEG 10
Db 152 YYVDSVEG 159
||:|||||

RESULT 10
PK61_DROME ID PK61_DROME STANDARD; PRT; 755 AA.
AC Q9W0V1; Q9W0V2; Q9W0V3; O62534;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Serine/threonine-protein kinase PK61C (EC 2.7.1.37) (dSTPK61).
GN PK61C OR CG1201 OR CG1210.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RA MacDougall C.N.;
RT "Cloning and characterisation of a gene encoding sex-specific
RT transcripts in Drosophila melanogaster."
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
RC STRAIN=Berkely;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benson P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fodor C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattai B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

```

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.:
RT "The genome sequence of *Drosophila melanogaster*";
RL Science 287:2185-2195(2000).
RN [3]
RP FUNCTION.
RX MEDLINE=98035195; PubMed=9368760;
RA MacDougall C.N., Todman M., Bowles M.;
RL Unpublished results, cited by:
RL Alessi D.R., Deak M., Casamayor A., Caudwell F.B., Morrice N.A.,
RL Norman D.G., Gaffney P.R.J., Reese C.B., MacDougall C.N., Harbison D.,
RL Ashworth A., Bowles M.;
RL Curr. Biol. 7:776-789(1997).
CC -!- FUNCTION: Implicated in the regulation of sexual differentiation,
CC oogenesis and spermatogenesis. May be implicated in the activation
CC of dPKB.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- ALTERNATIVE PRODUCTS: 3 isoforms; 1 (shown here), 2 and 3; may be
CC produced by alternative splicing.
CC -!- PTM: Phosphorylated on tyrosine and serine/threonine (By
CC similarity).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. PDK1
CC SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 1 PH DOMAIN.
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CC -----
DR EMBL; Y07908; CAA69216.1; -.
DR EMBL; AE003467; AAF47328.1; -.
DR EMBL; AE003467; AAF47329.1; -.
DR EMBL; AE003467; AAF47331.1; -.
DR FlyBase; FBgn0020386; PK61C.
DR InterPro; IPR000719; Euk_Pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR Transferrase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation; Alternative splicing.
FT DOMAIN 165 490
FT PROTEIN KINASE.
FT DOMAIN 592 684
FT NP_BIND 171 179 ATP (BY SIMILARITY).
FT BINDING 194 194 ATP (BY SIMILARITY).
FT ACT_SITE 289 289 BY SIMILARITY.
FT DOMAIN 126 154
FT POLY-GLN.
FT VARSPIC 1 3
FT VARSPIC 1 213 MISSING (IN ISOFORM 2).
FT VARSPIC 119 120 MISSING (IN ISOFORM 3).
FT CONFLICT 362 362 QQ -> HE (IN REF. 1).
FT CONFLICT 362 362 G -> R (IN REF. 1).
SQ SEQUENCE 755 AA; 85613 MW; 6375A99A25089FDD CRC64;
Query Match 69.8%; Score 37; DB 1; Length 755;
Best Local Similarity 77.8%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 TYLDTVEG 10

Db 658 TVYLDDEG 666
||||| ||
RESULT 11
GLNA_ANASP
ID GLNA_ANASP STANDARD; PRT; 473 AA.
AC P00964;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Glutamine synthetase (EC 6.3.1.2) (Glutamate--ammonia ligase).
GN GLNA OR ALR2328.
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RA Tumer N.E., Robinson S.J., Haselkorn R.;
RT "Different promoters for the Anabaena glutamine synthetase gene
RT during growth using molecular or fixed nitrogen.";
RL Nature 306:337-342(1983).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriiguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain PCC 7120.";
RL DNA Res. 8:203-213(2001).
CC -!- CATALYTIC ACTIVITY: ATP + L-glutamate + NH(3) = ADP + phosphate +
CC L-glutamine.
CC -!- SUBUNIT: OLIGOMER OF 12 SUBUNITS ARRANGED IN THE FORM OF TWO
CC HEXAGONS.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- MISCELLANEOUS: IN ANABAENA, IT IS PRESENT IN AMMONIA-GROWN
CC VEGETATIVE CELLS AS WELL AS IN HETEROCYSTES (FOR NITROGEN
CC FIXATION).
CC -!- SIMILARITY: BELONGS TO THE GLUTAMINE SYNTHETASE FAMILY.
CC -----
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CC -----
DR EMBL; X00147; CAA24982.1; -.
DR EMBL; AP003589; BAB74027.1; -.
DR PIR; A01192; AJA1Q.
DR HSP; P06201; ILGR.
DR InterPro; IPR001691; GLN_synth.
DR InterPro; IPR004809; GlnA.
DR InterPro; IPR001637; GlnA_adenyltn.
DR Pfam; PF00120; gln-synt; 1.
DR Pfam; PD001057; GlnA_adenyltn; 1.
DR TIGRfams; TIGR00653; GlnA; 1.
DR PROSITE; PS00180; GLNA_1; 1.
DR PROSITE; PS00181; GLNA_1; 1.
DR PROSITE; PS00182; GLNA_ADENYLATION; 1.
KW Nitrogen fixation; Ligase; Heterocyst; Complete proteome.
FT INIT_MET 0 106 BY SIMILARITY.
FT CONFLICT 106 106 R -> P (IN REF. 1; CAA24982).
SQ SEQUENCE 473 AA; 53005 MW; 373C7F949443A4E9 CRC64;
Query Match 67.9%; Score 36; DB 1; Length 473;
Best Local Similarity 75.0%; Pred. No. 17;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

QY      3 YYLDTVEG 10
Db      150 YFLDSVEG 157

RESULT 12
YB34_YEAST
ID YB34_YEAST STANDARD; PRT; 523 AA.
AC P38299;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Hypothetical 60.6 kDa protein in SMP1-MBAL intergenic region.
GN YBR184W OR YBR1306.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=95176710; PubMed=7871891;
RA Demolis N., Jacquet M., Mallet L.;
RT "A 12.5 kb fragment of the yeast chromosome II contains two adjacent
RT genes encoding ribosomal proteins and six putative new genes, one of
RT which encodes a putative transcriptional factor.";
RL Yeast 10:1511-1525(1994).
CC -----
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CC -----
DR EMBL; U02073; AAB60278.1; -
DR EMBL; Z36053; CAA85145.1; -
DR PIR; S46056; S46056.
DR SGD; S0000388; YBR184W.
KW Hypothetical protein.
SQ SEQUENCE 523 AA; 60642 MW; 9BFFBD192C85472F CRC64;

Query Match 67.9%; Score 36; DB 1; Length 523;
Best Local Similarity 70.0%; Pred. No. 19;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 STYYLDTVEG 10
Db      441 STYRLDSAE 450

RESULT 13
HV02_CANFA
ID HV02_CANFA STANDARD; PRT; 117 AA.
AC P01785;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region MOO.
OS Canis familiaris (dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE OF 1-112.
RX MEDLINE=77242268; PubMed=407924;
RA Wasserman R.L., Capra J.D.;
RT "Primary structure of the variable regions of two canine
RT immunoglobulin heavy chains.";
RL Biochemistry 16:3160-3168(1977).
RN [2]
RP SEQUENCE OF 113-117.

```

```

RX MEDLINE=80077682; PubMed=117299;
RA McCumber L.J., Capra J.D.;
RT "The complete amino-acid sequence of a canine mu chain.";
RL Mol. Immunol. 16:565-570(1979).
CC -!- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR PIR; A02058; MHDGMO.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region.
FT NON_TER 117
SQ SEQUENCE 117 AA; 12703 MW; FCE07309E0A84B35 CRC64;

Query Match 66.0%; Score 35; DB 1; Length 117;
Best Local Similarity 66.7%; Pred. No. 5.7;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      2 TYLDTVEG 10
Db      57 TYADAVG 65

RESULT 14
HV3L_HUMAN
ID HV3L_HUMAN STANDARD; PRT; 119 AA.
AC P01773;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-III region BUR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE (MYELOMA PROTEIN BUR).
RX MEDLINE=79151016; PubMed=107164;
RA Putnam F.W., Liu Y.-S.V., Low T.L.K.;
RT "Primary structure of a human IgA1 immunoglobulin. IV. Streptococcal
RT IgA1 protease, digestion, Fab and Fc fragments, and the complete
RT amino acid sequence of the alpha 1 heavy chain.";
RL J. Biol. Chem. 254:2865-2874(1979).
DR PIR; A02056; ALHUBR.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Glycoprotein.
FT MOD_RES 1
FT DISULFID 22
FT CARBOHYD 28
FT NON_TER 119
SQ SEQUENCE 119 AA; 12981 MW; 12A709A75344D024 CRC64;

Query Match 66.0%; Score 35; DB 1; Length 119;
Best Local Similarity 66.7%; Pred. No. 5.9;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      2 TYLDTVEG 10
Db      58 TYADSVRG 66

RESULT 15
YK27_AQUAE
ID YK27_AQUAE STANDARD; PRT; 364 AA.
AC O67821;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)

```

```
DE Hypothetical protein AQ_2027.
GN AQ_2027.
OS Aquifex aeolicus.
OC Bacteria; Aquificae; Aquificae (class); Aquificales; Aquificaceae;
OC Aquifex.
OX NCBI_TaxID=63363;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VF5;
RX MEDLINE=98196666; PubMed=9537320;
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Sneed M.A., Keller M., Aujay M., Huber R.,
RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
RL aeolicus."
RL Nature 392:353-358(1998).
CC -!- SIMILARITY: TO B.BURGDORFERI BB0374.
CC -----
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CC -----
DR EMBL; AE000768; AAC07788.1; -.
DR InterPro; IPR002819; HD.
DR InterPro; IPR003607; ME_Pplase_HDc.
DR Pfam; PF01966; HD; 1.
DR SMART; SM00471; HDc; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 364 AA; 42016 MW; 4022756E079B7276 CRC64;

Query Match          66.0%; Score 35; DB 1; Length 364;
Best Local Similarity 60.0%; Pred. No. 20;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 STYYLDTVVEG 10
Db | | | | | : |
203 SFYYLDSITG 212
```

Search completed: November 18, 2002, 17:33:22
Job time : 3.45098 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:01 ; Search time 10.4412 Seconds
(without alignments)
197.341 Million cell updates/sec

Title: US-09-016-061-58
Perfect score: 53
Sequence: 1 STYYLDTVEG 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTEMBL21.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp Vertebrate.*
- 14: sp Unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	75.5	121	4 Q9UL71	Q9UL71 homo sapien
2	40	75.5	211	11 Q9D8R6	Q9D8R6 mus musculu
3	40	75.5	597	4 Q96BB9	Q96BB9 homo sapien
4	40	75.5	1642	13 Q9L132	Q9L132 naja naja
5	39	73.6	289	17 Q8TJU0	Q8TJU0 methanosarc
6	38	71.7	262	13 Q9PWM6	Q9PWM6 brachydanio
7	38	71.7	473	2 O50210	O50210 synechococc
8	37	69.8	116	10 Q9LHW3	Q9LHW3 oryza sativ
9	37	69.8	479	11 Q9LWP5	Q9LWP5 mus musculu
10	36	67.9	118	4 Q9UL72	Q9UL72 homo sapien
11	36	67.9	258	2 Q9RA41	Q9RA41 trichodesmi
12	36	67.9	268	16 Q9RS44	Q9RS44 deinococcus
13	36	67.9	339	2 Q32822	Q32822 listeria mo
14	36	67.9	474	2 Q9RHZ1	Q9RHZ1 anabaena az
15	36	67.9	491	16 Q928B4	Q928B4 listeria in
16	36	67.9	491	16 Q8Y4G5	Q8Y4G5 listeria mo

17	36	67.9	603	5 Q95ZK6	Q95ZK6 caenorhabdi
18	36	67.9	977	5 Q95ZK7	Q95ZK7 caenorhabdi
19	35	66.0	195	5 Q9VZM0	Q9VZM0 drosophila
20	35	66.0	211	4 Q9BQA2	Q9BQA2 homo sapien
21	35	66.0	214	5 O18547	O18547 drosophila
22	35	66.0	275	5 Q8SZ10	Q8SZ10 drosophila
23	35	66.0	290	5 Q9VRT2	Q9VRT2 drosophila
24	35	66.0	322	17 Q97V57	Q97V57 sulfolobus
25	35	66.0	328	16 Q68786	Q68786 yersinia pe
26	35	66.0	400	5 Q95Y18	Q95Y18 caenorhabdi
27	35	66.0	473	11 Q91205	Q91205 mus musculu
28	35	66.0	499	16 Q55174	Q55174 synechocyst
29	35	66.0	508	16 Q8X718	Q8X718 escherichia
30	35	66.0	545	4 Q96SL2	Q96SL2 homo sapien
31	35	66.0	683	10 Q8S771	Q8S771 oryza sativ
32	35	66.0	867	13 Q9PW49	Q9PW49 gallus gall
33	35	66.0	1170	10 Q48573	Q48573 arabidopsis
34	35	66.0	1176	4 Q96Q05	Q96Q05 homo sapien
35	35	66.0	1186	16 Q8UDE9	Q8UDE9 agrobacteri
36	35	66.0	4472	2 Q33954	Q33954 streptomyce
37	34	64.2	119	11 Q920E7	Q920E7 mus musculu
38	34	64.2	142	16 Q8Y6P9	Q8Y6P9 listeria mo
39	34	64.2	227	2 Q9X319	Q9X319 bacillus an
40	34	64.2	243	17 Q9HIF1	Q9HIF1 thermoplasma
41	34	64.2	248	5 Q95WI8	Q95WI8 anopheles s
42	34	64.2	259	2 P94454	P94454 bacillus st
43	34	64.2	308	5 Q16503	Q16503 caenorhabdi
44	34	64.2	333	9 Q8SDE7	Q8SDE7 pseudomonas
45	34	64.2	349	2 Q9L8M5	Q9L8M5 prochloroco

ALIGNMENTS

RESULT 1

Q9UL71	ID	Q9UL71	PRELIMINARY;	PRT;	121 AA.
AC	Q9UL71;				
DT	01-MAY-2000 (Tremblrel. 13, Created)				
DT	01-MAY-2000 (Tremblrel. 13, Last sequence update)				
DT	01-DEC-2001 (Tremblrel. 19, Last annotation update)				
DE	Myosin-reactive immunoglobulin heavy chain variable region (Fragment).				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=98277139; PubMed=9614934;				
RA	Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,				
RA	Young D.C.;				
RT	"Myosin-reactive autoantibodies in rheumatic carditis and normal fetus".				
RL	Clin. Immunol. Immunopathol. 87:184-192(1998).				
DR	EMBL; AF035043; AAD56279.1; -.				
DR	HSSP; P01772; 2FB4.				
DR	InterPro; IPR003006; Ig_MHC.				
DR	InterPro; IPR003596; Ig_V.				
DR	Pfam; PF00047; Ig; 1.				
DR	SMART; SM00406; IGV; 1.				
FT	NON_TER 1 1				
FT	NON_TER 121 121				
SQ	SEQUENCE 121 AA; 13154 MW; 2F045CCFA5D50736 CRC64;				

Query Match 75.5%; Score 40; DB 4; Length 121;
Best Local Similarity 70.0%; Pred. No. 3.9;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 STYYLDTVEG 10

|||||:|:|

Db 57 STYYADSVKG 66

RESULT 2

Q9DBR6 PRELIMINARY; PRT; 211 AA.
 AC Q9DBR6
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE L81004A24RIK protein.
 GN L81004A24RIK
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=PANCREAS;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shingawa A., Shibata K., Konno H., Adachi J., Fukuda S.,
 RA Arakawa T., Hara A., Fukunishi Y., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
 RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 DR EMBL: AK007766; BAB25242.1; -;
 DR MGD: MGI:1923760; L81004A24RIK.
 SQ SEQUENCE 211 AA; 23482 MW; 018A8D093CACBBD8 CRC64;

Query Match 75.5%; Score 40; DB 11; Length 211;
 Best Local Similarity 77.8%; Pred. No. 7.3;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYLDVTE 9

||:|||||

DB 150 STYYLDVTE 158

RESULT 3

Q96BB9 PRELIMINARY; PRT; 597 AA.
 AC Q96BB9;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Hypothetical 65.0 kDa protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=B-CCELL;
 RL Strausberg R.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC015760; AAH15760.1; -;
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00047; Ig; 5.
 DR PROSITE: PS00290; IG_MHC; UNKNOWN_3.
 DE Hypothetical protein.

SQ SEQUENCE 597 AA; 65039 MW; 4FCA3AD8ECE263D9 CRC64;

Query Match 75.5%; Score 40; DB 4; Length 597;
 Best Local Similarity 70.0%; Pred. No. 23;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYLDVTE 10

|||||:|

DB 76 STYYADSVKG 85

RESULT 4

Q91132 PRELIMINARY; PRT; 1642 AA.
 ID Q91132
 AC Q91132;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Cobra venom factor precursor.
 OS Naja naja (Indian cobra).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroides;
 OC Elapidae; Elapinae; Naja.
 OC NCBI_TaxID=35670;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=VENOM GLAND;
 RX MEDLINE=95108041; PubMed=7809120;
 RA Fritzinger D.C., Bredehorst R., Vogel C.W.;
 RT "Molecular cloning and derived primary structure of cobra venom
 RT factor."
 RL Proc. Natl. Acad. Sci. U.S.A. 91:12775-12779(1994).
 DR EMBL: U09969; AAA68989.1; -;
 DR HSP; P01024; IC3D.
 DR InterPro: IPR002890; A2M_N.
 DR InterPro: IPR000020; Anaphylatoxin.
 DR InterPro: IPR001840; Anaphylatoxn.
 DR InterPro: IPR002048; EF-hand.
 DR InterPro: IPR001599; MacrogloblnA2.
 DR InterPro: IPR001134; Netrin_C.
 DR Pfam: PF00207; A2M; 1.
 DR Pfam: PF01835; A2M_N; 1.
 DR Pfam: PF01821; ANATO; 1.
 DR Pfam: PF01759; NTR; 1.
 DR PRINTS: PR00004; ANAPHYLATOXN
 DR ProDom: PD003264; Anaphylatoxin; 1.
 DR SMART: SM00104; ANATO; 1.
 DR PROSITE: PS00477; ALPHA_2_MACROGLOBULIN; 1.
 DR PROSITE: PS01178; ANAPHYLATOXIN_2; 1.
 DR PROSITE: PS00018; EF_HAND; UNKNOWN_1.
 KW Signal.
 FT SIGNAL 1 22 POTENTIAL.
 FT CHAIN 23 648 ALPHA CHAIN OF COBRA VENOM FACTOR.
 FT CHAIN 1264 1642 BETA CHAIN OF COBRA VENOM FACTOR.
 SQ SEQUENCE 1642 AA; 184517 MW; 2A71B2BD61D612A3 CRC64;

Query Match 75.5%; Score 40; DB 13; Length 1642;

Best Local Similarity 77.8%; Pred. No. 71;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYLDVTE 9

|||||

DB 1007 ATYYLDVTE 1015

RESULT 5

Q8TJU0 PRELIMINARY; PRT; 289 AA.
 ID Q8TJU0
 AC Q8TJU0;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Hypothetical protein MA3687.

GN MA3687.2
 OS Methanosarcina acetivorans.
 OC Archaea: Euryarchaeota: Methanococci: Methanosarcinales;
 OC Methanosarcinaceae; Methanosarcina.
 OX NCBI_TaxID=2214;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C2A / ATCC 35395 / DSM 2834;
 RX MEDLINE=21929760; PubMed=11932238;
 RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,
 RA Fitzhugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,
 RA Allen N., Naylor J., Stange-Thomann N., Dearellano K., Johnson R.,
 RA Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
 RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,
 RA Hedderich R., Ingram-Smith C., Kuettnner H.C., Krzycki J.A.,
 RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
 RA Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,
 RA Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,
 RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
 RA Metcalf W.W., Birren B.;
 RT "The genome of Methanosarcina acetivorans reveals extensive metabolic
 RT and physiological diversity.";
 RL Genome Res. 12:532-542(2002).
 DR EMBL; AE011078; AA07042.1;
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 289 AA; 32541 MW; 8886F22245794725 CRC64;
 Query Match 73.6%; Score 39; DB 17; Length 289;
 Best Local Similarity 60.0%; Pred. No. 16;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 STYYLDTVEG 10
 Db :||||| :|
 17 NTYYLDPIKG 26
 RESULT 6
 Q9PWW6 PRELIMINARY; PRT; 262 AA.
 AC Q9PWW6;
 DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
 DE Homeobox protein.
 GN HOXD9A.
 OS Brachydanio rerio (zebrafish) (zebra danio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99051425; PubMed=9831563;
 RA Anores A., Force A., Yan Y.-L., Wang Y.-L., Fritz A., Prince V.,
 RA Ho R., Anemlya C., Langeland J., Westerfield M., Ekker M.,
 RA Postlethwait J.;
 RT "Zebrafish hox clusters and vertebrate genome evolution.";
 RL Science 282:1711-1714(1998).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 DR EMBL; AF071268; AAD15961.1;
 DR HSSP; P02834; I881.
 DR TRANSFAC; T03653;
 DR 2FIN; ZDB-GENE-990415-121; hoxd9a.
 DR InterPro; IPR001356; Homeobox.
 DR InterPro; IPR000047; HTH repress.
 DR Pfam; PF00046; homeobox; 1.
 DR PRINTS; PR00024; HOMEBOX.
 DR PRINTS; PR00031; HTHREPRESS.
 DR ProDom; PD000010; Homeobox; 1.
 DR SMART; SM00389; HOX; 1.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PSS0071; HOMEBOX_2; 1.
 KW DNA-binding; Homeobox; Nuclear protein.

SQ SEQUENCE 262 AA; 29731 MW; 93BC979F8677CA27 CRC64;
 Query Match 71.7%; Score 38; DB 13; Length 262;
 Best Local Similarity 60.0%; Pred. No. 23;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 STYYLDTVEG 10
 Db :||||| :|
 8 SSYYVDITMG 17
 RESULT 7
 O50210 PRELIMINARY; PRT; 473 AA.
 AC O50210;
 DT 01-JUN-1998 (TRENBLrel. 06, Created)
 DT 01-JUN-1998 (TRENBLrel. 06, Last sequence update)
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
 DE Glutamine synthetase (EC 6.3.1.2).
 GN GLNA.
 OS Synecococcus sp. (strain PCC 7942) (Anacystis nidulans R2).
 OC Bacteria; Cyanobacteria; Chroococcales; Synecococcus.
 OX NCBI_TaxID=1140;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PCC 7942;
 RA Cohen-Kupiec R.;
 RT "Nitrogen regulation of non-nitrogen fixing cyanobacteria: the glnA
 RT gene of Synecococcus 7942 as a model.";
 RL Thesis (1993), Unknown Institution.
 RN [2]
 RP PARTIAL SEQUENCE FROM N.A.
 RC STRAIN=PCC 7942;
 RA Phung L.T.;
 RT "Molecular genetics of Synecococcus PCC 7942: genes for fatty acid
 RT biosynthesis and a copper translocating ATPase.";
 RL Thesis (1997), Unknown Institution.
 RN [3]
 RP SEQUENCE OF 1-4 FROM N.A.
 RC STRAIN=PCC 7942;
 RX MEDLINE=94064573; PubMed=7902350;
 RA Cohen-Kupiec R., Gurevitz M., Zilberstein A.;
 RT "Expression of glnA in the cyanobacterium Synecococcus sp. strain PCC
 RT 7942 is initiated from a single nif-like promoter under various
 RT nitrogen conditions.";
 RL J. Bacteriol. 175:7727-7731(1993).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PCC 7942;
 RA Phung L.T., Cohen-Kupiec R.;
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE + NH(3) = ADP + PHOSPHATE +
 CC L-GLUTAMINE.
 CC -1- SIMILARITY: BELONGS TO THE GLUTAMINE SYNTHETASE FAMILY.
 DR EMBL; AF031129; AAB87965.1;
 DR HSSP; P06201; ILGR.
 DR InterPro; IPR004809; GlnA.
 DR InterPro; IPR001637; GlnA_adenyltn.
 DR InterPro; IPR001691; GLN_synth.
 DR Pfam; PF00120; gln-synt; 1.
 DR ProDom; PD001057; GlnA_adenyltn; 1.
 DR TIGRFAMS; TIGR00653; GlnA; 1.
 DR PROSITE; PS00180; GLNA_1; 1.
 KW Ligase.
 SQ SEQUENCE 473 AA; 53045 MW; F228C865640D2555 CRC64;
 Query Match 71.7%; Score 38; DB 2; Length 473;
 Best Local Similarity 60.0%; Pred. No. 44;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 STYYLDTVEG 10
 Db :||||| :|
 150 SSYYVDSIEG 159

```

RESULT 8
Q9LHW3 ID Q9LHW3 PRELIMINARY; PRT; 116 AA.
AC Q9LHW3; 2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical protein.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophytá;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC
RT clone:p0515G01.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AP001633; BAA94223.1;
KW Hypothetical protein.
SQ SEQUENCE 116 AA; 12974 MW; 628AFC798CBB8EC CRC64;

Query Match 69.8%; Score 37; DB 10; Length 116;
Best Local Similarity 66.7%; Pred. No. 15;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYLDTVE 9
   |||||
Db 44 STYYFDTL 52

RESULT 9
Q91WP5 ID Q91WP5 PRELIMINARY; PRT; 479 AA.
AC Q91WP5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical 51.6 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COLON;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC013656; AAH13656.1;
DR InterPro: IPR003598; Ig_MHC.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig; 4.
DR SMART: SM00408; Igc2; 1.
DR PROSITE: PS00290; Ig_MHC; UNKNOWN_2.
KW Hypothetical protein; Immunoglobulin domain.
SQ SEQUENCE 479 AA; 51603 MW; ECB2D087748584F CRC64;

Query Match 69.8%; Score 37; DB 11; Length 479;
Best Local Similarity 60.0%; Pred. No. 71;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYLDTVEG 10
   :||| |||
Db 76 NTYYSDTMKG 85

RESULT 10
Q9UL72 ID Q9UL72 PRELIMINARY; PRT; 118 AA.

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AC Q9UL72;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035042; AAD56278.1;
DR HSSP: P01772; 2FB4.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR NON_TER 1
FT NON_TER 118
SQ SEQUENCE 118 AA; 12872 MW; B4D1A5944B2D5CCA CRC64;

Query Match 67.9%; Score 36; DB 4; Length 118;
Best Local Similarity 60.0%; Pred. No. 23;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYLDTVEG 10
   ||||| |||
Db 56 SSYYADSVKG 65

RESULT 11
Q9RA41 ID Q9RA41 PRELIMINARY; PRT; 258 AA.
AC Q9RA41;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Glutamine synthase (EC 6.3.1.2) (Fragment).
OS GLNA.
OS Trichodesmium sp. (strain IMS101).
OC Bacteria; Cyanobacteria; Oscillatoriales; Trichodesmium.
OX NCBI_TaxID=57878;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IMS101;
RA Dominic B., Zehr J.P.;
RT "Transcriptional analysis of the global nitrogen control gene ntca and
RT nitrogen assimilation gene glna in relation to nif genes of
RT Trichodesmium sp. IMS101.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE + NH(3) -> ADP + PHOSPHATE +
CC L-GLUTAMINE.
CC -!- SIMILARITY: BELONGS TO THE GLUTAMINE SYNTHETASE FAMILY.
DR EMBL: AF169960; AAD53079.1;
DR HSSP: P06201; 1LGR.
DR InterPro: IPR001637; GlnA_adenyltn.
DR InterPro: IPR001691; GlnA_synth.
DR Pfam: PF00120; gln-synt; 1.
DR ProDom: PD001057; GlnA_adenyltn; 1.
DR PROSITE: PS00181; GLNA_ATP; 1.
KW Ligase.
FT NON_TER 1
FT NON_TER 258
SQ SEQUENCE 258 AA; 28741 MW; A9A98E7AA78E9CC2 CRC64;

Query Match 67.9%; Score 36; DB 2; Length 258;

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Best Local Similarity 62.5%; Pred. No. 56;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 YYLDTVEG 10
Db 24 YYVDSIEG 31

RESULT 12
Q9RS44 PRELIMINARY; PRT; 268 AA.
AC Q9RS44;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Manganese ABC transporter, permease protein, putative.
GN D2283.
OS Deinococcus radiodurans.
OC Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales;
OC Deinococcaceae; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RI;
RX MEDLINE=20036896; PubMed=10567266;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Vamathevan J.J., Lam P., McDonald L., Utterback T., Zaleski C.,
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "genome sequence of the radioresistant bacterium Deinococcus
RT radiodurans RI."
RL Science 286:1571-1577(1999).
DR EMBL: AE002060; AAF11829.1; -.
DR TIGR: DR2283; -.
DR InterPro: IPR001626; ABCtransprtr3.
DR Pfam: PF00950; ABC-3; 1.
KW Complete proteome.
SQ SEQUENCE 268 AA; 27919 MW; 2D16BE531E8D9033 CRC64;

Query Match 67.9%; Score 36; DB 16; Length 268;
Best Local Similarity 60.0%; Pred. No. 58;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 STYYLDTVEG 10
Db 239 ASYYLDTAPG 248

RESULT 13
Q32822 PRELIMINARY; PRT; 339 AA.
AC Q32822;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical 39.7 kDa protein (Fragment).
OS Listeria monocytogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Listeriaceae; Listeria.
OX NCBI_TaxID=1639;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EGD;
RA Borovok I., Mislovati M., Cohen G., Aharonowitz Y.;
RT "Isolation, cloning and characterization of the Listeria monocytogenes
RT thioredoxin reductase gene, trxB."
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF009622; AAB63803.1; -.
DR InterPro: IPR001440; TPR.
KW Hypothetical protein.
```

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FT NON_TER 1
SQ SEQUENCE 339 AA; 39702 MW; 601CE3B46B06D006 CRC64;

Query Match 67.9%; Score 36; DB 2; Length 339;
Best Local Similarity 70.0%; Pred. No. 76;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 STYYLDTVEG 10
Db 148 SSYILGDSVEG 157

RESULT 14
Q9RHZ1 PRELIMINARY; PRT; 474 AA.
AC Q9RHZ1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Glutamine synthetase (EC 6.3.1.2).
GN GLNA.
OS Anabaena azollae.
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
OX NCBI_TaxID=1164;
RN [1]
RP SEQUENCE FROM N.A.
RA Francisco F.J.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20050636; PubMed=10583418;
RA Crespo J.L., Guerrero M.G., Florencio F.J.;
RT "Mutational analysis of Asp-51 of Anabaena azollae glutamine
RT synthetase. D51E mutation confers resistance to the active site
RT inhibitors L-methionine-DL-sulfoximine and phosphinothricin."
RL Eur. J. Biochem. 266:1202-1209(1999)
CC -|- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE + NH(3) -> ADP + PHOSPHATE +
CC L-GLUTAMINE.
CC -|- SUBUNIT: OLIGOMER OF 12 SUBUNITS ARRANGED IN THE FORM OF TWO
CC HEXAGON (BY SIMILARITY).
CC -|- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -|- SIMILARITY: BELONGS TO THE GLUTAMINE SYNTHETASE FAMILY.
DR EMBL: AJ249658; CAB64594.1; -.
DR HSSP: P06201; ILGR.
DR InterPro: IPR004809; GlnA.
DR InterPro: IPR001637; GlnA_adenyltn.
DR InterPro: IPR001691; Gln_synth.
DR Pfam: PF00120; gln-synt; 1.
DR ProDom: PD001057; GlnA_adenyltn; 1.
DR TIGRFAMs: TIGR00653; GlnA; 1.
DR PROSITE: PS00180; GLNA_1; 1.
DR PROSITE: PS00182; GLNA_ADENYLATION; 1.
DR PROSITE: PS00181; GLNA_ATP; 1.
KW Ligase.
SQ SEQUENCE 474 AA; 52993 MW; 54FDF2975DF5EFBC CRC64;

Query Match 67.9%; Score 36; DB 2; Length 474;
Best Local Similarity 75.0%; Pred. No. 11e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 YYLDTVEG 10
Db 151 YFLDSVEG 158

RESULT 15
Q928B4 PRELIMINARY; PRT; 491 AA.
AC Q928B4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein lin2622.
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GN LIN2622.
OS Listeria innocua.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Listeriaceae; Listeria.
OX NCBI_TaxID=1642;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CLIP 11262 / SEROVAR 6A;
RX PubMed=11679669;
RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouni F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Gobel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Rammel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
DR EMBL; AL596173; CAC97849.1; -.
DR Listlist; LIN2622; -.
DR InterPro; IPR001440; TPR.
DR Pfam; PF00515; TPR; 3.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 491 AA; 57742 MW; B03FAAFCAAE9AE53 CRC64;

Query Match 67.9%; Score 36; DB 16; Length 491;
Best Local Similarity 77.8%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 STYYLDTFVE 9
Db 300 SAYYLDVEVE 308

Search completed: November 18, 2002, 17:40:41
Job time : 12.4912 secs

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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:21:57 ; Search time 13.8235 Seconds
(without alignments)
96.394 Million cell updates/sec

Title: US-09-016-061-58
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Scoring table: BLOSUM62
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Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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19: /SID22/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
20: /SID22/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
21: /SID22/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22: /SID22/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	53	100.0	10	19	LM609 grafted anti
2	53	100.0	10	22	Mutant VH CDR2 pep
3	50	94.3	10	19	LM609 grafted anti
4	50	94.3	10	22	LM609 VH CDR2 pep
5	50	94.3	17	22	Enhanced 6H6LH hea
6	50	94.3	117	19	Vitaxin antibody h
7	50	94.3	117	19	LM609 antibody hea
8	50	94.3	117	20	Murine monoclonal
9	50	94.3	117	22	A heavy chain vari
10	50	94.3	117	22	A heavy chain vari

11	50	94.3	117	22	AA661359	Vitaxin heavy chai
12	50	94.3	117	22	AA661361	Antibody LM609 hea
13	50	94.3	130	20	AAU06379	Murine monoclonal
14	45	84.9	121	22	AA667069	Murine G250 antibo
15	45	84.9	352	23	AAU87031	Adenovirus 5 fiber
16	45	84.9	465	23	AAU87033	Adenovirus 5 fiber
17	45	84.9	565	23	AAU87034	Adenovirus 5 fiber
18	44	83.0	124	22	AAE07018	Human heavy chain
19	43	81.1	10	19	AAW76018	LM609 grafted anti
20	43	81.1	10	22	AA661376	Mutant VH CDR2 pep
21	43	81.1	17	22	AA661400	Enhanced LM609 VH
22	43	81.1	21	20	AAW99565	Immunoglobulin IgG
23	43	81.1	30	20	AAW98570	Immunoglobulin IgG
24	43	81.1	30	21	AAU78332	Anti-DNA monoclonal
25	43	81.1	30	22	AAU78332	Peptide #2. Synth
26	43	81.1	30	22	AAU78332	Peptide P3. Homo
27	43	81.1	30	23	AAE23169	Monoclonal antibody
28	43	81.1	30	23	AAE16153	Anti-DNA antibody
29	43	81.1	31	20	AAW98572	Immunoglobulin IgG
30	43	81.1	33	20	AAW99571	Immunoglobulin IgG
31	43	81.1	49	20	AAW99573	Immunoglobulin IgG
32	43	81.1	17	18	AAW27342	CDR2 from murine a
33	42	79.2	17	22	AAU07738	Human heavy chain
34	42	79.2	87	22	AAE06990	Mouse germline hea
35	42	79.2	98	22	AAE06978	Mouse germline hea
36	42	79.2	112	22	AAU07743	Human heavy chain
37	42	79.2	117	16	AAU79155	Human IgE receptor
38	42	79.2	117	18	AAW27357	Heavy chain variab
39	42	79.2	117	18	AAW27526	Heavy chain variab
40	42	79.2	117	18	AAW27354	Heavy chain variab
41	42	79.2	118	16	AAW79161	Human IgE receptor
42	42	79.2	120	17	AAW00240	EGF receptor chime
43	42	79.2	125	22	AA648937	Anti-TrkA murine m
44	42	79.2	127	15	AAU47510	LSH241 heavy chai
45	42	79.2	139	18	AAW21652	Humanised reshaped

ALIGNMENTS

RESULT 1
AAW76019
ID AAW76019 standard; Protein; 10 AA.
XX
AC AAW76019;
XX
DT 02-NOV-1998 (first entry)
XX
DE LM609 grafted antibody V-H region CDR2 protein fragment #5.
XX
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
XX
OS Mus sp.
XX
PN WO9833919-A2.
XX
PD 06-AUG-1998.
XX
PF 30-JAN-1998; 98WO-US01826.
XX
PR 30-JAN-1997; 97US-0791391.
XX
PA (IXSY-) IXSYS INC.
XX
PI Glaser SM, Huse WD;
XX
DR WPI; 1998-437472/37.
N-PSDB; AAV49856.

XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
XX Claim 61; Page 41; 129pp; English.
XX
CC AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
CC antibodies contain non-murine framework regions so are suitable for use
CC in humans. Enhanced types of LM609 have affinity more than 90 times
CC greater than that of parent the parent antibody.
XX
XX Sequence 10 AA;
SQ
Query Match 100.0%; Score 53; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 STYYLDTVVEG 10
Db 1 STYYLDTVVEG 10
|||||
RESULT 2
AAB61377
ID AAB61377 standard; peptide; 10 AA.
AC AAB61377;
XX
XX 03-APR-2001 (first entry)
XX
XX Mutant VH CDR2 peptide #3.
XX
XX LM609; grafted antibody; alphaVbeta_3 integrin; angiogenesis;
KW inflammatory; cancer; retina; restenosis; osteoporosis.
XX
XX Unidentified.
XX
XX WO200078815-A1.
XX
XX 28-DEC-2000.
XX
XX 23-JUN-2000; 2000WO-US17454.
XX
XX 24-JUN-1999; 99US-0339922.
XX
XX (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX
XX Huse WD, Wu H;
XX
XX WPI; 2001-050110/06.
XX
XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
PT osteoporosis -
XX
XX Disclosure; Page 41; 132pp; English.
XX
XX The present invention relates to enhanced LM609 grafted antibodies
CC exhibiting selective binding affinity to alphavbeta_3 integrin or
CC their functional fragments. The antibodies or their functional
CC fragments can be used in the diagnosis and treatment of
CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory

CC diseases (such as psoriasis and chronic articular rheumatism),
CC disorders associated with inappropriate or inopportune invasion of
CC vessels (such as diabetic retinopathy, neovascular glaucoma and
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
CC diseases (such as macular degeneration), restenosis and
CC osteoporosis.
XX
XX Sequence 10 AA;
SQ
Query Match 100.0%; Score 53; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 STYYLDTVVEG 10
Db 1 STYYLDTVVEG 10
|||||
RESULT 3
AAW76009
ID AAW76009 standard; Protein; 10 AA.
XX
XX AAW76009;
AC
XX 02-NOV-1998 (first entry)
DT
XX
XX LM609 grafted antibody V-H region CDR2 protein fragment #2.
DE
XX
XX Vitaxin; antibody; variable region; heavy chain; light chain; Integrin;
KW LM609; inhibitor; Integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
XX
XX Mus sp.
OS
XX
XX WO9833919-A2.
XX
XX 06-AUG-1998.
XX
XX 30-JAN-1998; 98WO-US01826.
XX
XX 30-JAN-1997; 97US-0791391.
XX
XX (IXSY-) IXSYS INC.
XX
XX Glaser SM, Huse WD;
PI
XX
XX WPI; 1998-437472/37.
XX
XX N-PSDB; AAV49846.
XX
XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
XX Disclosure; Page 40; 129pp; English.
XX
XX AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
CC antibodies contain non-murine framework regions so are suitable for use
CC in humans. Enhanced types of LM609 have affinity more than 90 times
CC greater than that of parent the parent antibody.
XX
XX Sequence 10 AA;
SQ

Query Match 94.3%; Score 50; DB 19; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.0097;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYLDTVQV 10
 | | | | | | | | | |
 Db 1 STYLDTVQV 10

RESULT 4

AAB61367
 ID AAB61367 standard; peptide; 10 AA.

XX
 AC AAB61367;

DT 03-APR-2001 (first entry)

DE LM609 VH CDR2 peptide #2.

XX LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis.
 XX

OS Unidentified.

PN WO200078815-A1.

XX 28-DEC-2000.

XX 23-JUN-2000; 2000WO-US17454.

XX 24-JUN-1999; 99US-0339922.

XX (MOLE-) APPLIED MOLECULAR EVOLUTION.

PI Huse WD, Wu H;

XX WPI; 2001-050110/06.

XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -

PS Disclosure; Page 39; 132pp; English.

XX The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphavbeta_3 integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.

XX Sequence 10 AA;

Query Match 94.3%; Score 50; DB 22; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.0097;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYLDTVQV 10
 | | | | | | | | | |
 Db 1 STYLDTVQV 10

RESULT 5

AAB61399
 ID AAB61399 standard; peptide; 17 AA.

XX

AC AAB61399;

DT 03-APR-2001 (first entry)

XX Enhanced 6H6LH heavy chain CDR2.

XX LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis.
 XX

OS Unidentified.

PN WO200078815-A1.

XX 28-DEC-2000.

XX 23-JUN-2000; 2000WO-US17454.

XX 24-JUN-1999; 99US-0339922.

XX (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX Huse WD, Wu H;

XX WPI; 2001-050110/06.

XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -

PS Claim 4; Page 46; 132pp; English.

XX The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphavbeta_3 integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.

XX Sequence 17 AA;

Query Match 94.3%; Score 50; DB 22; Length 17;
 Best Local Similarity 90.0%; Pred. No. 0.018;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYLDTVQV 10
 | | | | | | | | | |
 Db 8 STYLDTVQV 17

RESULT 6

AAB61399
 ID AAB61399 standard; Protein; 117 AA.

XX AAB61399;

DT 02-NOV-1998 (first entry)

XX Vitaxin antibody heavy chain variable region protein fragment.

XX Vitaxin; antibody; variable region; heavy chain; light chain; Integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.

XX Mus sp.


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PN WO9833919-A2.
XX
PD 06-AUG-1998.
XX
PF 30-JAN-1998; 98WO-US01826.
XX
PR 30-JAN-1997; 97US-0791391.
XX
PA (IXSY-) IXSYS INC.
XX
PI Glaser SM, Huse WD;
XX
DR WPI; 1998-437472/37.
DR N-PSDB; AAV49820.
XX
PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
PS Claim 1; Fig 1a; 129pp; English.
XX
CC This sequence represents a fragment of the vitaxin antibody variable
CC heavy chain region. Vitaxin and the antibody LM609 bind selectively to
CC integrin alphavbeta3 and can be used to inhibit binding of alphavbeta3
CC to a ligand and thus block integrin-mediated signal transduction. This is
CC useful in the treatment, prevention and diagnosis of alphavbeta3-mediated
CC disease, specifically angiogenesis and restenosis (but also e.g.
CC (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,
CC cancer, psoriasis, rheumatoid arthritis, macular degeneration,
CC osteoporosis etc.). The antibodies contain non-murine framework regions
CC so are suitable for use in humans. Enhanced types of LM609 have affinity
CC more than 90 times greater than that of parent the parent antibody.
XX
SQ Sequence 117 AA;

Query Match 94.3%; Score 50; DB 19; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.15;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYLDTVEG 10
Db 57 STYYLDTVQG 66
|||||||:|

RESULT 7
AAW76003
ID AAW76003 standard; Protein; 117 AA.
XX
AC AAW76003;
XX
DT 02-NOV-1998 (first entry)
XX
DE LM609 antibody heavy chain variable region protein fragment.
XX
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis.
XX
OS Mus sp.
XX
PN WO9833919-A2.
XX
PD 06-AUG-1998.
XX
PF 30-JAN-1998; 98WO-US01826.
XX
PR 30-JAN-1997; 97US-0791391.
XX
PA (IXSY-) IXSYS INC.
XX

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PI Glaser SM, Huse WD;
XX
DR WPI; 1998-437472/37.
DR N-PSDB; AAV49822.
XX
PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
PS Claim 43; Fig 2a; 129pp; English.
XX
CC This sequence represents the LM609 antibody variable heavy chain region.
CC LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3
CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus
CC block integrin-mediated signal transduction. This is useful in the
CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,
CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
CC etc.). The antibodies contain non-murine framework regions so are
CC suitable for use in humans. Enhanced types of LM609 have affinity more
CC than 90 times greater than that of parent the parent antibody.
XX
SQ Sequence 117 AA;

Query Match 94.3%; Score 50; DB 19; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.15;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYLDTVEG 10
Db 57 STYYLDTVQG 66
|||||||:|

RESULT 8
AAW06381
ID AAW06381 standard; Protein; 117 AA.
XX
AC AAW06381;
XX
DT 06-SEP-1999 (first entry)
XX
DE Murine monoclonal antibody LM609 VH region.
XX
KW Humanised antibody; antibody humanisation; antibody engineering;
KW LM609; monoclonal antibody; complementarity determining region;
KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
KW cancer; therapy; diagnosis.
XX
OS Mus musculus.
XX
PN WO9929888-A1.
XX
PD 17-JUN-1999.
XX
PF 04-DEC-1998; 98WO-US25828.
XX
PR 05-DEC-1997; 97US-0986016.
XX
PA (SCRI) SCRIPPS RES INST.
XX
PI Barbas CF, Rader C;
XX
DR WPI; 1999-394979/33.
XX
PT Production of humanized mouse monoclonal antibodies
XX
PS Disclosure; Page 52-53; 55pp; English.
XX
CC This sequence represents the heavy chain variable region of murine
CC monoclonal antibody LM609. LM609 is directed to integrin
CC alpha-v beta-3. It selectively promotes apoptosis of vascular

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CC cells that have been stimulated to undergo angiogenesis, making it
 CC a tool for cancer diagnosis and therapy. The invention provides
 CC humanised antibodies, especially humanised LM609. In such humanized
 CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
 CC grafted onto a human light chain, and a heavy chain CDR from a mouse
 CC antibody is grafted onto a human antibody heavy chain to produce
 CC libraries from which a humanised murine antibody having the desired
 CC specificity is selected. By preserving the original CDR sequences
 CC such as the HCDR3 and LCDR3 sequences of LM609 (see AAY06371-72), the
 CC humanisation strategy ensures epitope conservation.

XX SQ Sequence 117 AA;

Query Match 94.3%; Score 50; DB 20; Length 117;

Best Local Similarity 90.0%; Pred. No. 0.15;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STYYLDTVEG 10

|||||||:|

Db 57 STYYLDTVQG 66

RESULT 9

AAG63587

ID AAG63587 standard; Protein; 117 AA.

XX AC AAG63587;

XX 15-OCT-2001 (first entry)

XX A heavy chain variable region of LM609 grafted antibody.

XX Grafted antibody; LM609; integrin; alphavbeta3; inflammatory disorder;

XX chronic articular rheumatism; psoriasis; diabetic retinopathy;

XX neovascular glaucoma; capillary proliferation; atherosclerotic plaque;

XX cancer.

XX Synthetic.

XX Mus sp.

XX US2001011125-A1.

XX 02-AUG-2001.

XX 30-JAN-1997; 97US-0790540.

XX 30-JAN-1997; 97US-0790540.

XX (HUSE/) HUSE W D.

XX Huse WD;

XX WPI: 2001-496171/54.

XX N-PSDB; AAH74623.

XX New LM609 grafted antibody exhibiting selective binding affinity to
 PT alphavbeta3, comprising at least one LM609 grafted heavy and light
 PT chain polypeptide, useful for diagnosing and treating e.g. inflammatory
 PT disorders or cancer
 XX Claim 1; Fig 1A; 25pp; English.

XX The present sequence represents the heavy chain variable region of the
 CC grafted monoclonal antibody LM609. LM609 is a murine antibody which
 CC specifically recognises the integrin alphavbeta3, and inhibits is
 CC functional activity. The LM609 grafted antibody has the
 CC complementarity determining regions (CDRs) substituted into a non-murine
 CC framework. Nucleic acids encoding LM609 grafted heavy and light chain
 CC polypeptides and fragments are useful in diagnostic and therapeutic
 CC purposes, such as in the production of LM609 grafted antibodies and
 CC fragments having binding specificity and inhibitory activity against
 CC the integrin alphavbeta3. The antibody can be used for the diagnosis
 CC or treatment of alphavbeta3-mediated diseases (e.g. inflammatory

CC disorders, chronic articular rheumatism, psoriasis, disorders
 CC associated with inappropriate or inopportune invasion of vessels such
 CC as diabetic retinopathy, neovascular glaucoma and capillary
 CC proliferation in atherosclerotic plaques, or cancers), and to inhibit
 CC binding activity of alphavbeta3 that are necessary for progression of
 CC an alphavbeta3-mediated disease.

XX SQ Sequence 117 AA;

Query Match 94.3%; Score 50; DB 22; Length 117;

Best Local Similarity 90.0%; Pred. No. 0.15;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STYYLDTVEG 10

|||||||:|

Db 57 STYYLDTVQG 66

RESULT 10

AAG63589

ID AAG63589 standard; Protein; 117 AA.

XX AC AAG63589;

XX 15-OCT-2001 (first entry)

XX A heavy chain variable region of LM609 antibody.

XX Grafted antibody; LM609; integrin; alphavbeta3; inflammatory disorder;
 XX chronic articular rheumatism; psoriasis; diabetic retinopathy;
 XX neovascular glaucoma; capillary proliferation; atherosclerotic plaque;
 XX cancer.

XX Mus sp.

XX US2001011125-A1.

XX 02-AUG-2001.

XX 30-JAN-1997; 97US-0790540.

XX 30-JAN-1997; 97US-0790540.

XX (HUSE/) HUSE W D.

XX Huse WD;

XX WPI: 2001-496171/54.

XX N-PSDB; AAH74625.

XX New LM609 grafted antibody exhibiting selective binding affinity to
 PT alphavbeta3, comprising at least one LM609 grafted heavy and light
 PT chain polypeptide, useful for diagnosing and treating e.g. inflammatory
 PT disorders or cancer
 XX Disclosure; Fig 2A; 25pp; English.

XX The present sequence represents the heavy chain variable region of the
 CC monoclonal antibody LM609. LM609 is a murine antibody which specifically
 CC recognises the integrin alphavbeta3, and inhibits is functional activity.
 CC The specification describes a LM609 grafted antibody which has the
 CC complementarity determining regions (CDRs) substituted into a non-murine
 CC framework. Nucleic acids encoding LM609 grafted heavy and light chain
 CC polypeptides and fragments are useful in diagnostic and therapeutic
 CC purposes, such as in the production of LM609 grafted antibodies and
 CC fragments having binding specificity and inhibitory activity against
 CC the integrin alphavbeta3. The antibody can be used for the diagnosis
 CC or treatment of alphavbeta3-mediated diseases (e.g. inflammatory
 CC disorders, chronic articular rheumatism, psoriasis, disorders
 CC associated with inappropriate or inopportune invasion of vessels such
 CC as diabetic retinopathy, neovascular glaucoma and capillary
 CC proliferation in atherosclerotic plaques, or cancers), and to inhibit
 CC binding activity of alphavbeta3 that are necessary for progression of

CC an alphavbeta3-mediated disease.

SQ Sequence 117 AA;

Query Match 94.3%; Score 50; DB 22; Length 117;

Best Local Similarity 90.0%; Pred. No. 0.15;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYLDIVVEG 10

|||||||:|

Db 57 STYYLDIVVQG 66

RESULT 11

AAB61359

ID AAB61359 standard; protein; 117 AA.

XX

AC AAB61359;

XX

DT 03-APR-2001 (first entry)

XX

DE Vitaxin heavy chain variable region protein.

XX

KW LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;

KW inflammatory; cancer; retina; restenosis; osteoporosis.

XX

OS Unidentified.

XX

PN WO200078815-A1.

XX

PD 28-DEC-2000.

XX

PF 23-JUN-2000; 2000WO-US17454.

XX

PR 24-JUN-1999; 99US-0339922.

XX

PA (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX

PI Huse WD, Wu H;

XX

DR WPI; 2001-050110/06.

XX

PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity

PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of

PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and

PT osteoporosis -

XX

PS Disclosure; Fig 1; 132pp; English.

XX

CC The present invention relates to enhanced LM609 grafted antibodies

CC exhibiting selective binding affinity to alphavbeta_3 integrin or

CC their functional fragments. The antibodies or their functional

CC fragments can be used in the diagnosis and treatment of

CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory

CC diseases (such as psoriasis and chronic articular rheumatism),

CC disorders associated with inappropriate or inopportune invasion of

CC vessels (such as diabetic retinopathy, neovascular glaucoma and

CC cancer disorders such as tumours and Kaposi's sarcoma), retinal

CC osteoporosis.

XX

SQ Sequence 117 AA;

Query Match

Best Local Similarity 94.3%; Score 50; DB 22; Length 117;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYLDIVVEG 10

|||||||:|

Db 57 STYYLDIVVQG 66

RESULT 12

AAB61361

ID AAB61361 standard; protein; 117 AA.

XX

AC AAB61361;

XX

DT 03-APR-2001 (first entry)

XX

DE Antibody LM609 heavy chain variable region protein.

XX

KW LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;

KW inflammatory; cancer; retina; restenosis; osteoporosis.

XX

OS Unidentified.

XX

PN WO200078815-A1.

XX

PD 28-DEC-2000.

XX

PF 23-JUN-2000; 2000WO-US17454.

XX

PR 24-JUN-1999; 99US-0339922.

XX

PA (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX

PI Huse WD, Wu H;

XX

DR WPI; 2001-050110/06.

XX

PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of angiogenesis, inflammatory diseases e.g. psoriasis, cancers and osteoporosis -

XX

PS Disclosure; Fig 2; 132pp; English.

XX

CC The present invention relates to enhanced LM609 grafted antibodies

CC exhibiting selective binding affinity to alphavbeta_3 integrin or

CC their functional fragments. The antibodies or their functional

CC fragments can be used in the diagnosis and treatment of

CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory

CC diseases (such as psoriasis and chronic articular rheumatism),

CC disorders associated with inappropriate or inopportune invasion of

CC vessels (such as diabetic retinopathy, neovascular glaucoma and

CC cancer disorders such as tumours and Kaposi's sarcoma), retinal

CC diseases (such as macular degeneration), restenosis and

CC osteoporosis.

XX

SQ Sequence 117 AA;

Query Match

Best Local Similarity 94.3%; Score 50; DB 22; Length 117;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYLDIVVEG 10

|||||||:|

Db 57 STYYLDIVVQG 66

RESULT 13

AAV06379

ID AAV06379 standard; Protein; 130 AA.

XX

AC AAV06379;

XX

DT 06-SEP-1999 (first entry)

XX

DE Murine monoclonal antibody LM609 V kappa.

XX

KW Humanised antibody; antibody humanisation; antibody engineering;

KW LM609; monoclonal antibody; complementarity determining region;

KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;

KW cancer; therapy; diagnosis.

XX

XX	Disclosure; Page 95-99; 163pp; English.				
XX					
CC	The invention describes a modified virus comprising non-native				
CC	polypeptides which has framework moieties each containing binding				
CC	moieties, where the virus has altered tropism conferred by the binding				
CC	moieties. The polypeptides can be expressed in the cytoplasm and nucleus				
CC	of mammalian host cell in conformation which is maintained in absence of				
CC	ligands for the binding moieties, where the conformation allows the				
CC	binding moiety subsequently to bind with the ligand. The modified virus				
CC	is useful in therapy for the preparation of a medicament for treating				
CC	tumour cells, cancer, proliferating cells, vascular diseases,				
CC	inflammatory diseases and infectious diseases such as Human				
CC	immunodeficiency virus (HIV). The altered tropisms allow the virus to be				
CC	used in treatment of disease in human or animal subjects, either by in				
CC	vivo treatment of, or ex vivo treatment of cells of, the subject				
CC	requiring treatment. The problems associated with the expression of				
CC	functional non-native viral components in the nucleus and cytosol of				
CC	host cells is solved by using the modified virus for the purpose. This				
CC	sequence represents an amino acid sequence used in the creation of the				
CC	modified virus containing non-native polypeptides.				
XX					
SQ	Sequence 352 AA;				
	Query Match 84.9%; Score 45; DB 23; Length 352;				
	Best Local Similarity 88.9%; Pred. No. 4.3;				
	Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;				
Oy	2 TYILDRTVEG 10				
Db	183 TYILDRTVKG 191				

Search completed: November 18, 2002, 17:31:36
Job time : 14.8235 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:54:45 ; Search time 1.96078 Seconds
(without alignments)
76.811 Million cell updates/sec

Title: US-09-016-061-58
Perfect score: 53
Sequence: 1 STYLDTEG 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 97044 seqs, 15060890 residues

Total number of hits satisfying chosen parameters: 97044

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/RCTUS_PUBCOMB pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	50	94.3	117	8	US-08-790-540A-2
2	50	94.3	117	8	US-08-790-540A-6
3	50	94.3	117	8	US-08-791-391A-2
4	50	94.3	117	8	US-08-791-391A-6
5	44	83.0	124	10	US-09-840-459-81
6	42	79.2	87	10	US-09-840-459-53
7	42	79.2	98	10	US-09-840-459-41
8	41	77.4	245	9	US-09-956-086-5
9	41	77.4	245	9	US-09-956-087-5
10	41	77.4	265	9	US-09-985-442-5
11	41	77.4	265	10	US-09-983-580-5
12	40	75.5	17	9	US-09-968-561A-14
13	40	75.5	17	9	US-09-968-561A-38
14	40	75.5	17	9	US-09-968-561A-68
15	40	75.5	17	9	US-09-968-561A-74
16	40	75.5	17	9	US-09-968-561A-80
17	40	75.5	17	9	US-09-968-561A-86
18	40	75.5	17	9	US-09-968-561A-92
19	40	75.5	17	9	US-09-968-561A-122

20	40	75.5	17	9	US-09-968-561A-128	Sequence 128, App
21	40	75.5	17	9	US-09-968-561A-134	Sequence 134, App
22	40	75.5	17	9	US-09-968-561A-140	Sequence 140, App
23	40	75.5	17	9	US-09-968-561A-146	Sequence 146, App
24	40	75.5	17	9	US-09-968-561A-188	Sequence 188, App
25	40	75.5	17	9	US-09-968-561A-194	Sequence 194, App
26	40	75.5	17	9	US-09-968-561A-212	Sequence 212, App
27	40	75.5	17	9	US-09-968-561A-218	Sequence 218, App
28	40	75.5	17	9	US-09-968-561A-236	Sequence 236, App
29	40	75.5	17	9	US-09-968-561A-260	Sequence 260, App
30	40	75.5	17	9	US-09-968-561A-266	Sequence 266, App
31	40	75.5	17	9	US-09-968-561A-272	Sequence 272, App
32	40	75.5	17	9	US-09-968-561A-284	Sequence 284, App
33	40	75.5	17	9	US-09-968-561A-296	Sequence 296, App
34	40	75.5	17	9	US-09-968-561A-308	Sequence 308, App
35	40	75.5	17	9	US-09-968-561A-314	Sequence 314, App
36	40	75.5	17	10	US-09-192-854-10	Sequence 10, Appl
37	40	75.5	98	10	US-09-864-761-44343	Sequence 44343, A
38	40	75.5	98	10	US-09-822-698A-18	Sequence 18, Appl
39	40	75.5	98	12	US-10-025-687-19	Sequence 19, Appl
40	40	75.5	111	10	US-09-899-896-7	Sequence 7, Appl
41	40	75.5	113	10	US-09-056-160B-11	Sequence 11, Appl
42	40	75.5	116	10	US-09-840-459-80	Sequence 80, Appl
43	40	75.5	117	10	US-09-840-459-83	Sequence 83, Appl
44	40	75.5	119	10	US-09-811-123-3	Sequence 3, Appl
45	40	75.5	120	10	US-09-840-459-85	Sequence 85, Appl

ALIGNMENTS

RESULT 1
US-08-790-540A-2
; Sequence 2, Application US/08790540A
; Patent No. US20010011125A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,540A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-790-540A-2

Query Match 94.3%; Score 50; DB 8; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.014;

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Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYLDTVQ 10
Db 57 STYYLDTVQ 66

RESULT 2
US-08-790-540A-6
; Sequence 6, Application US/08790540A
; Patent No. US2001001125A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TELECOMMUNICATION INFORMATION:
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,540A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-790-540A-6

Query Match 94.3%; Score 50; DB 8; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.014;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYLDTVQ 10
Db 57 STYYLDTVQ 66

RESULT 3
US-08-791-391A-2
; Sequence 2, Application US/08791391A
; Patent No. US20010016645A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TELECOMMUNICATION INFORMATION:
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122

Query Match 94.3%; Score 50; DB 8; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.014;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYLDTVQ 10
Db 57 STYYLDTVQ 66

RESULT 4
US-08-791-391A-6
; Sequence 6, Application US/08791391A
; Patent No. US20010016645A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TELECOMMUNICATION INFORMATION:
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,391A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-391A-6
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COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,391A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-391A-2

Query Match 94.3%; Score 50; DB 8; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.014;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYLDTVQ 10
Db 57 STYYLDTVQ 66

RESULT 4
US-08-791-391A-6
; Sequence 6, Application US/08791391A
; Patent No. US20010016645A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TELECOMMUNICATION INFORMATION:
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,391A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-391A-6
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Query Match 94.3%; Score 50; DB 8; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.014;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYLDTVEG 10
Db 57 STYYLDTVVG 66
|||||:|

RESULT 5

US-09-840-459-81
; Sequence 81, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 81
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-840-459-81

Query Match 83.0%; Score 44; DB 10; Length 124;
Best Local Similarity 80.0%; Pred. No. 0.19;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYLDTVEG 10
Db 57 STYYADSVGE 66
|||||:|

RESULT 6

US-09-840-459-53
; Sequence 53, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22

; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 53
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-840-459-53

Query Match 79.2%; Score 42; DB 10; Length 87;
Best Local Similarity 80.0%; Pred. No. 0.29;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYLDTVEG 10
Db 46 STYYPDTVKG 55
|||||:|

RESULT 7

US-09-840-459-41
; Sequence 41, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 41
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-840-459-41

Query Match 79.2%; Score 42; DB 10; Length 98;
Best Local Similarity 80.0%; Pred. No. 0.33;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYLDTVEG 10
Db 57 STYYPDTVKG 66
|||||:|

RESULT 8

US-09-956-086-5
; Sequence 5, Application US/09956086
; Patent No. US20020155498A1
; GENERAL INFORMATION:
; APPLICANT: FILPULA, DAVID
; WANG, MAOLIANG
; SHORR, ROBERT
; WHITLOW, MARC
; LEE, LIHSYNG S.
; TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS
; CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF
; NUMBER OF SEQUENCES: 33

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;; STREET: 1100 NEW YORK AVE., NW, SUITE 600
;; CITY: WASHINGTON
;; STATE: DC
;; COUNTRY: USA
;; ZIP: 20005
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/956,086
;; FILING DATE: 20-Sep-2001
;; CLASSIFICATION: <Unknown>
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 09/069,821
;; FILING DATE: <Unknown>
;; APPLICATION NUMBER: US 60/063,074
;; FILING DATE: 27-OCT-1997
;; APPLICATION NUMBER: US 60/050,472
;; FILING DATE: 23-JUN-1997
;; APPLICATION NUMBER: US 60/044,449
;; FILING DATE: 30-APR-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: KIM, JUDITH U.
;; REGISTRATION NUMBER: 40,679
;; REFERENCE/DOCKET NUMBER: 0977.2280003
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202)371-2600
;; TELEFAX: (202)371-2540
;;
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 245 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: NO. US20020155498A1 Relevant
;; MOLECULE TYPE: peptide
;; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-956-086-5

Query Match 77.4%; Score 41; DB 9; Length 245;
Best Local Similarity 77.8%; Pred. No. 1.4;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 TTYLDTVEG 10
| | | | | : | |
DB 183 TTYLDSVKG 191

RESULT 9
US-09-956-087-5
; Sequence 5, Application US/09956087
; Patent No. US20020161201A1
; GENERAL INFORMATION:
; APPLICANT: FILPULA, DAVID
; WANG, MAOLIANG
; SHORR, ROBERT
; WHITLOW, MARC
; LEE, LIHSYNG S.
; TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS
; CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/956,087
;; FILING DATE: 20-Sep-2001
;; CLASSIFICATION: <Unknown>
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 09/069,821
;; FILING DATE: 1998-04-30
;; APPLICATION NUMBER: US 60/063,074
;; FILING DATE: 27-OCT-1997
;; APPLICATION NUMBER: US 60/050,472
;; FILING DATE: 23-JUN-1997
;; APPLICATION NUMBER: US 60/044,449
;; FILING DATE: 30-APR-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: KIM, JUDITH U.
;; REGISTRATION NUMBER: 40,679
;; REFERENCE/DOCKET NUMBER: 0977.2280003
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202)371-2600
;; TELEFAX: (202)371-2540
;;
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 245 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: not relevant
;; MOLECULE TYPE: peptide
;; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-956-087-5

Query Match 77.4%; Score 41; DB 9; Length 245;
Best Local Similarity 77.8%; Pred. No. 1.4;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 TTYLDTVEG 10
| | | | | : | |
DB 183 TTYLDSVKG 191

RESULT 10
US-09-985-442-5
; Sequence 5, Application US/09985442
; Patent No. US20020156248A1
; GENERAL INFORMATION:
; APPLICANT: FILPULA, David R.
; APPLICANT: Wang, Maoliang
; APPLICANT: Whitlow, Marc D.
; TITLE OF INVENTION: No. US20020156248A1el Method for Targeted Delivery of Nucleic
; FILE REFERENCE: 0977.2300003
; CURRENT APPLICATION NUMBER: US/09/985.442
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: 09/420,592
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/104,949
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 265
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: A33/218 sFv
US-09-985-442-5

Query Match 77.4%; Score 41; DB 9; Length 265;
Best Local Similarity 77.8%; Pred. No. 1.5;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 TTYLDTVEG 10

Db 183 TYYLDSVKG 191
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RESULT 11
US-09-983-580-5
; Sequence 5, Application US/09983580
; Patent No. US20020151061A1
; GENERAL INFORMATION:
; APPLICANT: Filipula, David R.
; APPLICANT: Wang, Maoliang
; APPLICANT: Whitlow, Marc D.
; TITLE OF INVENTION: No. US20020151061A1 Method for Targeted Delivery of Nucleic Acid
; FILE REFERENCE: 0577.2300002
; CURRENT APPLICATION NUMBER: US/09/983,580
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: 09/420,592
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/104,949
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 265
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: A33/218 sFv
US-09-983-580-5

Query Match 77.4%; Score 41; DB 10; Length 265;
Best Local Similarity 77.8%; Pred. No. 1.5;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 TYYLDTVEG 10
|||||:|:|
Db 183 TYYLDSVKG 191

RESULT 12
US-09-968-561A-14
; Sequence 14, Application US/09968561A
; Patent No. US20020164642A1
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, Ian M
; APPLICANT: Winter, Gregory
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
; FILE REFERENCE: 8039/1073B
; CURRENT APPLICATION NUMBER: US/09/968,561A
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: GB 9722131.1
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/065,248
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/066,729
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: PCT/GB98/03135
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: US 09/511,939
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-968-561A-14

Query Match 75.5%; Score 40; DB 9; Length 17;
Best Local Similarity 70.0%; Pred. No. 0.11;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYLDTVEG 10

Db 8 STYYADSVKG 17
|||||:|:|

RESULT 13
US-09-968-561A-38
; Sequence 38, Application US/09968561A
; Patent No. US20020164642A1
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, Ian M
; APPLICANT: Winter, Gregory
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligand
; FILE REFERENCE: 8039/1073B
; CURRENT APPLICATION NUMBER: US/09/968,561A
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: GB 9722131.1
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/065,248
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/066,729
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: PCT/GB98/03135
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: US 09/511,939
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-968-561A-38

Query Match 75.5%; Score 40; DB 9; Length 17;
Best Local Similarity 70.0%; Pred. No. 0.11;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYLDTVEG 10
|||||:|:|
Db 8 STYYADSVKG 17

RESULT 14
US-09-968-561A-68
; Sequence 68, Application US/09968561A
; Patent No. US20020164642A1
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, Ian M
; APPLICANT: Winter, Gregory
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligand
; FILE REFERENCE: 8039/1073B
; CURRENT APPLICATION NUMBER: US/09/968,561A
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: GB 9722131.1
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/065,248
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/066,729
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: PCT/GB98/03135
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: US 09/511,939
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-968-561A-68

Query Match 75.5%; Score 40; DB 9; Length 17;
Best Local Similarity 70.0%; Pred. No. 0.11;

Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYLDTVEG 10
|||||1:1:1
Db 8 STYYADSVKG 17

RESULT 15
US-09-968-561A-74
; Sequence 74, Application US/09968561A
; Patent No. US20020164642A1
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, Ian M
; APPLICANT: Winter, Gregory
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
; FILE REFERENCE: 8039/1073B
; CURRENT APPLICATION NUMBER: US/09/968,561A
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: GB 9722131.1
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/065,248
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/066,729
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: PCT/GB98/03135
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: US 09/511,939
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 74
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-968-561A-74

Query Match 75.5%; Score 40; DB 9; Length 17;
Best Local Similarity 70.0%; Pred. No. 0.11;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYLDTVEG 10
|||||1:1:1
Db 8 STYYADSVKG 17

Search completed: November 18, 2002, 18:45:14
Job time : 1.96078 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:01 ; Search time 4.2402 Seconds
(without alignments)
69.390 Million cell updates/sec

Title: US-09-016-061-58
Perfect score: 53
Sequence: 1 STYLDTVG 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	43	81.1	30	4	US-09-336-093-4
2	42	79.2	125	1	US-08-331-398A-65
3	42	79.2	125	2	US-08-331-397B-65
4	42	79.2	125	2	US-08-759-804A-64
5	42	79.2	158	2	US-08-653-402B-6
6	42	79.2	158	2	US-08-653-402B-10
7	41	77.4	117	4	US-08-752-693A-3
8	41	77.4	117	4	US-08-752-693A-4
9	41	77.4	117	4	US-08-253-877C-57
10	41	77.4	136	2	US-08-452-164A-57
11	41	77.4	136	4	US-08-976-183A-31
12	41	77.4	136	4	US-08-976-183A-32
13	41	77.4	136	4	US-08-976-183A-33
14	41	77.4	136	4	US-08-976-183A-34
15	41	77.4	150	4	US-08-976-183A-55
16	41	77.4	237	2	US-08-224-591-16
17	41	77.4	237	2	US-08-926-789-16
18	41	77.4	241	2	US-08-224-591-18
19	41	77.4	241	2	US-08-936-789-18
20	41	77.4	245	4	US-09-069-821-5
21	41	77.4	265	4	US-09-420-592A-5
22	40	75.5	17	1	US-08-264-093-22
23	40	75.5	95	4	US-09-043-514-2
24	40	75.5	113	3	US-08-974-899-6
25	40	75.5	116	3	US-08-545-809A-135
26	40	75.5	116	3	US-08-983-607-36
27	40	75.5	117	2	US-08-428-197-36

28	40	75.5	117	3	US-08-545-809A-109	Sequence 109, Appl
29	40	75.5	117	4	US-08-983-607-46	Sequence 46, Appl
30	40	75.5	117	5	PCT-US93-10555-36	Sequence 36, Appl
31	40	75.5	118	2	US-08-652-816A-11	Sequence 11, Appl
32	40	75.5	118	2	US-08-652-816A-12	Sequence 12, Appl
33	40	75.5	118	2	US-08-379-057-30	Sequence 30, Appl
34	40	75.5	118	3	US-08-545-809A-125	Sequence 125, App
35	40	75.5	119	4	US-08-983-607-22	Sequence 22, Appl
36	40	75.5	120	1	US-08-264-093-14	Sequence 14, Appl
37	40	75.5	120	2	US-08-428-197-20	Sequence 20, Appl
38	40	75.5	120	2	US-08-428-197-22	Sequence 22, Appl
39	40	75.5	120	2	US-08-428-197-24	Sequence 24, Appl
40	40	75.5	120	2	US-08-428-197-26	Sequence 26, Appl
41	40	75.5	120	2	US-08-428-197-28	Sequence 28, Appl
42	40	75.5	120	2	US-08-428-197-30	Sequence 30, Appl
43	40	75.5	120	2	US-08-428-197-32	Sequence 32, Appl
44	40	75.5	120	2	US-08-428-197-34	Sequence 34, Appl
45	40	75.5	120	2	US-08-428-197-40	Sequence 40, Appl

ALIGNMENTS

RESULT 1
US-09-336-093-4
; Sequence 4, Application US/09336093A
; Patent No. 6348185
; GENERAL INFORMATION:
; APPLICANT: Washington University School of Medicine
; TITLE OF INVENTION: MEMBRANE-PERMEANT PEPTIDE COMPLEXES FOR MEDICAL
; FILE REFERENCE: WSHU 2001
; CURRENT APPLICATION NUMBER: US/09/336,093A
; CURRENT FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: peptide
; OTHER INFORMATION: derivable from the heavy chain variable region of
; OTHER INFORMATION: an anti-DNA monoclonal antibody
US-09-336-093-4

Query Match 81.1%; Score 43; DB 4; Length 30;
Best Local Similarity 80.0%; Pred.No. 0.21;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYLDTVG 10
Db 10 STYSDTVKG 19
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RESULT 2
US-08-331-398A-65
; Sequence 65, Application US/08331398A
; Patent No. 5608039
; GENERAL INFORMATION:
; APPLICANT: Postan, Ira
; APPLICANT: Willingham, Mark
; APPLICANT: Fitzgerald, David
; APPLICANT: Brinkmann, Ulrich
; APPLICANT: Pai, Lee
; TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins
; TITLE OF INVENTION: and Their Uses (as amended)
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Plaza
; CITY: San Francisco
; STATE: California

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; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,398A
; FILING DATE: 28-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 015280-126110US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 125 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..125
; OTHER INFORMATION: /note= "Mouse monoclonal antibody B5 Fv
; OTHER INFORMATION: Heavy chain region"
; US-08-331-398A-65

Query Match 79.2%; Score 42; DB 1; Length 125;
Best Local Similarity 80.0%; Pred. No. 1.5;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYLDTVEG 10
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Db 57 STYPTDVKG 66

RESULT 3
US-08-331-397B-65
; Sequence 65, Application US/08331397B
; Patent No. 5981726
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Benhar, Itai
; TITLE OF INVENTION: Chimeric and Mutationally Stabilized Tumor-
; TITLE OF INVENTION: Specific Antibody Fragments, Fusion Proteins, and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,397B
; FILING DATE: 28-OCT-1994

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; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 015280-126120US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 125 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..125
; OTHER INFORMATION: /note= "Mouse monoclonal antibody B5 Fv
; OTHER INFORMATION: Heavy chain region"
; US-08-331-397B-65

Query Match 79.2%; Score 42; DB 2; Length 125;
Best Local Similarity 80.0%; Pred. No. 1.5;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYLDTVEG 10
   |||| |||:|
Db 57 STYPTDVKG 66

RESULT 4
US-08-759-804A-64
; Sequence 64, Application US/08759804A
; Patent No. 5990296
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Willingham, Mark
; APPLICANT: Fitzgerald, David J.
; APPLICANT: Brinkmann, Ulrich
; APPLICANT: Pal, Lee
; TITLE OF INVENTION: Tumor-Specific Antibody Fragments,
; TITLE OF INVENTION: Fusion Proteins, and Uses Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/759,804A
; FILING DATE: 03-DEC-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/331,398
; FILING DATE: 28-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:

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APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen L., 32, 762
REGISTRATION NUMBER: 015280-12614005
REFERENCE/DOCKET NUMBER:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 125 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Region
LOCATION: 1..125
OTHER INFORMATION: /note="Mouse monoclonal antibody B5 Fv
Heavy chain region"
US-08-759-80A-64

Query Match 79.2%; Score 42; DB 2; Length 125;
Best Local Similarity 80.0%; Pred. No. 1.5;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 STYYLDTVEG 10
|||||
Db 57 STYYPDTVKG 66

RESULT 5
US-08-653-402B-6
Sequence 6, Application US/08653402B
Patent No. 5969107
GENERAL INFORMATION:
APPLICANT: CARCELLER, Ana
APPLICANT: ROSELL, Elisabet
APPLICANT: GOMEZ, Alicia
APPLICANT: ADEN, Jaume
APPLICANT: PIULATS, Jaume
TITLE OF INVENTION: Anti-idiotypic antibodies which induce an
TITLE OF INVENTION: Immune response against epidermal growth factor receptor.
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
STREET: 2200 Clarendon Boulevard, Suite 1400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/653,402B
FILING DATE: 24-MAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95107967.2
FILING DATE: 26-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Lebovitz, Richard M.
REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: MERCK 1781
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 125 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-653-402B-6

LENGTH: 158 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-653-402B-6

Query Match 79.2%; Score 42; DB 2; Length 158;
Best Local Similarity 80.0%; Pred. No. 1.9;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 STYYLDTVEG 10
|||||
Db 76 STYYPDTVKG 85

RESULT 6
US-08-653-402B-10
Sequence 10, Application US/08653402B
Patent No. 5969107
GENERAL INFORMATION:
APPLICANT: CARCELLER, Ana
APPLICANT: ROSELL, Elisabet
APPLICANT: GOMEZ, Alicia
APPLICANT: ADEN, Jaume
APPLICANT: PIULATS, Jaume
TITLE OF INVENTION: Anti-idiotypic antibodies which induce an
TITLE OF INVENTION: Immune response against epidermal growth factor receptor.
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
STREET: 2200 Clarendon Boulevard, Suite 1400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/653,402B
FILING DATE: 24-MAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95107967.2
FILING DATE: 26-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Lebovitz, Richard M.
REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: MERCK 1781
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 158 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-653-402B-10

Query Match 79.2%; Score 42; DB 2; Length 158;
Best Local Similarity 80.0%; Pred. No. 1.9;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 STYYLDTVEG 10
|||||
Db 76 STYYPDTVKG 85

RESULT 7
US-08-752-693A-3

; Sequence 3, Application US/08752693A
; Patent No. 6190640
; GENERAL INFORMATION:
; APPLICANT: Sydney Welt
; Leonard Cohen
; Clarence William Jr.
; Elizabeth Carswell Richards
; Mary John
; TITLE OF INVENTION: METHOD FOR TREATING NEOPLASIA
; USING HUMANIZED ANTIBODIES WHICH
; BIND TO ANTIGEN A33
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski LLP
; STREET: 666 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
; COMPUTER: IBM PAULINE STASIAK, PH.D./2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/752.693A
; FILING DATE: 19-No. 6190640-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/07321
; FILING DATE: May 21, 1996
; APPLICATION NUMBER: 08/020.223
; FILING DATE: February 16, 1993
; APPLICATION NUMBER: 07/673.153
; FILING DATE: March 18, 1991
; APPLICATION NUMBER: 07/327.765
; FILING DATE: March 23, 1989
; APPLICATION NUMBER: 07/118.411
; FILING DATE: No. 6190640ember 6, 1987
; APPLICATION NUMBER: 06/724.991
; FILING DATE: April 19, 1985
; ATTORNEY/AGENT INFORMATION:
; NAME: Mary Anne Schofield
; REGISTRATION NUMBER: 36,669
; REFERENCE/DOCKET NUMBER: LUD 5381.1 CIP - JEL/MAS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 318-3400
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: <Unknown>
; DESCRIPTION: SEQ ID NO: 3
; ORIGINAL SOURCE:
; ORGANISM: Mice A33
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-08-752-693A-3

Query Match 77.4%; Score 41; DB 4; Length 117;
Best Local Similarity 77.8%; Pred. No. 2.1;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 TYILDVEG 10
|111111|
Db 58 TYILDSVK 66

RESULT 8
US-08-752-693A-4

; Sequence 4, Application US/08752693A
; Patent No. 6190640
; GENERAL INFORMATION:
; APPLICANT: Sydney Welt
; Gerd Ritter
; Leonard Cohen
; Clarence William Jr.
; Elizabeth Carswell Richards
; Mary John
; TITLE OF INVENTION: METHOD FOR TREATING NEOPLASIA
; USING HUMANIZED ANTIBODIES WHICH
; BIND TO ANTIGEN A33
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski LLP
; STREET: 666 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
; COMPUTER: IBM PAULINE STASIAK, PH.D./2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/752.693A
; FILING DATE: 19-No. 6190640-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/07321
; FILING DATE: May 21, 1996
; APPLICATION NUMBER: 08/020.223
; FILING DATE: February 16, 1993
; APPLICATION NUMBER: 07/673.153
; FILING DATE: March 18, 1991
; APPLICATION NUMBER: 07/327.765
; FILING DATE: March 23, 1989
; APPLICATION NUMBER: 07/118.411
; FILING DATE: No. 6190640ember 6, 1987
; APPLICATION NUMBER: 06/724.991
; FILING DATE: April 19, 1985
; ATTORNEY/AGENT INFORMATION:
; NAME: Mary Anne Schofield
; REGISTRATION NUMBER: 36,669
; REFERENCE/DOCKET NUMBER: LUD 5381.1 CIP - JEL/MAS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 318-3400
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: <Unknown>
; DESCRIPTION: SEQ ID NO: 4
; ORIGINAL SOURCE:
; ORGANISM: Human A33
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-08-752-693A-4

Query Match 77.4%; Score 41; DB 4; Length 117;
Best Local Similarity 77.8%; Pred. No. 2.1;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 TYILDVEG 10
|111111|
Db 58 TYILDSVK 66

RESULT 9
US-08-253-877C-57

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; Sequence 57, Application US/08253877C
; Patent No. 5773001
; GENERAL INFORMATION:
; APPLICANT: Hamann, Phillip R.
; APPLICANT: Hinman, Lois
; APPLICANT: Hollander, Irwin
; APPLICANT: Holcomb, Ryan
; APPLICANT: Hallett, William
; APPLICANT: Tsou, Hwei-Ru
; APPLICANT: Weiss, Martin J.
; TITLE OF INVENTION: Conjugates of Methyltrithio Antitumor
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07470-8426
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/253,877C
; FILING DATE: 03-JUN-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 32,368
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-831-3246
; TELEFAX: 201-831-3305
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 136 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-253-877C-57

Query Match 77.4%; Score 41; DB 1; Length 136;
Best Local Similarity 77.8%; Pred. No. 2.5;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 TTYLDIVVEG 10
Db 77 TTYLDSVKG 85

RESULT 10
US-08-452-164A-57
; Sequence 57, Application US/08452164A
; Patent No. 5877296
; GENERAL INFORMATION:
; APPLICANT: Hamann, Phillip R.
; APPLICANT: Hinman, Lois
; APPLICANT: Hollander, Irwin
; APPLICANT: Holcomb, Ryan
; APPLICANT: Hallett, William
; APPLICANT: Tsou, Hwei-Ru
; APPLICANT: Weiss, Martin J.
; TITLE OF INVENTION: Conjugates of Methyltrithio Antitumor
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Home Products Corporation
; STREET: One Campus Drive
; CITY: Parsippany
; STATE: New Jersey

Query Match 77.4%; Score 41; DB 1; Length 136;
Best Local Similarity 77.8%; Pred. No. 2.5;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 TTYLDIVVEG 10
Db 77 TTYLDSVKG 85

RESULT 10
US-08-452-164A-57
; Sequence 57, Application US/08452164A
; Patent No. 5877296
; GENERAL INFORMATION:
; APPLICANT: Hamann, Phillip R.
; APPLICANT: Hinman, Lois
; APPLICANT: Hollander, Irwin
; APPLICANT: Holcomb, Ryan
; APPLICANT: Hallett, William
; APPLICANT: Tsou, Hwei-Ru
; APPLICANT: Weiss, Martin J.
; TITLE OF INVENTION: Conjugates of Methyltrithio Antitumor
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Home Products Corporation
; STREET: One Campus Drive
; CITY: Parsippany
; STATE: New Jersey

Query Match 77.4%; Score 41; DB 2; Length 136;
Best Local Similarity 77.8%; Pred. No. 2.5;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 TTYLDIVVEG 10
Db 77 TTYLDSVKG 85

RESULT 11
US-08-976-183A-31
; Sequence 31, Application US/08976183A
; Patent No. 6307026
; GENERAL INFORMATION:
; APPLICANT: King, David J.
; APPLICANT: Adair, John R.
; APPLICANT: Owens, Raymond J.
; TITLE OF INVENTION: HUMANISED ANTIBODIES DIRECTED AGAINST A33
; TITLE OF INVENTION: ANTIGEN
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K. Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/976,183A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/595,848
; FILING DATE: 02-FEB-1996
; APPLICATION NUMBER: PCT/GB93/02529
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9225853.2
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9315249.4
; FILING DATE: 22-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Bernhard D. Saxe
```


; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 40283/151/CARA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 136 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-976-183A-31

Query Match 77.4%; Score 41; DB 4; Length 136;
Best Local Similarity 77.8%; Pred. No. 2.5;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 TYVLDTVEG 10
|||||:|
Db 77 TYVLDVKG 85

RESULT 12
US-08-976-183A-32
; Sequence 32, Application US/08976183A
; Patent No. 6307026
; GENERAL INFORMATION:
; APPLICANT: King, David J.
; APPLICANT: Adair, John R.
; APPLICANT: Owens, Raymond J.
; TITLE OF INVENTION: HUMANISED ANTIBODIES DIRECTED AGAINST A33
; TITLE OF INVENTION: ANTIGEN
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K. Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/976,183A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/595,848
; FILING DATE: 02-FEB-1996
; APPLICATION NUMBER: PCT/GB93/02529
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9225853.2
; FILING DATE: 10-DEC-1993

; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 136 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 40283/151/CARA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 136 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

Query Match 77.4%; Score 41; DB 4; Length 136;
Best Local Similarity 77.8%; Pred. No. 2.5;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 TYVLDTVEG 10
|||||:|
Db 77 TYVLDVKG 85

; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-976-183A-32
; Query Match 77.4%; Score 41; DB 4; Length 136;
; Best Local Similarity 77.8%; Pred. No. 2.5;
; Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
; QY 2 TYVLDTVEG 10
; |||||:|
; Db 77 TYVLDVKG 85
; RESULT 13
; US-08-976-183A-33
; Sequence 33, Application US/08976183A
; Patent No. 6307026
; GENERAL INFORMATION:
; APPLICANT: King, David J.
; APPLICANT: Adair, John R.
; APPLICANT: Owens, Raymond J.
; TITLE OF INVENTION: HUMANISED ANTIBODIES DIRECTED AGAINST A33
; TITLE OF INVENTION: ANTIGEN
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K. Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/976,183A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/595,848
; FILING DATE: 02-FEB-1996
; APPLICATION NUMBER: PCT/GB93/02529
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9225853.2
; FILING DATE: 10-DEC-1993
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 136 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-976-183A-33

Query Match 77.4%; Score 41; DB 4; Length 136;
Best Local Similarity 77.8%; Pred. No. 2.5;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 TYVLDTVEG 10
|||||:|
Db 77 TYVLDVKG 85

RESULT 14

US-08-976-183A-34
; Sequence 34, Application US/08976183A
; Patent No. 6307026
; GENERAL INFORMATION:
; APPLICANT: King, David J.
; APPLICANT: Adair, John R.
; APPLICANT: Owens, Raymond J.
; TITLE OF INVENTION: HUMANISED ANTIBODIES DIRECTED AGAINST A33
; TITLE OF INVENTION: ANTIGEN
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K. Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/976,183A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/595,848
; FILING DATE: 02-FEB-1996
; APPLICATION NUMBER: PCT/GB93/02529
; FILING DATE: 10-DEC-1993
; APPLICATION NUMBER: GB 9225853.2
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9315249.4
; FILING DATE: 22-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Bernhard D. Saxe
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 40283/151/CARA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 136 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; US-08-976-183A-34

Query Match 77.4%; Score 41; DB 4; Length 136;
Best Local Similarity 77.8%; Pred. No. 2.5;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TYLDTVEG 10
|||||:|
Db 77 TYLDSVKG 85

RESULT 15

US-08-976-183A-55
; Sequence 55, Application US/08976183A
; Patent No. 6307026
; GENERAL INFORMATION:
; APPLICANT: King, David J.
; APPLICANT: Adair, John R.
; APPLICANT: Owens, Raymond J.
; TITLE OF INVENTION: HUMANISED ANTIBODIES DIRECTED AGAINST A33

; TITLE OF INVENTION: ANTIGEN
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K. Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/976,183A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/595,848
; FILING DATE: 02-FEB-1996
; APPLICATION NUMBER: PCT/GB93/02529
; FILING DATE: 10-DEC-1993
; APPLICATION NUMBER: GB 9225853.2
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9315249.4
; FILING DATE: 22-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Bernhard D. Saxe
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 40283/151/CARA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 150 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; US-08-976-183A-55

Query Match 77.4%; Score 41; DB 4; Length 150;
Best Local Similarity 77.8%; Pred. No. 2.7;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TYLDTVEG 10
|||||:|
Db 84 TYLDSVKG 92

Search completed: November 18, 2002, 17:43:35
Job time : 5.2402 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:01 ; Search time 4.90196 Seconds
(without alignments)
196.114 Million cell updates/sec

Title: US-09-016-061-60
Perfect score: 58
Sequence: 1 ARNHGSPAY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	39	67.2	196	2 H64968	acetyl CoA acetyl
2	39	67.2	222	2 G81124	DnaA-related prote
3	39	67.2	243	2 B81896	hypothetical prote
4	37	63.8	150	2 D69081	deoxyuridine 5-tri
5	37	63.8	227	2 B81155	conserved hypothet
6	37	63.8	227	2 C81949	hypothetical prote
7	37	63.8	731	1 JC2464	probable copper-tr
8	36	62.1	108	2 S26316	Ig heavy chain v r
9	36	62.1	110	2 S26317	Ig heavy chain v r
10	36	62.1	470	2 H71667	glutamate-tRNA lig
11	36	62.1	473	2 D70405	glutamate-tRNA lig
12	36	62.1	495	2 AD1927	hypothetical prote
13	35	60.3	233	2 B82163	arginyl-tRNA-prote
14	35	60.3	272	2 S27819	vitelline B1 precu
15	35	60.3	272	2 S27820	vitelline B2 precu
16	35	60.3	282	2 T46541	hypothetical prote
17	35	60.3	289	2 AD3394	lipoprotein releas
18	35	60.3	335	2 AC2686	cation efflux syst
19	35	60.3	338	2 H97467	probable inner mem
20	35	60.3	388	2 AC2011	hypothetical prote
21	35	60.3	448	1 A60003	nucleosid prote
22	35	60.3	480	2 C69438	hypothetical prote
23	35	60.3	538	2 T51272	hypothetical prote
24	35	60.3	538	2 T28874	hypothetical prote
25	35	60.3	628	1 A56707	protein-tyrosine k
26	35	60.3	651	2 F84743	similar to mammali
27	35	60.3	722	2 S64492	hypothetical prote
28	35	60.3	736	2 T06757	hypothetical prote
29	35	60.3	977	2 H85058	hypothetical prote

30	35	60.3	1797	2 T21889	hypothetical prote
31	35	60.3	1805	2 T21888	hypothetical prote
32	34	58.6	129	2 H70727	hypothetical prote
33	34	58.6	154	2 E72126	conserved hypothet
34	34	58.6	154	2 H86497	CT296 hypothetical
35	34	58.6	170	2 D75554	hypothetical prote
36	34	58.6	207	2 B97320	S-adenosylmethioni
37	34	58.6	208	2 AC2830	pyrazinamidase/nic
38	34	58.6	219	1 Q8EAS5	hypothetical 23.4K
39	34	58.6	219	2 C90938	hypothetical prote
40	34	58.6	219	2 G85786	hypothetical prote
41	34	58.6	225	2 H97607	hypothetical prote
42	34	58.6	231	1 ISECP4	L-ribulose-phospha
43	34	58.6	231	2 S47804	L-ribulose-5-phosp
44	34	58.6	231	2 A90637	L-ribulose-5-phosp
45	34	58.6	231	2 A85488	L-ribulose-5-phosp

ALIGNMENTS

RESULT 1

H64968
acetyl CoA acetyltransferase - Escherichia coli (strain K-12)
C:Species: Escherichia coli
C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C:Accession: H64968; I69646; I69656
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A.: Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: H64968
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-196 <BLAT>
A:Cross-references: GB:A6000294; GB:U00096; NID:91788338; PIDN:AAC75094.1; PID:917883
A:Experimental source: strain K-12, substrain MG1655
R:Yao, Z.; Valvano, M.A.
J. Bacteriol. 176, 4133-4143, 1994
A:Title: Genetic analysis of the O-specific lipopolysaccharide biosynthesis region (r
erotypes y and 4a.
A:Reference number: 155053; MUID:94292434; PMID:7517390
A:Accession: I69646
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-167, 'LFRKYCHC', 177-186, 'IMR', 190-196 <RES>
A:Cross-references: EMBL:U03041; NID:9501028; PIDN:AAC31635.1; PID:9510256
R:Stevenson, G.; Neal, B.; Liu, D.; Hobbs, M.; Packer, N.H.; Batley, M.; Redmond, J.W
J. Bacteriol. 176, 4144-4156, 1994
A:Title: Structure of the O antigen of Escherichia coli K-12 and the sequence of its
A:Reference number: 155054; MUID:94292435; PMID:7517391
A:Accession: I69656
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-167, 'LFRKYCHC', 177-186, 'IMR', 190-196 <RE2>
A:Cross-references: EMBL:U09876; NID:9508236; PID:9508245
C:Genetics:
A:Gene: yefH
A:Map position: 45 min
C:Superfamily: galactoside acetyltransferase

Query Match 67.2%; Score 39; DB 2; Length 196;
Best Local Similarity 75.0%; Pred. No. 7.7;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 HNHGSFAY 10
|||||
Db 105 HNHGSFKH 112

RESULT 2

G81124

```

DnaA-related protein NMB1076 [imported] - Neisseria meningitidis (strain MC58 serogroup
C:Species: Neisseria meningitidis
C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C:Accession: G81124
R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masingani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A:Reference number: A81000; MUID:20175755; PMID:10710307
A:Accession: G81124
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-222 <TET>
A:CROSS-references: GB:AE002458; GB:AE002098; NID:g7226311; PIDN:AAF41471.1; PID:g722631
A:Experimental source: serogroup B, strain MC58
C:Genetics:
A:Gene: NMB1076

Query Match 67.2%; Score 39; DB 2; Length 222;
Best Local Similarity 66.7%; Pred. No. 8.7;
Matches 6; Conservative 0; Mismatches 0; Indels 3; Gaps 0;

QY 2 RHNGSFAY 10
DB 32 RHKGQFIY 40

RESULT 3
B81896
hypothetical protein NMA1279 [imported] - Neisseria meningitidis (strain Z2491 serogroup
C:Species: Neisseria meningitidis
C>Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C:Accession: B81896
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A:Reference number: A81775; MUID:20222556; PMID:10761919
A:Accession: B81896
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-243 <PAR>
A:CROSS-references: GB:AL162755; GB:AL157959; NID:g7379742; PIDN:CAB84531.1; PID:g737995
A:Experimental source: serogroup A, strain Z2491
C:Genetics:
A:Gene: NMA1279

Query Match 67.2%; Score 39; DB 2; Length 243;
Best Local Similarity 66.7%; Pred. No. 9.5;
Matches 6; Conservative 0; Mismatches 0; Indels 3; Gaps 0;

QY 2 RHNGSFAY 10
DB 53 RHKGQFIY 61

RESULT 4
D69081
deoxyuridine 5-triphosphate nucleotidohydrolase related protein MTH1605 [imported] - Met
C:Species: Methanobacterium thermoautotrophicum
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 31-Mar-2000
C:Accession: D69081
R:Smith, D.R.; Doucette-Stamm, L.A.; Delonghery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiواني, N.
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A:Reference number: A69000; MUID:98037514; PMID:9371463
A:Accession: D69081
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA

```

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A:Residues: 1-150 <MTH>
A:CROSS-references: GB:AE000920; GB:AE000666; NID:g2622729; PIDN:AA886078.1; PID:g2622
A:Experimental source: strain Delta H
C:Genetics:
A:Gene: MTH1605
C:Superfamily: dCTP deaminase

Query Match 63.8%; Score 37; DB 2; Length 150;
Best Local Similarity 62.5%; Pred. No. 14;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 HHNGSFAY 10
DB 115 HHNGEYEV 122

RESULT 5
B81155
conserved hypothetical protein NMB0803 [imported] - Neisseria meningitidis (strain MC
C:Species: Neisseria meningitidis
C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C:Accession: B81155
R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen,
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masingani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.;
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A:Reference number: A81000; MUID:20175755; PMID:10710307
A:Accession: B81155
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-257 <TET>
A:CROSS-references: GB:AE002435; GB:AE002098; NID:g7226049; PIDN:AAF41216.1; PID:g722
A:Experimental source: serogroup B, strain MC58
C:Genetics:
A:Gene: NMB0803

Query Match 63.8%; Score 37; DB 2; Length 257;
Best Local Similarity 62.5%; Pred. No. 23;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HHNGSFAY 10
DB 246 HHNSAYAY 253

RESULT 6
C81949
hypothetical protein NMA1013 [imported] - Neisseria meningitidis (strain Z2491 serogr
C:Species: Neisseria meningitidis
C>Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C:Accession: C81949
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mo
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandre
Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491
A:Reference number: A81775; MUID:20222556; PMID:10761919
A:Accession: C81949
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-257 <PAR>
A:CROSS-references: GB:AL162754; GB:AL157959; NID:g7379424; PIDN:CAB84282.1; PID:g737
A:Experimental source: serogroup A, strain Z2491
C:Genetics:
A:Gene: NMA1013

Query Match 63.8%; Score 37; DB 2; Length 257;
Best Local Similarity 62.5%; Pred. No. 23;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HHNGSFAY 10
DB 246 HHNSAYAY 253

```

Db 246 HNHGSFAY 253

RESULT 7

JC2464

probable copper-transporting ATPase (EC 3.6.1.1) HRA-1 - Enterobacteriaceae spp.
 C:Species: Enterobacteriaceae spp.
 C:Date: 16-Oct-1998 #sequence_revision 16-Oct-1998 #text_change 18-Jun-1999
 C:Accession: JC2464
 R:Trenor III., C.; Lin, W.; Andrews, N.C.
 Biochem. Biophys. Res. Commun. 205, 1644-1650, 1994
 A:Title: Novel bacterial P-type ATPases with histidine-rich heavy-metal-associated sequence
 A:Reference number: JC2464; MUID:95110304; PMID:7811248
 A:Accession: JC2464
 A:Molecule type: mRNA
 A:Residues: 1-731 <TRE>
 A:Cross-references: GB:016658; NID:9643612; PIDN:AAA62113.1; PID:g643613
 A:Experimental source: human small intestine cDNA library
 A:Note: the source species is uncertain; the cloned sequence did not hybridize with human
 C:Superfamily: Enterococcus copper-transporting ATPase copB; ATPase nucleotide-binding d
 C:Keywords: ATP; copper transport; hydrolase; ion transport; phosphoprotein; transmembr
 F:7-92/Region: His-rich
 F:135-477/Domain: ATPase transduction domain homology <ATP>
 F:544-685/Domain: ATPase nucleotide-binding domain homology <ATN>
 F:287/Active site: Glu #status predicted
 F:431/Active site: Asp (aspartylphosphate intermediate) #status predicted

Query Match 63.8% Score 37; DB 1; Length 731;
 Best Local Similarity 75.0%; Pred. No. 65;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARNHGGSF 8

Db 88 AHHHGSF 95

RESULT 8

S26316

Ig heavy chain V region - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
 C:Accession: S26316
 R:Stark, S.E.; Caton, A.J.
 J. Exp. Med. 174, 613-624, 1991
 A:Title: Antibodies that are specific for a single amino acid interchange in a protein e
 A:Reference number: S26309; MUID:91341421; PMID:1908510
 A:Accession: S26316
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-108 <STA>
 A:Cross-references: EMBL:X59190; NID:g52066; PIDN:CAA41900.1; PID:g1334035
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:2-85/Domain: immunoglobulin homology <IMM>

Query Match 62.1% Score 36; DB 2; Length 108;
 Best Local Similarity 60.0%; Pred. No. 15;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARNHGGSFAY 10

Db 84 ARGNYGNAY 93

RESULT 9

S26317

Ig heavy chain V region - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 21-Jan-2000
 C:Accession: S26317
 R:Stark, S.E.; Caton, A.J.
 J. Exp. Med. 174, 613-624, 1991
 A:Title: Antibodies that are specific for a single amino acid interchange in a protein e

A:Reference number: S26309; MUID:91341421; PMID:1908510
 A:Accession: S26317
 A:Molecule type: mRNA
 A:Residues: 1-110 <STA>
 A:Cross-references: EMBL:X59186
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:4-87/Domain: immunoglobulin homology <IMM>

Query Match 62.1% Score 36; DB 2; Length 110;
 Best Local Similarity 60.0%; Pred. No. 15;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARNHGGSFAY 10

Db 86 ARGNYGNAY 95

RESULT 10

H71667

glutamate-tRNA ligase (EC 6.1.1.17) (gltX2) RP623 - Rickettsia prowazekii
 C:Species: Rickettsia prowazekii
 C:Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 03-Jun-2002
 C:Accession: H71667
 R:Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark
 Nature 396, 133-140, 1998
 A:Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.
 A:Reference number: A71630; MUID:99039499; PMID:9823893
 A:Accession: H71667
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-470 <AND>
 A:Cross-references: GB:AJ235272; GB:AJ235269; NID:g3861033; PIDN:CAA15066.1; PID:g386
 A:Experimental source: strain Madrid E
 C:Genetics:

A:Gene: gltX2; RP623
 C:Superfamily: glutamate-tRNA ligase; glutamine-tRNA ligase homology
 C:Keywords: aminocyl-tRNA synthetase; ligase; protein biosynthesis
 F:4-281/Domain: glutamine-tRNA ligase homology <EGL>

Query Match 62.1% Score 36; DB 2; Length 470;
 Best Local Similarity 75.0%; Pred. No. 64;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARNHGGSF 8

Db 31 ARHHNGKF 38

RESULT 11

D70405

glutamate-tRNA ligase (EC 6.1.1.17) - Aquifex aeolicus
 C:Species: Aquifex aeolicus
 C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 03-Jun-2002
 C:Accession: D70405
 R:Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.;
 Nature 392, 353-358, 1998
 A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
 A:Reference number: A70300; MUID:98196666; PMID:9537320
 A:Accession: D70405
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-473 <AQF>
 A:Cross-references: GB:AE000729; NID:g2983659; PIDN:AAC07230.1; PID:g2983664; GB:AE00
 A:Experimental source: strain VF5
 C:Genetics:

A:Gene: gltX
 C:Superfamily: glutamate-tRNA ligase; glutamine-tRNA ligase homology
 C:Keywords: aminocyl-tRNA synthetase; ligase; protein biosynthesis
 F:4-276/Domain: glutamine-tRNA ligase homology <EGL>

Query Match 62.1% Score 36; DB 2; Length 473;

Best Local Similarity 75.0%; Pred. No. 65;
Matches 6; Conservative 1; Mismatches 0; Gaps 0;

QY 1 ARNHGGSF 8
|||||
Db 31 ARNHGGSF 38

RESULT 12
AD1927
hypothetical protein all0967 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp.
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C:Accession: AD1927
R:Kazaki, N.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena PCC 7120
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AD1927
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-495 <KUR>
A:Cross-references: GB:BA000019; PIDN:BA072924.1; PID:g17130313; GSPDB:GN00179
C:Genetics:
A:Gene: all0967
C:Superfamily: Synechocystis hypothetical protein slr1535

Query Match 62.1%; Score 36; DB 2; Length 495;
Best Local Similarity 75.0%; Pred. No. 68;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNHGSFAY 10
|||
Db 88 HNAFAFAY 95

RESULT 13
H82163
arginyl-tRNA-protein transferase-related protein VCI736 [imported] - Vibrio cholerae (strain 569B)
C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C:Accession: H82163
R:Heidelberger, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.; Chardson, D.; Emolaeva, M.D.; Vamathevan, J.; Bass, S.; Qian, H.; Dragoi, I.; Sellers, P.; R. R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: H82163
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-233 <HEI>
A:Cross-references: GB:AE004251; GB:AE003852; NID:g9656248; PIDN:AAF94886.1; GSPDB:GN00179
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VCI736
A:Map position: 1

Query Match 60.3%; Score 35; DB 2; Length 233;
Best Local Similarity 85.7%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARNHGGS 7
|||||
Db 117 ANRHGGS 123

RESULT 14
S27819
vitelline B1 precursor - liver fluke

Best Local Similarity 60.3%; Score 35; DB 2; Length 272;
Best Local Similarity 75.0%; Pred. No. 57;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

N;Alternate names: eggshell protein B1
C:Species: Fasciola hepatica (liver fluke)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 04-Feb-2000
C:Accession: A48436; A48437; B48437; A59161; S27819
R:Rice-Ficht, A.C.; Dusek, K.A.; Kochevar, G.J.; Waite, J.H.
Mol. Biochem. Parasitol. 54, 129-141, 1992
A:Title: Eggshell precursor proteins of Fasciola hepatica, I. Structure and expression
A:Reference number: A48436; MUID:93063029; PMID:1435854
A:Accession: A48436
A:Molecule type: mRNA; protein
A:Residues: 1-272 <RIC>
A:Cross-references: EMBL:M03024; NID:g159065; PIDN:AAA29144.1; PID:g159066
A:Note: Sequence extracted from NCBI backbone (NCBIN:117208, NCBIP:117210)
R:Waite, J.H.; Rice-Ficht, A.C.
Mol. Biochem. Parasitol. 54, 143-151, 1992
A:Title: Eggshell precursor proteins of Fasciola hepatica, II. Microheterogeneity in
A:Reference number: A48437; MUID:93063030; PMID:1435855
A:Accession: A48437
A>Status: preliminary
A:Molecule type: protein
A:Residues: 20-47 <WAI>
A:Cross-references: PID:g259030; PIDN:AAB23982.1
A:Note: Sequence extracted from NCBI backbone (NCBIP:117211)
A:Accession: B48437
A>Status: preliminary
A:Molecule type: protein
A:Residues: 172-193 <WA2>
A:Cross-references: PID:g259031; PIDN:AAB23983.1
A:Note: Sequence extracted from NCBI backbone (NCBIP:117213)
R:Waite, J.H.
Anal. Biochem. 192, 429-433, 1991
A:Title: Detection of peptidyl-3,4-dihydroxyphenylalanine by amino acid analysis and
A:Reference number: A59161; MUID:91241559; PMID:1903612
A:Accession: A59161
A:Molecule type: protein
A:Residues: 62-70 <WA3>
A:Experimental source: egg shell
C:Keywords: egg shell
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-272/Product: vitelline B1 #status predicted <WAT>
F:63/Modified site: 3',4'-dihydroxyphenylalanine (Tyr) #status experimental

Query Match 60.3%; Score 35; DB 2; Length 272;
Best Local Similarity 75.0%; Pred. No. 57;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARNHGGSF 8
|||||
Db 19 ARPHGKF 26

RESULT 15
S27820
vitelline B2 precursor - liver fluke
N;Alternate names: eggshell protein B2
C:Species: Fasciola hepatica (liver fluke)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 04-Feb-2000
C:Accession: S27820
R:Rice-Ficht, A.C.; Dusek, K.A.; Kochevar, G.J.; Waite, J.H.
submitted to the EMBL Data Library, May 1992
A:Description: Eggshell precursor proteins of Fasciola hepatica: I. structure and exp
A:Reference number: S27819
A:Accession: S27820
A:Molecule type: mRNA
A:Residues: 1-272 <RIC>
A:Cross-references: EMBL:M03025; NID:g159067; PIDN:AAA29144.1; PID:g159068
C:Keywords: egg shell
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-272/Product: vitelline B2 #status predicted <WAT>

Query Match 60.3%; Score 35; DB 2; Length 272;
Best Local Similarity 75.0%; Pred. No. 57;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ARPHGKF 8
 | | | | |
Db 19 ARPHGKF 26

Search completed: November 18, 2002, 17:47:02
Job time : 5.90196 secs

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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:00 ; Search time 2.45098 Seconds
(without alignments)
169.223 Million cell updates/sec

Title: US-09-016-061-60
Perfect score: 58
Sequence: 1 ARNHGSFAY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	67.2	196	1 WBJL_ECOLI	P37750 escherichia
2	36	62.1	218	1 Y4VH_RHISN	Q53216 rhizobium s
3	36	62.1	470	1 SYE2_RICPR	Q92ct8 rickettsia
4	36	62.1	473	1 SYE_AQUAE	O67271 aquifex aeo
5	35	60.3	197	1 EGG5_FASHE	P07915 fasciola he
6	35	60.3	448	1 NCAP_CVHOC	P33469 human coron
7	35	60.3	567	1 CC45_XENLA	Q9yhz6 xenopus lae
8	35	60.3	629	1 KSYK_RAT	Q64725 rattus norv
9	35	60.3	722	1 PBPI_YEAST	P53297 saccharomyc
10	34	58.6	129	1 YP56_MYCTU	Q50742 mycobacteri
11	34	58.6	213	1 PNCA_ECOLI	P21369 escherichia
12	34	58.6	231	1 ARAD_ECOLI	P08203 escherichia
13	34	58.6	231	1 ARAD_SALTY	P06190 salmonella
14	34	58.6	231	1 SGBE_ECOLI	P37680 escherichia
15	34	58.6	231	1 SGBE_HABIN	P44989 haemophilus
16	34	58.6	284	1 YNB9_YEAST	P53975 saccharomyc
17	34	58.6	284	1 YND3_YEAST	P53964 saccharomyc
18	34	58.6	297	1 YC24_ANTSP	Q02857 antithamio
19	34	58.6	339	1 LYCA_BPCP1	P15057 bacterioph
20	34	58.6	339	1 LYCA_BPCP9	P19386 bacterioph
21	34	58.6	349	1 PTEI_YEAST	P41903 saccharomyc
22	34	58.6	491	1 SYE_LISIN	Q92f38 listeria in
23	34	58.6	491	1 SYE_LISMO	Q8yab3 listeria mo
24	34	58.6	538	1 MADE_PSEAE	Q51353 pseudomonas
25	34	58.6	1446	1 IE18_PPRKA	P33479 pseudorabie
26	34	58.6	1461	1 IE18_PPRVF	P11675 pseudorabie
27	33.5	57.8	172	1 LGUL_PSEPU	P16635 pseudomonas
28	33	56.9	302	1 YE06_YEAST	P40049 saccharomyc
29	33	56.9	309	1 TSA2_HUMAN	Q8wyr4 homo sapien
30	33	56.9	480	1 SYE_HUMAN	P43818 haemophilus
31	33	56.9	966	1 MI72_HUMAN	Q14596 homo sapien
32	33	56.9	1403	1 YDF3_SCHPO	Q10475 schizosacch
33	32	55.2	190	1 SLVD_HAEIN	P44830 haemophilus

RESULT 1
WBJL_ECOLI
ID WBJL_ECOLI STANDARD: PRT: 196 AA.
AC P37750; P76375;
DT 01-OCT-1994 (Rel. 30, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Putative lipopolysaccharide biosynthesis O-acetyl transferase wbbJ
DE (EC 2.3.1.-).
GN WBJL OR B2033.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / W3110;
RX MEDLINE=94292434; PubMed=7517390;
RA Yao Z., Valvano M.A.;
RT "Genetic analysis of the O-specific lipopolysaccharide biosynthesis
region (rfb) of Escherichia coli K-12 W3110: identification of genes
that confer group 6 specificity to Shigella flexneri serotypes y and
4a.";
RL J. Bacteriol. 176:4133-4143(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / W31;
RX MEDLINE=94292435; PubMed=7517391;
RA Stevenson G., Neal B., Liu D., Hobbs M., Packer N.H., Batley M.,
Redmond J.W., Lindquist L., Reeves P.R.;
RT "Structure of the O antigen of Escherichia coli K-12 and the sequence
of its rfb gene cluster.";
RL J. Bacteriol. 176:4144-4156(1994).
RN [3]
RP REVISIONS TO 168-176 AND 187-189.
RC STRAIN=K12 / W31;
RA Stevenson G.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97251358; PubMed=9097040;
RA Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T.,
Isono K., Kasa H., Kimura S., Kitagawa M., Kitagawa M.,
Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T.,

O53117 rhodococcus
O84420 chlamydia t
O9PJY0 chlamydia m
Q11123 caenorhabdi
P11460 vibrio angu
Q9bbp4 lotus japon
P08431 saccharomyc
O08376 mycobacteri
P29723 treponema p
O13969 schizosacch
P51689 homo sapien
P43405 homo sapien


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RA Saito N., Sampei G., Seki Y., Sivasundaram S., Tagami H.,
RT Takeda J., Takenoto K., Wada C., Yamamoto Y., Horiuchi T.;
RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome
RL corresponding to the 40.1-50.0 min region on the linkage map.";
RT DNA Res. 3:379-392(1996).
CC -!- FUNCTION: PUTATIVE O-ACETYLTRANSFERASE THAT TRANSFERS AN O-ACETYL
CC ON THE O ANTIGEN.
CC -!- PATHWAY: Lipopolysaccharide biosynthesis.
CC -!- SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NOBL FAMILY OF
CC ACETYLTRANSFERASES, COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
CC -----
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CC -----
DR EMBL; U03041; AAC31635.1; -.
DR EMBL; U09876; AAB88406.1; -.
DR EMBL; AE000294; AAC75094.1; -.
DR EMBL; D90841; BAA15875.1; -.
DR EMBL; D90842; BAA15887.1; -.
DR EcoGene; EGI1984; wbbJ.
DR InterPro; IPR001451; Hexapep_transf.
DR Pfam; PF00132; hexapep; 4.
DR PROSITE; PS00101; HEXAPEP_TRANSFERASES; FALSE NEG.
KW Lipopolysaccharide biosynthesis; Transferrase; Acyltransferase; Repeat;
KW Complete proteome.
FT CONFLICT 168 176 SIPENTVIA -> LFRKYCHC (IN REF. 1).
FT CONFLICT 187 189 NHE -> IMR (IN REF. 1).
SQ SEQUENCE 196 AA; 21675 MW; D1C2FA7D3B29A1B1 CRC64;

Query Match 67.2%; Score 39; DB 1; Length 196;
Best Local Similarity 75.0%; Pred. No. 2.2;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNHGSFAY 10
DB 105 HNHGSFKH 112
|||||
ID Y4VH_RH1SN STANDARD; PRT; 218 AA.
AC Q53216;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Hypothetical 24.6 kDa protein Y4VH.
GN Y4VH.
OS Rhizobium sp. (strain NGR234).
OG Plasmid sym pNGR234a.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=394;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97305956; PubMed=9163424;
RA Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
RA Perret X.;
RT "Molecular basis of symbiosis between Rhizobium and legumes.";
RL Nature 387:394-401(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96389014; PubMed=8796346;
RA Freiberg C., Perret X., Broughton W.J., Rosenthal A.;
RT "Sequencing the 500-kb GC-rich symbiotic replicon of Rhizobium sp.
RT NGR234 using the 500-kb GC-rich symbiotic replicon of Rhizobium sp.
RT beginning.";
RT Genome Res. 6:590-600(1996).
CC -!- SIMILARITY: NONE OBVIOUS.

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CC -----
DR EMBL; Z68203; CAA92423.1; -.
DR EMBL; AE000101; AAB91896.1; -.
KW Hypothetical protein; Plasmid.
SQ SEQUENCE 218 AA; 24594 MW; 501C6CB38A09A2E5 CRC64;

Query Match 62.1%; Score 36; DB 1; Length 218;
Best Local Similarity 66.7%; Pred. No. 9;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNHGSFA 9
DB 68 ARDNHGSYS 76
|||||
ID SYE2_RICPR STANDARD; PRT; 470 AA.
AC Q9ZCT8;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Glutamyl-tRNA synthetase 2 (EC 6.1.1.17) (Glutamate--tRNA ligase 2)
DE (Glurs 2).
GN GLTX2 OR RP623.
OS Rickettsia prowazekii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsieae; Rickettsia.
OX NCBI_TaxID=782;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Madrid E;
RX MEDLINE=99039499; PubMed=9823893;
RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,
RA Sacheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
RT "The genome sequence of Rickettsia prowazekii and the origin of
RT mitochondria.";
RL Nature 396:133-140(1998).
CC -!- CATALYTIC ACTIVITY: ATP + L-glutamate + tRNA(Glu) = AMP +
CC diphosphate + L-glutamyl-tRNA(Glu).
CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-tRNA SYNTHETASE FAMILY.
CC -----
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CC -----
DR EMBL; AJ235272; CAA15066.1; -.
DR HSPSP; P27000; IGLN.
DR InterPro; IPR004527; GLTX_bact.
DR InterPro; IPR000924; Glu-tRNA-synt_1c.
DR InterPro; IPR001412; tRNA-synt_1.
DR Pfam; PF00749; tRNA-synt_1c; 1.
DR PRINTS; PR00987; TRNASYNTHGLU.
DR TIGRams; TIGR00464; gltx_bact; 1.
DR PROSITE; PS00178; AA-tRNA_LIGASE_I; FALSE NEG.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
KW Complete proteome.
FT SITE 10 20 "HIGH" REGION.

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FT SITE      239      243      "KMSKS" REGION.
FT BINDING   242      242      ATP (BY SIMILARITY).
SQ SEQUENCE  470 AA; 53696 MW; DFCE50A20B8A9FD CRC64;

Query Match      62.1%; Score 36; DB 1; Length 470;
Best Local Similarity 75.0%; Pred. No. 20;
Matches 6; Conservative 1; Mismatches 0; Gaps 0;

QY 1 ARHNHGSF 8
    |||||
Db 31 ARHNNGKF 38

RESULT 4
SYE_AQUAE
ID SYE_AQUAE STANDARD; PRT; 473 AA.
AC O67271;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Glutamyl-tRNA synthetase (EC 6.1.1.17) (Glutamate--tRNA ligase)
DE (GluRS).
GN GLTX OR AQ.1221.
OS Aquifex aeolicus.
OC Bacteria; Aquificae; Aquificae (class); Aquificales; Aquificaceae;
OC Aquifex.
OX NCBI_TaxID=63363;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VF5;
RX MEDLINE=98196666; PubMed=9537320;
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Snead M.A., Keller M., AuJay M., Huber R.,
RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus";
RL Nature 392:353-358(1998).
CC -1- CATALYTIC ACTIVITY: ATP + L-glutamate + tRNA(Glu) = AMP +
CC diphosphate + L-glutamyl-tRNA(Glu).
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
-----
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-----
DR EMBL; AE000729; AAC07230.1; -
DR HSP; P27000; IGLN.
DR InterPro; IPR004527; Gltx_bact.
DR InterPro; IPR000924; Glu-trna-synt_lc.
DR InterPro; IPR001412; trna-synt_I.
DR Pfam; PF00749; trna-synt_lc; 1.
DR PRINTS; PR00987; TRNASYNTHGLU.
DR TIGRFAMs; TIGR00464; gltx_bact; 1.
DR PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
KW Complete proteome.
FT SITE      10      20      "HIGH" REGION.
FT SITE      242      246      "KMSKS" REGION.
FT BINDING   245      245      ATP (BY SIMILARITY).
SQ SEQUENCE  473 AA; 55121 MW; 5CB4D1590973E07A CRC64;

Query Match      62.1%; Score 36; DB 1; Length 473;
Best Local Similarity 75.0%; Pred. No. 20;
Matches 6; Conservative 1; Mismatches 0; Gaps 0;

QY 1 ARHNHGSF 8
    |||||
Db 31 ARHNNGKF 38

us-09-016-061-60.rsp

Db 31 ARHNNGGF 38

RESULT 5
EGGS_FASHE
ID EGGS_FASHE STANDARD; PRT; 197 AA.
AC P07915;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Putative eggshell protein precursor.
DE Fasciola hepatica (Liver fluke).
OS Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
OC Echinostomida; Echinostomata; Fascioloidae; Fasciolidae; Fasciola.
OX NCBI_TaxID=6192;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87175670; PubMed=3470798;
RA Zurita M., Bieber D., Ringold G., Mansour T.E.;
RT "Cloning and characterization of a female genital complex cDNA from
RT the liver fluke Fasciola hepatica.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:2340-2344(1987).
CC -----
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-----
DR EMBL; M15871; AAA29138.1; -
DR Eggshell; Signal.
FT SIGNAL      1      17      PUTATIVE EGGSHELL PROTEIN.
FT CHAIN       18      197
SQ SEQUENCE  197 AA; 22470 MW; 72033ED203FC1A3E CRC64;

Query Match      60.3%; Score 35; DB 1; Length 197;
Best Local Similarity 75.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNHGSF 8
    |||||
Db 17 ARHPHGKF 24

RESULT 6
NCAP_CVHOC
ID NCAP_CVHOC STANDARD; PRT; 448 AA.
AC P33469;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE Nucleocapsid protein.
DE Human coronavirus (strain OC43).
OS Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=31631;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89243809; PubMed=2541577;
RA Kanahora T., Soe L.H., Lai M.M.C.;
RT "Sequence analysis of nucleocapsid gene and leader RNA of human
RT coronavirus OC43.";
RL Virus Res. 12:1-9(1989).
DR PIR; A60003; A60003.
DR InterPro; IPR001218; Corona_nucleocap.
DR Pfam; PF00937; Corona_nucleoca; 1.
KW Nucleocapsid.
SQ SEQUENCE  448 AA; 49316 MW; 5193AB1AE0D75626 CRC64;

Query Match      60.3%; Score 35; DB 1; Length 448;
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Best Local Similarity 85.7%; Pred. No. 29;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNHGSF 8
   ||| |||
Db 103 RHNHGSF 109

RESULT 7
CC45_XENLA STANDARD; PRT; 567 AA.
AC O3YH26;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE CDC45-related protein.
GN CDC45.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98429493; PubMed=9755170;
RA Mimura S., Takisawa H.;
RT "Xenopus Cdc45-dependent loading of DNA polymerase alpha onto
RL chromatin under the control of S-phase Cdk.";
EMBO J. 17:5699-5707(1998).
CC -!- FUNCTION: REQUIRED FOR INITIATION OF CHROMOSOMAL DNA REPLICATION.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: BELONGS TO THE CDC45 FAMILY.
-----
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-----
DR EMBL; AF062494; AAC67520.1; -
DR InterPro; IPR003874; CDC45_like.
DR Pfam; PF02724; CDC45; 1.
DR DNA replication; Cell cycle; Nuclear protein.
SQ SEQUENCE 567 AA; 65444 MW; 9A32FB20097F7C86 CRC64;

Query Match 60.3%; Score 35; DB 1; Length 567;
Best Local Similarity 71.4%; Pred. No. 38;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARNHGS 7
   :||||:
Db 251 SRNHGN 257

RESULT 8
KSYK_RAT STANDARD; PRT; 629 AA.
ID KSYK_RAT
AC Q64725;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tyrosine-protein kinase SYK (EC 2.7.1.112) (Spleen tyrosine kinase).
GN SYK.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95279402; PubMed=7759516;
RA Rowley R.N., Bolen J.B., Fargnoli J.;

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RT Molecular cloning of rodent p72Syk. Evidence of alternative mRNA
RT splicing.;
RL J. Biol. Chem. 270:12659-12664(1995).
CC -!- FUNCTION: MAY PARTICIPATE IN SIGNALING PATHWAYS. PLAYS A ROLE IN
CC LYMPHOCYTE ACTIVATION.
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; SYKA AND SYKB (SHOWN HERE);
CC ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -!- PTM: AUTOPHOSPHORYLATED (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SYK/ZAP-
CC 70 SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 2 SH2 DOMAINS.
-----
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-----
DR EMBL; U21684; AAA75167.1; -
DR EMBL; U21683; AAA75166.1; -
DR HSP; P43405; 1A81.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00017; SH2; 2.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00401; SH2DOMAIN.
DR ProDom; PD000001; Euk_pkinase; 1.
DR ProDom; PD000093; SH2; 2.
DR SMART; SM00252; SH2; 2.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS50001; SH2; 2.
KW Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
KW SH2 domain; Repeat; Alternative splicing.
FT DOMAIN 14 106 SH2 1.
FT DOMAIN 167 258 SH2 2.
FT DOMAIN 365 625 PROTEIN_KINASE.
FT NP_BIND 371 379 ATP (BY SIMILARITY).
FT BINDING 396 396 ATP (BY SIMILARITY).
FT ACT_SITE 488 488 BY SIMILARITY.
FT MOD_RES 519 519 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT VARSPIC 277 299 MISSING (IN ISOFORM SYKA).
SQ SEQUENCE 629 AA; 71528 MW; 81169A643EC6A6FE CRC64;

Query Match 60.3%; Score 35; DB 1; Length 629;
Best Local Similarity 77.8%; Pred. No. 42;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARNHGSFA 9
   ||| |||
Db 195 ARDNNGSFA 203

RESULT 9
PBPI_YEAST STANDARD; PRT; 722 AA.
ID PBPI_YEAST
AC P53297;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE PAB1-binding protein 1.
GN PBPI OR MRS16 OR YGR178C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;

```

```
[1] SEQUENCE FROM N.A.
RP Hebling U., Hofmann B., Dellus H.;
RA Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
[2] SEQUENCE FROM N.A.
RP STRAIN=BDY747;
RC Mecklenbrauker I.;
RA "Sequencing and characterization of a suppressor of the pet- phenotype
RT in a Saccharomyces cerevisiae strain without mitochondrial group II
RT introns.";
RL Thesis (1996), Vienna Biocentre, Austria.
[3] CHARACTERIZATION.
RX MEDLINE=99038243; PubMed=9819425;
RA Mangus D.A., Amrani N., Jacobson A.;
RT "pbp1, a factor interacting with Saccharomyces cerevisiae poly(A)-
RT binding protein, regulates polyadenylation.";
RL Mol. Cell. Biol. 18:7383-7396(1998).
CC -!- FUNCTION: APPEARS TO PROMOTE PROPER POLYADENYLATION. IN THE
CC ABSENCE OF PBP1P, THE 3'TERMINI OF PRE-MRNAs ARE PROPERLY CLEAVED
CC BUT LACK FULL-LENGTH POLY(A) TAILS. MAY ACT TO REPRESS THE ABILITY
CC OF PAB1 TO NEGATIVELY REGULATE POLYADENYLATION.
CC -!- SUBUNIT: INTERACTS WITH PAB1.
CC -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
CC
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CC
CC EMBL; 272963; CAAG7204.1; -.
DR EMBL; U46931; AAB94294.1; -.
DR SGD; S0003410; PBP1.
KW Nuclear protein.
SQ SEQUENCE 722 AA; 78781 MW; 92005F3A2346193E CRC64;

Query Match 60.3%; Score 35; DB 1; Length 722;
Best Local Similarity 85.7%; Pred. No. 48;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNHGSF 8
DB 474 RRNHGSF 480

RESULT 10
YP36_MYCTU STANDARD; PRT; 129 AA.
AC Q50742;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein RV2556c.
GN RV2556C OR MT2633 OR MTCY9C4.12.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S.,
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RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RL Nature 393:537-544(1998).
[2] SEQUENCE FROM N.A.
RP STRAIN=CDC 1551 / Oshkosh;
RC Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE UPF0047 FAMILY.
CC
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CC
CC EMBL; 277250; CAB01048.1; -.
DR EMBL; AE007098; AAK46945.1; -.
DR TIGR; MT2633; -.
DR TuberculList; RV2556c; -.
DR InterPro; IPR001602; UPF0047.
DR Pfam; PF01894; UPF0047.1.
DR ProDom; PD005232; UPF0047.1.
DR PROSITE; PS01314; UPF0047.1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 129 AA; 13925 MW; AABE57AE876B6923 CRC64;

Query Match 58.6%; Score 34; DB 1; Length 129;
Best Local Similarity 55.6%; Pred. No. 12;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNHGSFAY 10
DB 69 RHAHGSYGH 77

RESULT 11
PNCA_ECOLI STANDARD; PRT; 213 AA.
ID PNCA_ECOLI
AC P21369; P76229; P76910;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Pyrazinamidase/nicotinamidase [Includes: Pyrazinamidase (EC 3.5.1.-)
DE (PZAase); Nicotinamidase (EC 3.5.1.19) (Nicotine deamidase)].
GN PNCA OR NAM OR B1768.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=89357501; PubMed=2670682;
RA Jerlstrom P.G., Bezjak D.A., Jennings M.P., Beacham I.R.;
RT "Structure and expression in Escherichia coli K-12 of the
RT L-asparaginase I-encoding ansA gene and its flanking regions.";
RL Gene 78:37-46(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96338362; PubMed=8726014;
RA Frothingham R., Meeker-O'Connell W.A., Talbot E.A., George J.W.,
RA Kreuzer K.N.;
RT "Identification, cloning, and expression of the Escherichia coli
```

RT pyrazinamidase and nicotinamidase gene, pncA.";
 RL Antimicrob. Agents Chemother. 40:1426-1431(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:1453-1474(1997).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=97251357; PubMed=9057039;
 RA Aliba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,
 RA Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
 RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
 RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T., Saito N.,
 RA Sampei G., Seki Y., Sivasubram S., Tagami H., Takeda J.,
 RA Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;
 RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome
 corresponding to the 28.0-40.1 min region on the linkage map.";
 RL DNA Res. 3:363-377(1996).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=92334977; PubMed=1630901;
 RA Yura T., Mori H., Nagai H., Nagata T., Ishihama A., Fujita N.,
 RA Isono K., Mizobuchi K., Nakata A.;
 RT "Systematic sequencing of the Escherichia coli genome: analysis of
 the 0-2.4 min region.";
 RL Nucleic Acids Res. 20:3305-3308(1992).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:1453-1474(1997).
 RN [6]
 RP SEQUENCE OF 222-231 FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=91017565; PubMed=2217158;
 RA Bonner C.A., Hays S., McEntee K., Goodman M.F.;
 RT "DNA polymerase II is encoded by the DNA damage-inducible dna gene
 of Escherichia coli.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:7663-7667(1990).
 RN [7]
 RP SEQUENCE OF 158-231 FROM N.A.
 RC STRAIN=K12 / W3110;
 RX MEDLINE=91238699; PubMed=2034216;
 RA Iwasaki H., Ishino Y., Toh H., Nakata A., Shinagawa H.;
 RT "Escherichia coli DNA polymerase II is homologous to alpha-like DNA
 polymerases.";
 RL Mol. Gen. Genet. 226:24-33(1991).
 CC -|- CATALYTIC ACTIVITY: L-ribulose 5-phosphate - D-xylulose 5-
 phosphate.
 CC -|- COFACTOR: BINDS ONE ZINC ION PER MOLECULE (POTENTIAL).
 CC -|- PATHWAY: L-arabinose catabolism; third step.
 CC -|- SIMILARITY: BELONGS TO THE ALDOLASE CLASS II FAMILY. ARAD/FUCA
 SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL; M35263; AAA23464.1; -;
 CC EMBL; M35371; -; NOT_ANNOTATED_CDS.
 DR

Query Match 58.6%; Score 34; DB 1; Length 213;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 NHGSFA 9
 |||||
 Db 57 NHGSFA 62

RESULT 12
 ARAD_ECOLI
 ID ARAD_ECOLI STANDARD; PRT; 231 AA.
 AC P08203;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE L-ribulose-5-phosphate 4-epimerase (EC 5.1.3.4) (Phosphoribulose
 DE isomerase).
 GN ARAD OR B0061.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=B;
 RX MEDLINE=87163495; PubMed=3549454;
 RA Lee N., Gielow W., Martin R., Hamilton E., Fowler A.;
 RT "The organization of the arabAD operon of Escherichia coli.";
 RL Gene 47:231-244(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=91083835; PubMed=2261080;
 RA Chen H., Sun Y., Stark T., Beattie W., Moses R.E.;
 RT "Nucleotide sequence and deletion analysis of the polB gene of
 Escherichia coli.";
 RL DNA Cell Biol. 9:631-635(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=91067495; PubMed=2251150;
 RA Mineno J., Fukui H., Ishino Y., Kato I., Shinagawa H.;
 RT "Nucleotide sequence of the arab gene of Escherichia coli K12
 encoding the L-ribulose 5-phosphate 4-epimerase.";
 RL Nucleic Acids Res. 18:6722-6722(1990).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=92334977; PubMed=1630901;
 RA Yura T., Mori H., Nagai H., Nagata T., Ishihama A., Fujita N.,
 RA Isono K., Mizobuchi K., Nakata A.;
 RT "Systematic sequencing of the Escherichia coli genome: analysis of
 the 0-2.4 min region.";
 RL Nucleic Acids Res. 20:3305-3308(1992).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:1453-1474(1997).
 RN [6]
 RP SEQUENCE OF 222-231 FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=91017565; PubMed=2217158;
 RA Bonner C.A., Hays S., McEntee K., Goodman M.F.;
 RT "DNA polymerase II is encoded by the DNA damage-inducible dna gene
 of Escherichia coli.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:7663-7667(1990).
 RN [7]
 RP SEQUENCE OF 158-231 FROM N.A.
 RC STRAIN=K12 / W3110;
 RX MEDLINE=91238699; PubMed=2034216;
 RA Iwasaki H., Ishino Y., Toh H., Nakata A., Shinagawa H.;
 RT "Escherichia coli DNA polymerase II is homologous to alpha-like DNA
 polymerases.";
 RL Mol. Gen. Genet. 226:24-33(1991).
 CC -|- CATALYTIC ACTIVITY: L-ribulose 5-phosphate - D-xylulose 5-
 phosphate.
 CC -|- COFACTOR: BINDS ONE ZINC ION PER MOLECULE (POTENTIAL).
 CC -|- PATHWAY: L-arabinose catabolism; third step.
 CC -|- SIMILARITY: BELONGS TO THE ALDOLASE CLASS II FAMILY. ARAD/FUCA
 SUBFAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; M35263; AAA23464.1; -;
 CC EMBL; M35371; -; NOT_ANNOTATED_CDS.
 DR

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DR EMBL; J62646; AAA24405.1; -.
DR EMBL; D10483; BAA01332.1; -.
DR EMBL; AE000116; AAC73172.1; -.
DR EMBL; M37727; AAA23683.1; -.
DR EMBL; M38283; AAA63763.1; -.
DR EMBL; X56048; CAA39519.1; -.
DR PIR; D29022; ISECP4.
DR PIR; S13593; ISECK4.
DR PIR; A36236; A36236.
DR PIR; S40577; S40577.
DR ECO2DBASE; G028.1; 6TH EDITION.
DR EcoGene; EG10055; arad.
DR InterPro; IPR001303; Aldolase_II_N.
DR InterPro; IPR004661; Arad.
DR Pfam; PF00596; Aldolase_II; 1.
DR TIGRfams; TIGR00760; arad; 1.
KW Arabinose catabolism; Isomerase; Zinc; Complete proteome.
FT METAL 76 76 ZINC (BY SIMILARITY).
FT METAL 95 95 ZINC (BY SIMILARITY).
FT METAL 97 97 ZINC (BY SIMILARITY).
FT METAL 171 171 ZINC (BY SIMILARITY).
FT VARIANT 50 50 V -> I.
FT VARIANT 70 70 T -> A.
FT VARIANT 216 216 D -> N.
SQ SEQUENCE 231 AA; 25519 MW; 1753F75958332163 CRC64;

Query Match 58.6%; Score 34; DB 1; Length 231;
Best Local Similarity 62.5%; Pred. No. 23;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNHGSFAY 10
DB 169 HSHGPFAY 176

RESULT 13
ARAD_SALTY STANDARD; PRT; 231 AA.
AC P06130;
DT 01-JAN-1988 (Rel. 06, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE L-ribulose-5-phosphate 4-epimerase (EC 5.1.3.4) (Phosphoribulose
DE isomerase).
GN ARAD OR STM0101.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2;
RC MEDLINE=85232046; PubMed=3891514;
RA Lin H.-C., Lei S.-P., Studnicka G., Wilcox G.;
RT "The arabad operon of Salmonella typhimurium LT2. III. Nucleotide
RT sequence of arad and its flanking regions, and primary structure of
RT its product, L-ribulose-5-phosphate 4-epimerase.";
RL Gene 34:129-134(1985).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2 / SGSCI412 / ATCC 700720;
RC MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT LT2.";
RL Nature 413:852-856(2001).
CC -1- CATALYTIC ACTIVITY: L-ribulose 5-phosphate -> D-xylulose 5-
CC phosphate.
CC -1- COFACTOR: BINDS ONE ZINC ION PER MOLECULE (POTENTIAL).
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CC -1- PATHWAY: L-arabinose catabolism; third step.
CC -1- SIMILARITY: BELONGS TO THE ALDOLASE CLASS II FAMILY. ARAD/FUCA
CC SUBFAMILY.
CC -1- CAUTION: Ref.1 sequence differs from that shown due to a
CC frameshift in position 202.
CC -----
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CC -----
DR EMBL; M11047; AAA27025.1; ALT_FRAME.
DR EMBL; AE008698; AALJ9065.1; -.
DR PIR; A24986; ISEB4T.
DR StyGene; SG10015; arad.
DR InterPro; IPR001303; Aldolase_II_N.
DR InterPro; IPR004661; Arad.
DR Pfam; PF00596; Aldolase_II; 1.
DR TIGRfams; TIGR00760; arad; 1.
KW Arabinose catabolism; Isomerase; Zinc; Complete proteome.
FT METAL 76 76 ZINC (BY SIMILARITY).
FT METAL 95 95 ZINC (BY SIMILARITY).
FT METAL 97 97 ZINC (BY SIMILARITY).
FT METAL 171 171 ZINC (BY SIMILARITY).
SQ SEQUENCE 231 AA; 25531 MW; DA473505739284F9 CRC64;

Query Match 58.6%; Score 34; DB 1; Length 231;
Best Local Similarity 62.5%; Pred. No. 23;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNHGSFAY 10
DB 169 HSHGPFAY 176

RESULT 14
SGBE_ECOLI STANDARD; PRT; 231 AA.
ID SGBE_ECOLI
AC P37680;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable sugar isomerase sgbe (EC 5.1.3.4).
GN SGBE OR B3583.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RC MEDLINE=94316500; PubMed=8041620;
RA Sofia H.J., Burland V., Daniels D.L., Plunkett G. III, Blattner F.R.;
RT "Analysis of the Escherichia coli genome. V. DNA sequence of the
RT region from 76.0 to 81.5 minutes.";
RL Nucleic Acids Res. 22:2576-2586(1994).
RN [2]
RP DISCUSSION OF SEQUENCE.
RA Reizer J., Charbit A., Reizer A., Sailer M.H. Jr.;
RT "Novel phosphotransferases system genes revealed by bacterial genome
RT analysis: operons encoding homologues of sugar-specific permease
RT domains of the phosphotransferase system and pentose catabolic
RT enzymes.";
RL Genome Sci. Technol. 1:53-75(1996).
CC -1- FUNCTION: PROBABLE PENTULOSE-5-PHOSPHATE-4-EPIMERASE.
CC -1- COFACTOR: BINDS ONE ZINC ION PER MOLECULE (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE ALDOLASE CLASS II FAMILY. ARAD/FUCA
CC SUBFAMILY.
CC -----
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CC -----

DR EMBL; U00039; AAB18560.1; -;
DR EMBL; AF000435; AAC76607.1; -;
DR EcoGene; EG12287; sgbe.
DR InterPro; IPR001303; Aldolase_II_N.
DR Pfam; PF00596; Aldolase_II; 1.
KW Isomerase; Zinc; Complete proteome.
FT METAL 76 76 ZINC (BY SIMILARITY).
FT METAL 95 95 ZINC (BY SIMILARITY).
FT METAL 97 97 ZINC (BY SIMILARITY).
FT METAL 171 171 ZINC (BY SIMILARITY).
SQ SEQUENCE 231 AA; 25561 MW; F4FF4D7ECA80B3A CRC64;

Query Match 58.6%; Score 34; DB 1; Length 231;
Best Local Similarity 62.5%; Pred. No. 23;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 HNHGSFAY 10
I:| | | |
Db 169 HSHGPFAY 176

RESULT 15
SGBE_HAEIN STANDARD; PRT; 231 AA.
ID P44989;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Probable sugar isomerase sgbe (EC 5.1.-.-).
GN SGBE OR H1025.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
OX NCBI_TaxID=727;
[1]
RN
RP SEQUENCE FROM N.A.
RC STRAIN-Rd / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
Rd.";
RL Science 269:496-512(1995).
CC -!- FUNCTION: PROBABLE PENTULOSE-5-PHOSPHATE-4-EPIMERASE.
CC -!- COFACTOR: BINDS ONE ZINC ION PER MOLECULE (POTENTIAL).
CC -!- SIMILARITY: BELONGS TO THE ALDOLASE CLASS II FAMILY. ARAD/FUCA
CC SUBFAMILY.
CC -----
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CC -----
DR EMBL; U32783; AAC22685.1; -;
DR TIGR; H1025; -;
DR InterPro; IPR001303; Aldolase_II_N.

DR Pfam; PF00596; Aldolase_II; 1.
KW Isomerase; Zinc; Complete proteome.
FT METAL 76 76 ZINC (BY SIMILARITY).
FT METAL 95 95 ZINC (BY SIMILARITY).
FT METAL 97 97 ZINC (BY SIMILARITY).
FT METAL 171 171 ZINC (BY SIMILARITY).
SQ SEQUENCE 231 AA; 25980 MW; 9DE3485E54B10DC7 CRC64;

Query Match 58.6%; Score 34; DB 1; Length 231;
Best Local Similarity 62.5%; Pred. No. 23;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 HNHGSFAY 10
I:| | | |
Db 169 HSHGPFAY 176

Search completed: November 18, 2002, 17:33:23
Job time : 3.45098 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:01 ; Search time 10.4412 Seconds
(without alignments)
197.341 Million cell updates/sec

Title: US-09-016-061-60
Perfect score: 58
Sequence: 1 ARNHGSFAY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SPTEMBL21.*
2: sp_archaea.*
3: sp_bacteria.*
4: sp_fungi.*
5: sp_human.*
6: sp_invertebrate.*
7: sp_mammal.*
8: sp_mhc.*
9: sp_organella.*
10: sp_phase.*
11: sp_plant.*
12: sp_rodent.*
13: sp_virus.*
14: sp_vertebrate.*
15: sp_unclassified.*
16: sp_virus.*
17: sp_bacteriaph.*
17: sp_archaea.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	39	67.2	222	16 Q9JZF5	Q9JZF5 neisseria m
2	39	67.2	243	16 Q9JUT9	Q9JUT9 neisseria m
3	38	65.5	593	5 Q8T5L2	Q8T5L2 anopheles g
4	38	65.5	839	10 Q9LIE5	Q9LIE5 arabidopsis
5	38	65.5	1108	10 Q9FNO7	Q9FNO7 arabidopsis
6	37	63.8	150	17 Q27642	Q27642 methanobact
7	37	63.8	257	16 Q9K023	Q9K023 neisseria m
8	37	63.8	257	16 Q9J35	Q9J35 neisseria m
9	37	63.8	326	16 Q9RGJ3	Q9RGJ3 streptomyce
10	37	63.8	710	2 Q8VPE6	Q8VPE6 enterococu
11	37	63.8	731	2 Q59369	Q59369 escherichia
12	36	62.1	237	4 Q9H897	Q9H897 homo sapien
13	36	62.1	237	11 Q8VE10	Q8VE10 mus musculu
14	36	62.1	275	11 Q9DAI5	Q9DAI5 mus musculu
15	36	62.1	444	2 Q9AKB5	Q9AKB5 rickettsia
16	36	62.1	495	16 Q8Y84	Q8Y84 anabaena sp

17	36	62.1	649	9 Q8SCW1	Q8SCW1 pseudomonas
18	36	62.1	755	2 Q9F0F9	Q9F0F9 campylobact
19	36	62.1	999	4 Q9H0F0	Q9H0F0 homo sapien
20	36	62.1	1049	12 Q836L1	Q836L1 ectromelia
21	36	62.1	1061	4 Q8TC00	Q8TC00 homo sapien
22	35	60.3	105	12 Q9Q9I1	Q9Q9I1 avian adeno
23	35	60.3	134	10 Q84F4	Q84F4 arcea catec
24	35	60.3	233	16 Q9KRA6	Q9KRA6 vibrio chol
25	35	60.3	251	17 Q8TJ84	Q8TJ84 methanosarc
26	35	60.3	272	5 Q24950	Q24950 fasciola he
27	35	60.3	272	5 Q24951	Q24951 fasciola he
28	35	60.3	276	7 Q9GJN0	Q9GJN0 calman croc
29	35	60.3	282	2 Q9ZA29	Q9ZA29 streptomyce
30	35	60.3	282	2 Q9K578	Q9K578 fluoribacte
31	35	60.3	289	16 Q8YGM0	Q8YGM0 brucella me
32	35	60.3	305	10 Q8RUD9	Q8RUD9 glycine max
33	35	60.3	318	17 Q8TRU1	Q8TRU1 methanosarc
34	35	60.3	338	16 Q8UGZ4	Q8UGZ4 agrobacteri
35	35	60.3	388	16 Q8YWH2	Q8YWH2 anabaena sp
36	35	60.3	480	17 Q28764	Q28764 archaeoglob
37	35	60.3	483	10 Q9LES4	Q9LES4 arabidopsis
38	35	60.3	534	10 Q9LGI6	Q9LGI6 oryza sativ
39	35	60.3	551	11 Q8VCJ5	Q8VCJ5 mus musculu
40	35	60.3	615	11 Q63614	Q63614 rattus norv
41	35	60.3	651	10 Q22781	Q22781 arabidopsis
42	35	60.3	736	10 Q9SVX7	Q9SVX7 arabidopsis
43	35	60.3	762	5 Q9GIL2	Q9GIL2 caenorhabdl
44	35	60.3	788	4 Q9P2E5	Q9P2E5 homo sapien
45	35	60.3	977	10 Q9S9V3	Q9S9V3 arabidopsis

ALIGNMENTS

RESULT 1

Q9JZF5
ID Q9JZF5 PRELIMINARY; PRT; 222 AA.
AC Q9JZF5;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE DnaA-related protein.
GN NMB1076.
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58 / SEROGROUP B;
RX MEDLINE=20175755; PubMed=10710307;
RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A., Mason T., Ciecko A., Parksey D.S., Blair E., Clifton H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J., Gill J., Scarlato V., Maignani V., Pizzia M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
RA "Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.";
RT Science 287:1809-1815(2000).
RL EMBL; AF002458; AAF41471.1; -;
DR TIGR; NMB1076; -;
DR InterPro; IPR002078; Sig54_interact.
DR PROSITE; PS00675; SIGMA54_INTERACT_1; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 222 AA; 25427 MW; EC80D2AA88FC9086 CRC64;

Query Match 67.2%; Score 39; DB 16; Length 222;
Best Local Similarity 66.7%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 RHNGSFAY 10

Db 32 RHKGQFIY 40

RESULT 2

Q9JUJ9 PRELIMINARY; PRT; 243 AA.
 AC Q9JUJ9;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Hypothetical protein NMA1279.
 GN NMA1279.
 OS Neisseria meningitidis (serogroup A).
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OX NCBI_TaxID=65699;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=22491 / SEROGROUP A / SEROTYPE 4A;
 RX MEDLINE=2022256; PubMed=10761919;
 RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
 RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
 RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
 RA Jegels K., Leather S., Moule S., Mungall K., Quail M.A.,
 RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
 RA Whitehead S., Spratt B.G., Barrell B.G.;
 RT "Complete DNA sequence of a serogroup A strain of Neisseria
 meningitidis 22491";
 RL Nature 404:502-506(2000).
 DR EMBL; AL162755; CAB84531.1; -.
 DR InterPro; IPR002078; Sig54_INTERACT.
 DR PROSITE; PS00675; SIGMA54_INTERACT_1; UNKNOWN_1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 243 AA; 27882 MW; E03E4E1B9498A8DF CRC64;

Query Match 67.2%; Score 39; DB 16; Length 243;
 Best Local Similarity 66.7%; Pred. No. 23;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 RHNGSFAY 10

Db 53 RHKGQFIY 61

RESULT 3

Q8T5L2 PRELIMINARY; PRT; 593 AA.
 AC Q8T5L2;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Putative transcription factor.
 GN 4Fl1.4.
 OS Anopheles gambiae (African malaria mosquito).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
 OC Anopheles.
 OX NCBI_TaxID=7165;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PEST;
 RA Thomasova D., Ton L.O., Collins F.H., Kafatos F.C.;
 RT "Sequencing and analysis of Pen1 region from Anopheles gambiae
 chromosome 2R";
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ438610; CAD2476.1; -.
 SQ SEQUENCE 593 AA; 63339 MW; 65CFED4BC35B148F CRC64;

Query Match 65.5%; Score 38; DB 5; Length 593;
 Best Local Similarity 66.7%; Pred. No. 88;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARNHGSA 9

Db 573 AAHNHGQYA 581

RESULT 4

Q9LIE5 PRELIMINARY; PRT; 839 AA.
 AC Q9LIE5;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Far-red impaired response protein, mutator-like transposase-like
 protein, phytochrome A signaling protein-like.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RX MEDLINE=20363099; PubMed=10907853;
 RA Nakamura Y.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.
 RT Sequence features of the regions of 4,251,695 bp covered by ninety Pl.
 RT TAC and BAC clones";
 RL DNA Res. 7:217-221(2000).
 DR EMBL; AP001306; BAB03065.1; -.
 DR InterPro; IPR004330; FARI.
 DR InterPro; IPR001000; Glyco_hydro_10.
 DR Pfam; PF03101; FARI; 1.
 DR PROSITE; PS00591; GLYCOSYL_HYDROL_F10; UNKNOWN_1.
 SQ SEQUENCE 839 AA; 95996 MW; CBBF60DF8B6797F8 CRC64;

Query Match 65.5%; Score 38; DB 10; Length 839;
 Best Local Similarity 75.0%; Pred. No. 1.3e+02;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARNHGGSF 8

Db 274 SRHNGSF 281

RESULT 5

Q9FNQ7 PRELIMINARY; PRT; 1108 AA.
 AC Q9FNQ7;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE Similarity to histone deacetylase.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RX MEDLINE=98069011; PubMed=9405937;
 RA Kotani H., Nakamura Y., Sato S., Kaneko T., Asamizu E., Miyajima N.,
 RA Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. II.
 RT Sequence features of the regions of 1,044,062 bp covered by thirteen
 RT physically assigned pl clones";
 RL DNA Res. 4:291-300(1997).
 DR EMBL; AB006696; BAB10370.1; -.
 DR InterPro; IPR000286; His_deacetylase.

DR Pfam: PF00850; Hist_deacetyl1; 2.
 DR PRINTS: PR01270; HDASUPER.
 SQ SEQUENCE 1108 AA; 123609 MW; 9BCF5A2BCD90A1E2 CRC64;

Query Match 65.5%; Score 38; DB 10; Length 1108;
 Best Local Similarity 85.7%; Pred. No. 1.7e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RHNGSF 8
 ||:||||
 Db 255 RHGGSF 261

RESULT 6

O27642 PRELIMINARY; PRT; 150 AA.

AC O27642;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Deoxycytidine-triphosphate deaminase related protein.
 GN MTH1605.

OS Methanobacterium thermoautotrophicum.
 OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
 OC Methanobacteriaceae; Methanothermobacter.
 OX NCBI_TaxID=187420;
 RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=DELTA H;

RX MEDLINE=98037514; PubMed=9371463;

RA Smith D.R., Doucette-Stamm L.A., DeLoughery C., Lee H.-M., Dubois J.,
 RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
 RA Harrison D., Hoang L., Keagle P., Lum W., Pothier B., Qiu D.,
 RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
 RA Jiwan N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
 RA McDougall S., Shimer G., Goyal A., Pietrowski S., Church G.M.,
 RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
 RT "Complete genome sequence of Methanobacterium thermoautotrophicum
 RT deltaH: functional analysis and comparative genomics.";
 RL J. Bacteriol. 179:7135-7155(1997).

DR EMBL: AE009920; AAB86078.1; -.

DR InterPro: IPR001428; DeoxyUTase.

DR Pfam: PF00692; dUTase; 1.

KW Complete proteome.

SQ SEQUENCE 150 AA; 16996 MW; AFA09D55FB371648 CRC64;

Query Match 63.8%; Score 37; DB 17; Length 150;
 Best Local Similarity 62.5%; Pred. No. 32;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 HNHGSFAY 10
 ||||:|
 Db 115 HNHGEY 122

RESULT 7

O9K023 PRELIMINARY; PRT; 257 AA.

AC O9K023;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)

DE Hypothetical protein NMB0803.

GN NMB0803.

OS Neisseria meningitidis (serogroup B).

OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.

OX NCBI_TaxID=491;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=MC58 / SEROGROUP B;

RX MEDLINE=20175753; PubMed=10710307;

RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,

RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,

RA Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,
 RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
 RA Mason T., Ciecko A., Parksey D.S., Blair E., Citterone H., Clark E.B.,
 RA Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,
 RA Gill J., Scarlato V., Masignani V., Pizzo M., Grandi G., Sun L.,
 RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
 RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
 RT MC58.";

RL Science 287:1809-1815(2000).

DR EMBL: AE002434; AAF41216.1; -.

DR TIGR: NMB0803; -.

DR InterPro: IPR003801; DUF198.

DR Pfam: PF02649; DUF198; 1.

KW Hypothetical protein; Complete proteome.

SQ SEQUENCE 257 AA; 28718 MW; 0BD50624D6B90C77 CRC64;

Query Match 63.8%; Score 37; DB 16; Length 257;

Best Local Similarity 62.5%; Pred. No. 56;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 HNHGSFAY 10
 ||||:|

Db 246 HNHSAVAY 253

RESULT 8

O9JV35

ID O9JV35 PRELIMINARY; PRT; 257 AA.

AC O9JV35;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE Hypothetical protein NMA1013.

GN NMA1013.

OS Neisseria meningitidis (serogroup A).

OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.

OX NCBI_TaxID=65699;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Z2491 / SEROGROUP A / SEROTYPE 4A;

RX MEDLINE=20222556; PubMed=10761919;

RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,

RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,

RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,

RA Jagals K., Leather S., Moule S., Mungall K., Quail M.A.,

RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,

RA Whitehead S., Spratt B.G., Bartell B.G.;

RT "Complete DNA sequence of a serogroup A strain of Neisseria

RT meningitidis Z2491.";

RL Nature 404:502-506(2000).

DR EMBL: AL162754; CAB84282.1; -.

DR InterPro: IPR003801; DUF198.

DR Pfam: PF02649; DUF198; 1.

KW Hypothetical protein; Complete proteome.

SQ SEQUENCE 257 AA; 28734 MW; 021A28C018F35281 CRC64;

Query Match 63.8%; Score 37; DB 16; Length 257;

Best Local Similarity 62.5%; Pred. No. 56;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 HNHGSFAY 10
 ||||:|

Db 246 HNHSAVAY 253

RESULT 9

O9RJG3

ID O9RJG3 PRELIMINARY; PRT; 326 AA.

AC O9RJG3;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE Putative araC family transcriptional regulator.

```

GN SC00471 OR SCF76.11.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Murphy L., Harris D.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RX MEDLINE=97000351; PubMed=8843436;
RA Redenbach M., Kieser H.M., Denapite D., Eichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
RT the 8 Mb Streptomyces coelicolor A3(2) chromosome."
RL Mol. Microbiol. 21:77-96(1996).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
CC -1- SIMILARITY: BELONGS TO THE ARAC/XLYS FAMILY OF TRANSCRIPTIONAL
CC REGULATORS.
DR EMBL; ALJ21600; CAB56731.1; -.
DR InterPro; IPR000005; HTHArac.
DR Pfam; PF00165; HTH_Arac; 2.
DR SMART; SM00342; HTH_ARAC; 1.
DR PROSITE; PS01124; HTH_ARAC_FAMILY_2; 1.
KW DNA-binding; Transcription regulation.
SQ SEQUENCE 326 AA; 34425 MW; 2FEF5346ACAC80D6 CRC64;

Query Match 63.8%; Score 37; DB 16; Length 326;
Best Local Similarity 85.7%; Pred. No. 72;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNHGSF 8
Db 85 RHGHSF 91

RESULT 10
Q8VPE6 PRELIMINARY; PRT; 710 AA.
AC Q8VPE6;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Transferable copper resistance protein TcrB.
GN TCRB.
OS Enterococcus faecium (Streptococcus faecium).
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1352;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN=AL7SV1;
RA Hasman H., Arestrup F.M.;
RT "A novel gene conferring transferable copper resistance from
RT Enterococcus faecium: occurrence, transferability and linkage to
RT macrolide and glycopeptide resistance."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY048044; AAL05407.1; -.
DR InterPro; IPR001757; ATPase_E1-E2.
DR Pfam; PF00122; E1-E2_ATPase; 1.
DR Pfam; PF00702; Hydrolase; 1.
DR PRINTS; PR00119; CATATPASE.
DR PROSITE; PS00154; ATPASE_E1_E2; UNKNOWN1.
SQ SEQUENCE 710 AA; 76237 MW; 14AC9CC5080FAD7A CRC64;

Query Match 63.8%; Score 37; DB 2; Length 710;
Best Local Similarity 75.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARNHGSF 8
Db 67 AHHHGSF 74

RESULT 11
Q59369 PRELIMINARY; PRT; 731 AA.
AC Q59369;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Histidine rich P type ATPase.
GN HRA-1.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95110304; PubMed=7811248;
RA Trenor C.C., Lin W., Andrews N.C.;
RT "Novel bacterial p-type ATPases with histidine-rich heavy-metal-
RT associated sequences."
RL Biochem. Biophys. Res. Commun. 205:1644-1650(1994).
DR EMBL; U16658; AAA62113.1; -.
DR InterPro; IPR001757; ATPase_E1-E2.
DR InterPro; IPR001454; Hignase/Hydriase.
DR Pfam; PF00122; E1-E2_ATPase; 1.
DR Pfam; PF00702; Hydrolase; 1.
DR PROSITE; PS00154; ATPASE_E1_E2; UNKNOWN1.
KW Hydrolase; Transmembrane; Phosphorylation; ATP-binding.
FT MOD_RES 431 431 PHOSPHORYLATION (PROBABLE).
SQ SEQUENCE 731 AA; 78453 MW; 06237F159E151F0D CRC64;

Query Match 63.8%; Score 37; DB 2; Length 731;
Best Local Similarity 75.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARNHGSF 8
Db 88 AHHHGSF 95

RESULT 12
Q9H897 PRELIMINARY; PRT; 237 AA.
AC Q9H897;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE THYR01000855 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

```

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=THYROID;
RA Isozaki T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,
RA Tanase T., Nomura Y., Todoya S., Komai F., Hara R., Takeuchi K.,
RA Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,
RA Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK023910; BAB14720.1; -
DR InterPro: IPR000182; GCN5acetyltransf.
DR Pfam: PF00583; Acetyltransf; 1.
SQ SEQUENCE 237 AA; 27224 MW; AED75B58DB3FCE1 CRC64;

Query Match 62.1%; Score 36; DB 4; Length 237;
Best Local Similarity 44.4%; Pred. No. 78;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNGSFAY 10
Db 177 KHNHGAYQF 185

RESULT 13
Q8VE10 PRELIMINARY; PRT; 237 AA.
AC Q8VE10;
DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DE 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Similar to hypothetical protein FLJ13848.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC020020; AAH20020.1; -
DR InterPro: IPR000182; GCN5acetyltransf.
DR Pfam: PF00583; Acetyltransf; 1.
KW Hypothetical protein.
SQ SEQUENCE 237 AA; 27229 MW; A3574555906CDEE1 CRC64;

Query Match 62.1%; Score 36; DB 11; Length 237;
Best Local Similarity 44.4%; Pred. No. 78;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNGSFAY 10
Db 177 KHNHGAYQF 185

RESULT 14
Q9D4I5 PRELIMINARY; PRT; 275 AA.
AC Q9D4I5;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
DE 493143E08RIK protein.
GN 493143E08RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=TESTIS;

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RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Glissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Marzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK016504; BAB30275.1; -
DR MGD: MGI:1918249; 493143E08RIK.
DR InterPro: IPR000182; GCN5acetyltransf.
DR Pfam: PF00583; Acetyltransf; 1.
SQ SEQUENCE 275 AA; 31388 MW; C65476299762C60C CRC64;

Query Match 62.1%; Score 36; DB 11; Length 275;
Best Local Similarity 44.4%; Pred. No. 91;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNGSFAY 10
Db 215 KHNHGAYQF 223

RESULT 15
Q9AKB5 PRELIMINARY; PRT; 444 AA.
AC Q9AKB5;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DE 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Glutamyl-tRNA synthetase (Fragment).
GN GLTX2.
OS Rickettsia typhi.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsieae; Rickettsia.
OX NCBI_TaxID=785;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WILMINGTON;
RX MEDLINE=21219194; PubMed=11319266;
RA Andersson J.O., Andersson S.G.E.;
RT "Pseudogenes, junk DNA and the dynamics of Rickettsia genomes.";
RL Mol. Biol. Evol. 18:829-839(2001).
DR EMBL: AJ293325; CAC33753.1; -
DR HSSP: P27000; IGLN.
DR InterPro: IPR004527; GLTX_bact.
DR InterPro: IPR000924; Glu_tRNA-synt_1c.
DR Pfam: PF00749; tRNA-synt_1c; 1.
DR PRINTS: PR00987; TRNASYNTHGLU.
DR TIGRFAMs: TIGR00464; gltx_bact; 1.
KW Aminoacyl-tRNA synthetase.
FT NON_TER
SQ SEQUENCE 444 AA; 50791 MW; FF00E12E10FD6FCB CRC64;

Query Match 62.1%; Score 36; DB 2; Length 444;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ARNHGSF 8
Db 1 ARNHGSF 8

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Db 6 ARHNGKF 13

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Job time : 11.4912 secs

GenCore version 5.1.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:21:57 ; Search time 13.8235.Seconds
(without alignments)
96.394 Million cell updates/sec

Title: US-09-016-061-60
Perfect score: 58
Sequence: 1 ARNHGSPAY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	58	100.0	10	19	AAW76020
2	58	100.0	10	22	AAW76020
3	52	89.7	10	19	AAW76010
4	52	89.7	10	22	AAW76010
5	52	89.7	117	19	AAW76001
6	52	89.7	117	19	AAW76003
7	52	89.7	117	19	AAW76001
8	52	89.7	117	20	AAW76037
9	52	89.7	117	22	AAW76037
10	52	89.7	117	22	AAW76037

11	52	89.7	117	22	AAW76037	Vitaxin heavy chain
12	52	89.7	117	22	AAW76037	Antibody LM609 hea
13	52	89.7	118	20	AAW76037	Humanised LM609 an
14	52	89.7	118	20	AAW76037	Humanised LM609 an
15	52	89.7	118	20	AAW76037	Humanised LM609 an
16	52	89.7	118	20	AAW76037	Humanised LM609 an
17	52	89.7	130	20	AAW76037	Murine monoclonal
18	51	87.9	10	19	AAW76037	LM609 grafted anti
19	51	87.9	10	22	AAW76037	Multiple mutant VH
20	49	84.5	10	19	AAW76021	LM609 grafted anti
21	49	84.5	10	22	AAW76021	Mutant VH CDR3 pep
22	47	81.0	10	19	AAW76038	LM609 grafted anti
23	47	81.0	10	22	AAW76038	Multiple mutant VH
24	46	79.3	10	19	AAW76022	LM609 grafted anti
25	46	79.3	10	19	AAW76022	LM609 grafted anti
26	46	79.3	10	22	AAW76022	Mutant VH CDR3 pep
27	46	79.3	10	22	AAW76022	Mutant VH CDR3 pep
28	45	77.6	10	19	AAW76024	LM609 grafted anti
29	45	77.6	10	19	AAW76024	LM609 grafted anti
30	45	77.6	10	19	AAW76026	LM609 grafted anti
31	45	77.6	10	19	AAW76027	LM609 grafted anti
32	45	77.6	10	19	AAW76028	LM609 grafted anti
33	45	77.6	10	19	AAW76029	LM609 grafted anti
34	45	77.6	10	19	AAW76030	LM609 grafted anti
35	45	77.6	10	22	AAW76032	Mutant VH CDR3 pep
36	45	77.6	10	22	AAW76032	Mutant VH CDR3 pep
37	45	77.6	10	22	AAW76032	Mutant VH CDR3 pep
38	45	77.6	10	22	AAW76035	Mutant VH CDR3 pep
39	45	77.6	10	22	AAW76036	Mutant VH CDR3 pep
40	45	77.6	10	22	AAW76037	Mutant VH CDR3 pep
41	45	77.6	10	22	AAW76038	Mutant VH CDR3 pep
42	44	75.9	110	20	AAW84099	Vitronectin alpha
43	44	75.9	117	20	AAW84093	Murine vitronectin
44	44	75.9	117	20	AAW84097	Humanised anti- α 1p
45	43	74.1	8	20	AAW06371	Murine monoclonal

ALIGNMENTS

RESULT 1
AAW76020
ID AAW76020 standard; Protein; 10 AA.
XX AAW76020;
XX AAW76020;
DT 02-NOV-1998 (first entry)
XX LM609 grafted antibody V-H region CDR3 protein fragment #2.
DE Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
XX Mus sp.
XX WO9833919-A2.
XX 06-AUG-1998.
XX 30-JAN-1998; 98WO-US01826.
XX 30-JAN-1997; 97US-0791391.
XX (IXSY-) IXSYS INC.
XX Glaser SM, Huse WD;
XX WPI; 1998-437472/37.
XX N-PSDB; AAW49857.

XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
PT integrin - and related grafted antibodies based on murine monoclonal.
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
XX
PS Claim 62: Page 41; 129pp; English.
XX
CC AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
CC antibodies contain non-murine framework regions so are suitable for use
CC in humans. Enhanced types of LM609 have affinity more than 90 times
CC greater than that of parent the parent antibody.
XX
XX Sequence 10 AA;

Query Match 100.0%; Score 58; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00038;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNHGSFAY 10
| | | | | | | | | |
Db 1 ARHNHGSFAY 10

RESULT 2
AAB61378
ID AAB61378 standard; peptide; 10 AA.
XX
AC AAB61378;
XX
XX 03-APR-2001 (first entry)
XX
XX Mutant VH CDR3 peptide #1.
XX
XX LM609; grafted antibody; alphaVbeta_3 integrin; angiogenesis;
KW inflammatory; cancer; retina; restenosis; osteoporosis.
KW
XX Unidentified.
OS
XX WO200078815-A1.
PN
XX 28-DEC-2000.
PD
XX 23-JUN-2000; 2000WO-US17454.
XX
XX 24-JUN-1999; 99US-0339922.
XX
XX (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX
XX Huse WD, Wu H;
PI
XX WPI; 2001-050110/06.
XX
XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
PT osteoporosis.
XX
XX Disclosure; Page 41; 132pp; English.
PS
XX The present invention relates to enhanced LM609 grafted antibodies
CC exhibiting selective binding affinity to alphaVbeta_3 integrin or
CC their functional fragments. The antibodies or their functional
CC fragments can be used in the diagnosis and treatment of
CC alphaVbeta_3-mediated diseases such as angiogenesis, inflammatory

CC diseases (such as psoriasis and chronic articular rheumatism),
CC disorders associated with inappropriate or inopportune invasion of
CC vessels (such as diabetic retinopathy, neovascular glaucoma and
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
CC diseases (such as macular degeneration), restenosis and
CC osteoporosis.
XX
XX Sequence 10 AA;

Query Match 100.0%; Score 58; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00038;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNHGSFAY 10
| | | | | | | | | |
Db 1 ARHNHGSFAY 10

RESULT 3
AAW76010
ID AAW76010 standard; Protein; 10 AA.
XX
AC AAW76010;
XX
XX 02-NOV-1998 (first entry)
XX
XX LM609 grafted antibody V-H region CDR3 protein fragment #1.
XX
XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
XX
XX Mus sp.
XX
XX WO9833919-A2.
XX
XX 06-AUG-1998.
XX
XX 30-JAN-1998; 98WO-US01826.
XX
XX 30-JAN-1997; 97US-0791391.
XX
XX (IXSY-) IXSYS INC.
XX
XX Glaser SM, Huse WD;
PI
XX WPI; 1998-437472/37.
DR
XX N-PSDB; AAV49847.
XX
XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
XX Disclosure; Page 40; 129pp; English.
PS
XX
XX AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
CC antibodies contain non-murine framework regions so are suitable for use
CC in humans. Enhanced types of LM609 have affinity more than 90 times
CC greater than that of parent the parent antibody.
XX
XX Sequence 10 AA;
-SQ

Query Mgtch 89.7%; Score 52; DB 19; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.0046;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARNHGSEFAY 10
 ||||:||||
 Db 1 ARHNYGSFAY 10

RESULT 4

AA61368
 ID AAB61368 standard; peptide; 10 AA.

XX AC AAB61368;
 XX DT 03-APR-2001 (first entry)
 XX DE LM609 VH CDR3 peptide.
 XX KW LM609; grafted antibody; alphaVbeta3 integrin; angiogenesis;
 KW Inflammatory; cancer; retina; restenosis; osteoporosis.

XX OS Unidentified.

XX PN W0200078815-A1.

XX PD 28-DEC-2000.

XX XX 23-JUN-2000; 2000WO-US17454.

XX PR 24-JUN-1999; 99US-0339922.

XX PA (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX PI Huse WD, Wu H;

XX DR WPI; 2001-050110/06.

XX PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 to alpha(V)beta3 integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -

XX PS Disclosure; Page 39; 132pp; English.

XX CC The present invention relates to enhanced LM609 grafted antibodies
 exhibiting selective binding affinity to alphaVbeta3 integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphaVbeta3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.

XX SQ Sequence 10 AA;

Query Match 89.7%; Score 52; DB 22; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.0046;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARNHGSEFAY 10
 ||||:||||
 Db 1 ARHNYGSFAY 10

RESULT 5

AAW76001
 ID AAW76001 standard; Protein; 117 AA.

XX

AC AAW76001;
 XX 02-NOV-1998 (first entry)
 DT Vitaxin antibody heavy chain variable region protein fragment.
 XX DE Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.
 XX OS Mus sp.
 XX PN W09833919-A2.
 XX PD 06-AUG-1998.
 XX PF 30-JAN-1998; 98WO-US01826.
 XX PR 30-JAN-1997; 97US-0791391.
 XX PA (IXSY-).IXSYS INC.
 XX PI Glaser SM, Huse WD;
 XX DR WPI; 1998-437472/37.
 XX DR N-PSDB; AAV49820.
 XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX PS Claim 1; Fig 1a; 129pp; English.
 XX CC This sequence represents a fragment of the vitaxin antibody variable
 CC heavy chain region. Vitaxin and the antibody LM609 bind selectively to
 CC integrin alphaVbeta3 and can be used to inhibit binding of alphaVbeta3
 CC to a ligand and thus block integrin-mediated signal transduction. This is
 CC useful in the treatment, prevention and diagnosis of alphaVbeta3-mediated
 CC disease, specifically angiogenesis and restenosis (but also e.g.
 CC (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,
 CC cancer, psoriasis, rheumatoid arthritis, macular degeneration,
 CC osteoporosis etc.). The antibodies contain non-murine framework regions
 CC so are suitable for use in humans. Enhanced types of LM609 have affinity
 CC more than 90 times greater than that of parent the parent antibody.
 XX SQ Sequence 117 AA;
 Query Match 89.7%; Score 52; DB 19; Length 117;
 Best Local Similarity 90.0%; Pred. No. 0.063;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ARHNGSFAY 10
 ||||:||||
 Db 97 ARHNYGSFAY 106
 RESULT 6
 AAW76003
 ID AAW76003 standard; Protein; 117 AA.
 XX AC AAW76003;
 XX 02-NOV-1998 (first entry)
 DT LM609 antibody heavy chain variable region protein fragment.
 XX DE Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;

KW macular degeneration; osteoporosis.

XX Mus sp.

XX WO9833919-A2.

XX 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

XX Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

XX N-PSDB; AAV49822.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3 integrin - and related grafted antibodies based on murine monoclonal LM609, also related nucleic acid, used to treat, prevent or diagnose angiogenesis or restenosis

XX Claim 43; Fig 2a; 129pp; English.

XX This sequence represents the LM609 antibody variable heavy chain region. LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3 and can be used to inhibit binding of alphavbeta3 to a ligand and thus block integrin-mediated signal transduction. This is useful in the treatment, prevention and diagnosis of alphavbeta3-mediated disease, specifically angiogenesis and restenosis (but also e.g. (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis etc.). The antibodies contain non-murine framework regions so are suitable for use in humans. Enhanced types of LM609 have affinity more than 90 times greater than that of parent the parent antibody.

XX Sequence 117 AA;

Query Match 89.7%; Score 52; DB 19; Length 117;

Best Local Similarity 90.0%; Pred. No. 0.063;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNHGSFAY 10

||||:|||||

Db 97 ARHNHGSFAY 106

RESULT 7

AAY06381

ID AAY06381 standard; Protein; 117 AA.

XX AAY06381;

XX 06-SEP-1999 (first entry)

XX Murine monoclonal antibody LM609 VH region.

XX Humanised antibody; antibody humanisation; antibody engineering; LM609; monoclonal antibody; complementarity determining region; CDR grafting; mouse; human; integrin; apoptosis; angiogenesis; cancer; therapy; diagnosis.

XX Mus musculus.

XX WO9929888-A1.

XX 17-JUN-1999.

XX 04-DEC-1998; 98WO-US25828.

XX 05-DEC-1997; 97US-0986016.

XX (SCRI) SCRIPPS RES INST.

XX Barbas CF, Rader C;

XX WPI; 1999-394979/33.

XX Production of humanized mouse monoclonal antibodies

XX Disclosure; Page 52-53; 55pp; English.

XX This sequence represents the heavy chain variable region of murine monoclonal antibody LM609. LM609 is directed to integrin alpha-v beta-3. It selectively promotes apoptosis of vascular cells that have been stimulated to undergo angiogenesis, making it a tool for cancer diagnosis and therapy. The invention provides humanised antibodies, especially humanised LM609. In such humanized antibodies, a light chain CDR from a mouse antibody such as LM609 is grafted onto a human light chain, and a heavy chain CDR from a mouse antibody is grafted onto a human antibody heavy chain to produce a library from which a humanised murine antibody having the desired specificity is selected. By preserving the original CDR sequences such as the HCDR3 and LCDR3 sequences of LM609 (see AAY06371-72), the humanisation strategy ensures epitope conservation.

XX Sequence 117 AA;

Query Match 89.7%; Score 52; DB 20; Length 117;

Best Local Similarity 90.0%; Pred. No. 0.063;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNHGSFAY 10

||||:|||||

Db 97 ARHNHGSFAY 106

RESULT 8

AAY06387

ID AAY06387 standard; Protein; 117 AA.

XX AAY06387;

XX 06-SEP-1999 (first entry)

XX Humanised LM609 antibody VH domain.

XX Humanised antibody; antibody humanisation; antibody engineering; LM609; monoclonal antibody; complementarity determining region; CDR grafting; mouse; human; integrin; apoptosis; angiogenesis; cancer; therapy; diagnosis.

XX Homo sapiens.

XX Synthetic.

XX Key Location/Qualifiers

FT Peptide 1..2 /note= "vector-encoded residues"

FT Region 31..35 /note= "CDR1"

FT Region 50..66 /note= "CDR2"

FT Region 107..117 /note= "CDR3"

XX WO9929888-A1.

XX 17-JUN-1999.

XX 04-DEC-1998; 98WO-US25828.

XX 05-DEC-1997; 97US-0986016.

XX (SCRI) SCRIPPS RES INST.

XX Barba\$ CF, Rader C;
 XX WPI; 1999-394979/33.
 XX Production of humanized mouse monoclonal antibodies
 XX Disclosure; Page 52; 55pp; English.
 XX This sequence represents the heavy chain variable region of a
 CC humanised LM609 antibody. LM609 is directed to human integrin
 CC alpha-v beta-3. It selectively promotes apoptosis of vascular
 CC cells that have been stimulated to undergo angiogenesis, making it
 CC a tool for cancer diagnosis and therapy. The invention provides
 CC humanised antibodies, especially humanised LM609. In such humanized
 CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
 CC grafted onto a human light chain, and a heavy chain CDR from a mouse
 CC antibody is grafted onto a human antibody heavy chain to produce
 CC libraries from which a humanised murine antibody having the desired
 CC specificity is selected. By preserving the original CDR sequences
 CC such as the HCDR3 and LCDR3 sequences of LM609 (see AAY06371-72), the
 CC humanisation strategy ensures epitope conservation.
 XX Sequence 117 AA;
 SQ Query Match 89.7%; Score 52; DB 20; Length 117;
 Best Local Similarity 90.0%; Pred. NO. 0.063;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ARHNHGSFAY 10
 Db | | | | : | | | | |
 97 ARHNHGSFAY 106
 RESULT 9
 AAG63587
 ID AAG63587 standard; Protein; 117 AA.
 XX AC AAG63587;
 XX DT 15-OCT-2001 (first entry)
 XX DE A heavy chain variable region of LM609 grafted antibody.
 XX KW Grafted antibody; LM609; integrin; alphavbeta3; inflammatory disorder;
 KW chronic articular rheumatism; psoriasis; diabetic retinopathy;
 KW neovascular glaucoma; capillary proliferation; atherosclerotic plaque;
 KW cancer.
 XX OS Synthetic.
 XX Mus sp.
 XX US2001011125-A1.
 XX PD 02-AUG-2001.
 XX PF 30-JAN-1997; 97US-0790540.
 XX PR 30-JAN-1997; 97US-0790540.
 XX PA (HUSE/) HUSE W D.
 XX PI Huse WD;
 XX WPI; 2001-496171/54.
 XX DR N-PSDB; AAH74623.
 XX New LM609 grafted antibody exhibiting selective binding affinity to
 PT alphavbeta3, comprising at least one LM609 grafted heavy and light
 PT chain polypeptide, useful for diagnosing and treating e.g. inflammatory
 PT disorders or cancer -
 XX Claim 1; Fig 1A; 25pp; English.

XX The present sequence represents the heavy chain variable region of the
 CC grafted monoclonal antibody LM609. LM609 is a murine antibody which
 CC specifically recognises the integrin alphavbeta3, and inhibits its
 CC functional activity. The LM609 grafted antibody has the
 CC complementarity determining regions (CDRs) substituted into a non-murine
 CC framework. Nucleic acids encoding LM609 grafted heavy and light chain
 CC polypeptides and fragments are useful in diagnostic and therapeutic
 CC purposes, such as in the production of LM609 grafted antibodies and
 CC fragments having binding specificity and inhibitory activity against
 CC the integrin alphavbeta3. The antibody can be used for the diagnosis
 CC or treatment of alphavbeta3-mediated diseases (e.g. inflammatory
 CC disorders, chronic articular rheumatism, psoriasis, disorders
 CC associated with inappropriate or inopportune invasion of vessels such
 CC as diabetic retinopathy, neovascular glaucoma and capillary
 CC proliferation in atherosclerotic plaques, or cancers), and to inhibit
 CC binding activity of alphavbeta3 that are necessary for progression of
 CC an alphavbeta3-mediated disease.
 XX Sequence 117 AA;
 SQ Query Match 89.7%; Score 52; DB 22; Length 117;
 Best Local Similarity 90.0%; Pred. NO. 0.063;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ARHNHGSFAY 10
 Db | | | | : | | | | |
 97 ARHNHGSFAY 106
 RESULT 10
 AAG63589
 ID AAG63589 standard; Protein; 117 AA.
 XX AC AAG63589;
 XX DT 15-OCT-2001 (first entry)
 XX DE A heavy chain variable region of LM609 antibody.
 XX KW Grafted antibody; LM609; integrin; alphavbeta3; inflammatory disorder;
 KW chronic articular rheumatism; psoriasis; diabetic retinopathy;
 KW neovascular glaucoma; capillary proliferation; atherosclerotic plaque;
 KW cancer.
 XX OS Mus sp.
 XX US2001011125-A1.
 XX PD 02-AUG-2001.
 XX PF 30-JAN-1997; 97US-0790540.
 XX PR 30-JAN-1997; 97US-0790540.
 XX PA (HUSE/) HUSE W D.
 XX PI Huse WD;
 XX WPI; 2001-496171/54.
 XX DR N-PSDB; AAH74625.
 XX New LM609 grafted antibody exhibiting selective binding affinity to
 PT alphavbeta3, comprising at least one LM609 grafted heavy and light
 PT chain polypeptide, useful for diagnosing and treating e.g. inflammatory
 PT disorders or cancer -
 XX Disclosure; Fig 2A; 25pp; English.
 XX The present sequence represents the heavy chain variable region of the
 CC monoclonal antibody LM609. LM609 is a murine antibody which specifically
 CC recognises the integrin alphavbeta3, and inhibits its functional activity.
 CC The specification describes a LM609 grafted antibody which has the

CC complementarity determining regions (CDRs) substituted into a non-murine
 CC framework. Nucleic acids encoding LM609 grafted heavy and light chain
 CC polypeptides and fragments are useful in diagnostic and therapeutic
 CC purposes, such as in the production of LM609 grafted antibodies and
 CC fragments having binding specificity and inhibitory activity against
 CC the integrin alphavbeta3. The antibody can be used for the diagnosis
 CC or treatment of alphavbeta3-mediated diseases (e.g. inflammatory
 CC disorders, chronic articular rheumatism, psoriasis, disorders
 CC associated with inappropriate or inopportune invasion of vessels such
 CC as diabetic retinopathy, neovascular glaucoma and capillary
 CC proliferation in atherosclerotic plaques, or cancers), and to inhibit
 CC binding activity of alphavbeta3 that are necessary for progression of
 CC an alphavbeta3-mediated disease.

XX
 SQ Sequence 117 AA;

Query Match 89.7%; Score 52; DB 22; Length 117;
 Best Local Similarity 90.0%; Pred. No. 0.063;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNHGSFAY 10
 ||||:|||||
 Db 97 ARHNHGSFAY 106

RESULT 11

AAB61359
 ID AAB61359 standard; protein; 117 AA.

XX AAB61359;

XX 03-APR-2001 (first entry)

XX Vitaxin heavy chain variable region protein.

XX LM609; grafted antibody; alphaVbeta_3 integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis.

XX Unidentified.

XX WO200078815-A1.

XX 28-DEC-2000.

XX 23-JUN-2000; 2000WO-US17454.

XX 24-JUN-1999; 99US-0339922.

XX (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX Huse WD, Wu H;

XX WPI; 2001-050110/06.

XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -

PS Disclosure; Fig 1; 132pp; English.

XX The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphaVbeta_3 integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.

SQ Sequence 117 AA;

Query Match 89.7%; Score 52; DB 22; Length 117;
 Best Local Similarity 90.0%; Pred. No. 0.063;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNHGSFAY 10
 ||||:|||||
 Db 97 ARHNHGSFAY 106

RESULT 12

AAB61361
 ID AAB61361 standard; protein; 117 AA.

XX AAB61361;

XX 03-APR-2001 (first entry)

XX Antibody LM609 heavy chain variable region protein.

XX LM609; grafted antibody; alphaVbeta_3 integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis.

XX Unidentified.

XX WO200078815-A1.

XX 28-DEC-2000.

XX 23-JUN-2000; 2000WO-US17454.

XX 24-JUN-1999; 99US-0339922.

XX (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX Huse WD, Wu H;

XX WPI; 2001-050110/06.

XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -

PS Disclosure; Fig 2; 132pp; English.

XX The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphaVbeta_3 integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.

SQ Sequence 117 AA;

Query Match 89.7%; Score 52; DB 22; Length 117;
 Best Local Similarity 90.0%; Pred. No. 0.063;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNHGSFAY 10
 ||||:|||||
 Db 97 ARHNHGSFAY 106

RESULT 13

AAY06384
 ID AAY06384 standard; Protein; 118 AA.

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XX AC AAYQ6384;
XX DT
XX DE
XX DE 06-SEP-1999 (first entry)
XX DE Humanised LM609 antibody VH domain.
XX KW Humanised antibody; antibody humanisation; antibody engineering;
XX KW LM609; monoclonal antibody; complementarity determining region;
XX KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
XX KW cancer; therapy; diagnosis.
XX OS Homo sapiens.
XX OS Synthetic.
XX FH
XX FH Key Location/Qualifiers
XX FT Peptide 1..2
XX FT Region /note= "vector-encoded residues"
XX FT Region 31..37
XX FT Region /note= "CDR1"
XX FT Region 52..67
XX FT Region /note= "CDR2"
XX FT Region 100..107
XX FT Region /note= "CDR3"
XX PN WO9929888-A1.
XX PN
XX PD 17-JUN-1999.
XX PF 04-DEC-1998; 98WO-US25828.
XX PR 05-DEC-1997; 97US-0986016.
XX PR (SCRI ) SCRIPPS RES INST.
XX PA
XX PI Barbas CF, Rader C;
XX PI WPI; 1999-394979/33.
XX DR
XX DR Production of humanized mouse monoclonal antibodies
XX PT
XX PT Disclosure; Page 51; 55pp; English.
XX PS
XX CC This sequence represents the heavy chain variable region of a
XX CC humanised LM609 antibody. LM609 is directed to human integrin
XX CC alpha-v beta-3. It selectively promotes apoptosis of vascular
XX CC cells that have been stimulated to undergo angiogenesis, making it
XX CC a tool for cancer diagnosis and therapy. The invention provides
XX CC humanised antibodies, especially humanised LM609. In such humanized
XX CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
XX CC grafted onto a human light chain, and a heavy chain CDR from a mouse
XX CC antibody is grafted onto a human antibody heavy chain to produce
XX CC libraries from which a human antibody having the desired
XX CC specificity is selected. By preserving the original CDR sequences
XX CC such as the HCDR3 and LCDR3 sequences of LM609 (see AAY06371-72), the
XX CC humanisation strategy ensures epitope conservation.
XX SQ
XX Sequence 118 AA;
XX Query Match 89.7%; Score 52; DB 20; Length 118;
XX Best Local Similarity 90.0%; Pred. No. 0.064;
XX Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 ARNHGGSFAY 10
XX ||||:||||
XX Db 98 ARHNYGSFAY 107
XX RESULT 14
XX AAY06385
XX ID AAY06385 standard; Protein; 118 AA.
XX AC AAY06385;

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XX DT 06-SEP-1999 (first entry)
XX DE Humanised LM609 antibody VH domain.
XX KW Humanised antibody; antibody humanisation; antibody engineering;
XX KW LM609; monoclonal antibody; complementarity determining region;
XX KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
XX KW cancer; therapy; diagnosis.
XX OS Homo sapiens.
XX OS Synthetic.
XX FH
XX FH Key Location/Qualifiers
XX FT Peptide 1..2
XX FT Region /note= "vector-encoded residues"
XX FT Region 31..37
XX FT Region /note= "CDR1"
XX FT Region 52..67
XX FT Region /note= "CDR2"
XX FT Region 100..107
XX FT Region /note= "CDR3"
XX PN WO9929888-A1.
XX PN
XX PD 17-JUN-1999.
XX PF 04-DEC-1998; 98WO-US25828.
XX PR 05-DEC-1997; 97US-0986016.
XX PR (SCRI ) SCRIPPS RES INST.
XX PA
XX PI Barbas CF, Rader C;
XX PI WPI; 1999-394979/33.
XX DR
XX DR Production of humanized mouse monoclonal antibodies
XX PT
XX PT Disclosure; Page 51; 55pp; English.
XX PS
XX CC This sequence represents the heavy chain variable region of a
XX CC humanised LM609 antibody. LM609 is directed to human integrin
XX CC alpha-v beta-3. It selectively promotes apoptosis of vascular
XX CC cells that have been stimulated to undergo angiogenesis, making it
XX CC a tool for cancer diagnosis and therapy. The invention provides
XX CC humanised antibodies, especially humanised LM609. In such humanized
XX CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
XX CC grafted onto a human light chain, and a heavy chain CDR from a mouse
XX CC antibody is grafted onto a human antibody heavy chain to produce
XX CC libraries from which a humanised murine antibody having the desired
XX CC specificity is selected. By preserving the original CDR sequences
XX CC such as the HCDR3 and LCDR3 sequences of LM609 (see AAY06371-72), the
XX CC humanisation strategy ensures epitope conservation.
XX SQ
XX Sequence 118 AA;
XX Query Match 89.7%; Score 52; DB 20; Length 118;
XX Best Local Similarity 90.0%; Pred. No. 0.064;
XX Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 ARNHGGSFAY 10
XX ||||:||||
XX Db 98 ARHNYGSFAY 107
XX RESULT 15
XX AAY06386
XX ID AAY06386 standard; Protein; 118 AA.
XX AC AAY06386;
XX DT 06-SEP-1999 (first entry)

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XX DE Humanised LM609 antibody VH domain.
XX KW Humanised antibody; antibody humanisation; antibody engineering;
KW LM609; monoclonal antibody; complementarity determining region;
KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
KW cancer; therapy; diagnosis.
XX OS Homo sapiens.
OS Synthetic.
XX FH Key Location/Qualifiers
FT Peptide 1..2
FT Region /note= "vector-encoded residues"
FT Region 31..37
FT Region /note= "CDR1"
FT Region 52..67
FT Region /note= "CDR2"
FT Region 100..107
FT Region /note= "CDR3"
XX PN WO9929888-A1.
XX PD 17-JUN-1999.
XX PF 04-DEC-1998; 98WO-US25828.
XX PR 05-DEC-1997; 97US-0986016.
XX PA (SCRI ) SCRIPPS RES INST.
XX PI Barbas CF, Rader C;
XX DR WPI; 1999-394979/33.
XX PT Production of humanized mouse monoclonal antibodies
XX Disclosure; Page 51-52; 55pp; English.
XX CC This sequence represents the heavy chain variable region of a
CC humanised LM609 antibody. LM609 is directed to human integrin
CC alpha-v beta-3. It selectively promotes apoptosis of vascular
CC cells that have been stimulated to undergo angiogenesis, making it
CC a tool for cancer diagnosis and therapy. The invention provides
CC humanised antibodies, especially humanised LM609. In such humanized
CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
CC grafted onto a human light chain, and a heavy chain CDR from a mouse
CC antibody is grafted onto a human antibody heavy chain to produce
CC libraries from which a humanised murine antibody having the desired
CC specificity is selected. By preserving the original CDR sequences
CC such as the HCDR3 and LCDR3 sequences of LM609 (see AAY06371-72), the
CC humanisation strategy ensures epitope conservation.
XX SQ Sequence 118 AA;
Query Match 89.7%; Score 52; DB 20; Length 118;
Best Local Similarity 90.0%; Pred. No. 0.064;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 ARHNHGSFAY 10
Db 98 ARHNHGSFAY 107
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Job time : 13.8235 secs
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:54:45 ; Search time 1.96078 Seconds
(without alignments)
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Title: US-09-016-061-60
Perfect score: 58
Sequence: 1 ARNHGSFAY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 97044 seqs, 15060890 residues

Total number of hits satisfying chosen parameters: 97044

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- Published_Applications_AA:*
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 - 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB pep.*
 - 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match %	Score	Length	ID	Description
1	52	89.7	117	8	US-08-790-540A-2
2	52	89.7	117	8	US-08-790-540A-6
3	52	89.7	117	8	US-08-791-391A-2
4	52	89.7	117	8	US-08-791-391A-6
5	39	67.2	196	10	US-09-741-669-368
6	39	67.2	196	10	US-09-912-020-376
7	38	65.5	265	10	US-09-732-091-44
8	35	60.3	772	9	US-09-905-291A-339
9	35	60.3	772	10	US-09-909-320-339
10	35	60.3	772	10	US-09-909-088B-339
11	34	58.6	59	10	US-09-864-761-35802
12	34	58.6	349	10	US-09-766-366-4
13	34	58.6	482	10	US-09-815-242-4953
14	34	58.6	491	10	US-09-815-242-10940
15	34	58.6	554	10	US-09-981-649A-30
16	33	56.9	100	10	US-09-864-761-35983
17	33	56.9	138	10	US-09-796-744-15
18	33	56.9	480	10	US-09-815-242-10999
19	32	55.2	29	10	US-09-864-761-34610

Query Match 89.7%; Score 52; DB 8; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.0096;

20	32	55.2	189	9	US-09-992-738-1	Sequence 1, Appli
21	32	55.2	299	9	US-09-992-598-213	Sequence 213, App
22	32	55.2	299	10	US-09-989-722-213	Sequence 213, App
23	32	55.2	299	10	US-09-989-723-213	Sequence 213, App
24	32	55.2	299	10	US-09-989-279-213	Sequence 213, App
25	32	55.2	299	10	US-09-989-727-213	Sequence 213, App
26	32	55.2	299	10	US-09-989-731-213	Sequence 213, App
27	32	55.2	299	10	US-09-989-732-213	Sequence 213, App
28	32	55.2	299	10	US-09-991-073-213	Sequence 213, App
29	32	55.2	299	10	US-09-990-442-213	Sequence 213, App
30	32	55.2	299	10	US-09-991-163-213	Sequence 213, App
31	32	55.2	299	10	US-09-993-604-213	Sequence 213, App
32	32	55.2	299	10	US-09-990-456-213	Sequence 213, App
33	32	55.2	299	10	US-09-989-721-213	Sequence 213, App
34	32	55.2	299	12	US-10-052-586-164	Sequence 164, App
35	32	55.2	382	10	US-09-919-831-3	Sequence 3, Appli
36	32	55.2	679	10	US-09-815-242-5082	Sequence 5082, Ap
37	32	55.2	1741	9	US-09-971-536-68	Sequence 68, Appl
38	31	53.4	14	1	US-08-677-599B-22	Sequence 22, Appl
39	31	53.4	67	10	US-09-864-761-42935	Sequence 42935, A
40	31	53.4	101	10	US-09-764-853-432	Sequence 432, App
41	31	53.4	183	12	US-10-033-109-2	Sequence 37, Appl
42	31	53.4	245	8	US-08-424-550B-37	Sequence 5110, Ap
43	31	53.4	254	10	US-09-815-242-5110	Sequence 4, Appli
44	31	53.4	258	10	US-09-452-239-4	Sequence 38, Appl
45	31	53.4	258	10	US-09-452-239-38	

ALIGNMENTS

RESULT 1
US-08-790-540A-2
; Sequence 2, Application US/08790540A
; Patent No. US20010011125A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,540A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-790-540A-2

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARNHGSPAY 10
||||:|||||

Db 97 ARHNYGSFAY 106

RESULT 2
US-08-790-540A-6
; Sequence 6, Application US/08790540A
; Patent No. US20010011125A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,540A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122

Query Match 89.7%; Score 52; DB 8; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.0096;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARNHGSPAY 10
||||:|||||

Db 97 ARHNYGSFAY 106

RESULT 3
US-08-791-391A-2
; Sequence 2, Application US/08791391A
; Patent No. US20010016645A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,391A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-391A-2

Query Match 89.7%; Score 52; DB 8; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.0096;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNGSPAY 10
||||:|||||

Db 97 ARHNYGSFAY 106

RESULT 4
US-08-791-391A-6
; Sequence 6, Application US/08791391A
; Patent No. US20010016645A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,391A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-391A-6

Query Match
Best Local Similarity 89.7%; Score 52; DB 8; Length 117;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARNHGSFAY 10
 |||||
DB 97 ARHNYGSFAY 106

RESULT 5
US-09-741-669-368
; Sequence 368, Application US/09741669
; Patent No. US20020022718A1
; GENERAL INFORMATION:
; APPLICANT: Forsyth, R. Allyn
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; TITLE OF INVENTION: Genes identified as required for
; TITLE OF INVENTION: proliferation of E. coli
; FILE REFERENCE: ELITRA 009A
; CURRENT APPLICATION NUMBER: US/09/741,669
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 60/173005
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 481
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 368
; LENGTH: 196
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-741-669-368

Query Match
Best Local Similarity 67.2%; Score 39; DB 10; Length 196;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNHGSFAY 10
 |||||
DB 105 HNHGSFKH 112

RESULT 6
US-09-912-020-376
; Sequence 376, Application US/09912020
; Patent No. US20020045592A1
; GENERAL INFORMATION:
; APPLICANT: Zyskind, Judith
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Trawick, John
; APPLICANT: Forsyth, R. Allyn
; APPLICANT: Froelich, Jamie M.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION IN
; TITLE OF INVENTION: ESCHERICHIA COLI
; FILE REFERENCE: ELITRA 001DV1
; CURRENT APPLICATION NUMBER: US/09/912,020
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: 09/492,709
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 60/117,405
; PRIOR FILING DATE: 1999-01-27
; NUMBER OF SEQ ID NOS: 485
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 376
; LENGTH: 196
; TYPE: PRT
; ORGANISM: E. Coli
US-09-912-020-376

Query Match
Best Local Similarity 67.2%; Score 39; DB 10; Length 196;

Best Local Similarity 75.0%; Pred. No. 3.2;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 3 HNHGSFAY 10
 |||||
DB 105 HNHGSFKH 112

RESULT 7
US-09-732-091-44
; Sequence 44, Application US/09732091
; Patent No. US20020107368A1
; GENERAL INFORMATION:
; APPLICANT: Tian, Jing-Hui
; APPLICANT: Walker, Richard I.
; APPLICANT: Jackson, W. James
; TITLE OF INVENTION: Helicobacter proteins, gene sequences and uses
; TITLE OF INVENTION: thereof
; FILE REFERENCE: 7969-088
; CURRENT APPLICATION NUMBER: US/09/732,091
; CURRENT FILING DATE: 2000-12-07
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 265
; TYPE: PRT
; ORGANISM: Helicobacter sp.
US-09-732-091-44

Query Match
Best Local Similarity 65.5%; Score 38; DB 10; Length 265;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNHGSFAY 10
 |:|||||
DB 8 HHHGSMAY 15

RESULT 8
US-09-905-291A-339
; Sequence 339, Application US/09905291A
; Patent No. US20020160374A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,291A
; CURRENT FILING DATE: 2001-07-12

; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 339
; LENGTH: 772
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-905-291A-339

Query Match 60.3%; Score 35; DB 9; Length 772;
Best Local Similarity 60.0%; Pred. No. 66;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ARHNHGSFAY 10
||: ||| |
Db 220 ARYCHGGFGY 229

RESULT 9
US-09-909-320-339
; Sequence 339, Application US/09909320
; Patent No. US20020132240A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.

; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/909,320
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 339
; LENGTH: 772
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-909-320-339

Query Match 60.3%; Score 35; DB 10; Length 772;
Best Local Similarity 60.0%; Pred. No. 66;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ARHNHGSFAY 10
||: ||| |
Db 220 ARYCHGGFGY 229

RESULT 10
US-09-909-088B-339
; Sequence 339, Application US/09909088B
; Patent No. US20020146709A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone

APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ACIDS ENCODING THE SAME
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/909,088B
CURRENT FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 339
LENGTH: 772
TYPE: PRT
ORGANISM: Homo Sapien
US-09-909-088B-339

Query Match 60.3%; Score 35; DB 10; Length 772;
Best Local Similarity 60.0%; Pred. No. 66;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARNHGSFAY 10

||: ||| |

Db 220 ARYCHGGFGY 229

RESULT 11
US-09-864-761-35802
Sequence 35802, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aemica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 35802
LENGTH: 59
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC011307.1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.2
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 3.8
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 17
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 9.3
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.7
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.8
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 56
OTHER INFORMATION: EST_HUMAN HIT: A970601.1, EVALUE 7.00e-18
OTHER INFORMATION: SWISSPROT HIT: P27793, EVALUE 3.00e-01
US-09-864-761-35802

Query Match 58.6% Score 34; DB 10; Length 59;
Best Local Similarity 100.0%; Pred. No. 7.4; 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Gaps 0;

QY 4 NHGSFA 9
|||||
DB 16 NHGSFA 21

RESULT 12

US-09-766-366-4
; Sequence 4, Application US/09766366
; Patent No. US20010024786A1
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; Shah, Purvi
; Corley, Neil C.
; TITLE OF INVENTION: HUMAN PEROXISOMAL THIOESTERASE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:

FILING DATE: 18-Jan-2001

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/872,784

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0293 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-0555

TELEFAX: 415-845-4166

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 349 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: GenBank

CLONE: 854594

SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-766-366-4

Query Match 58.6% Score 34; DB 10; Length 349;
Best Local Similarity 60.0%; Pred. No. 44;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARNHGSFAY 10
|||: |||
DB 247 ARYNYVAFAY 256

RESULT 13

US-09-815-242-4953
; Sequence 4953, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.

; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4953
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Enterococcus faecalis

US-09-815-242-4953

Query Match 58.6% Score 34; DB 10; Length 482;
Best Local Similarity 75.0%; Pred. No. 61;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARNHGSF 8
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DB 29 ARHNDGEF 36

RESULT 14

US-09-815-242-10940
; Sequence 10940, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:

; APPLICANT: Haselbeck, Robert

; APPLICANT: Ohlsen, Karl L.

; APPLICANT: Zyskind, Judith W.

; APPLICANT: Wall, Daniel

; APPLICANT: Trawick, John D.

; APPLICANT: Carr, Grant J.

; APPLICANT: Yamamoto, Robert T.

; APPLICANT: Xu, H. Howard

; TITLE OF INVENTION: Identification of Essential Genes in

; TITLE OF INVENTION: Prokaryotes

; FILE REFERENCE: ELITRA.011A

; CURRENT APPLICATION NUMBER: US/09/815,242

; CURRENT FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,727

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/242,578

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/253,625

; PRIOR FILING DATE: 2000-11-27

; PRIOR APPLICATION NUMBER: 60/257,931

; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

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; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10940
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-815-242-10940
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Query Match      58.6%; Score 34; DB 10; Length 491;
Best Local Similarity 75.0%; Pred. No. 63;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 1 ARNHGSF 8
    |||||
Db 37 ARHNDGEF 44
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RESULT 15
US-09-981-649A-30
; Sequence 30, Application US/09981649A
; Patent No. US20020132250A1
; GENERAL INFORMATION:
; APPLICANT: Ford et al.
; TITLE OF INVENTION: EGF MOTIF PROTEIN, EGFL6, MATERIALS AND METHODS
; FILE REFERENCE: 28110/37665
; CURRENT APPLICATION NUMBER: US/09/981,649A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 09/687,860
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: US 09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US 09/363,316
; PRIOR FILING DATE: 1999-07-28
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 554
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-981-649A-30
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Query Match      58.6%; Score 34; DB 10; Length 554;
Best Local Similarity 66.7%; Pred. No. 71;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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QY 1 ARNHGSFA 9
    |||||
Db 26 ARHHGLLA 34
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Search completed: November 18, 2002, 18:45:15
Job time : 2.96078 secs
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:01 ; Search time 4.2402 Seconds
(without alignments)
69.390 Million cell updates/sec

Title: US-09-016-061-60

Perfect score: 58

Sequence: 1 ARNHGSEFAY 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/1/iaa/5A-COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B-COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A-COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B-COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS-COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	58.6	99	4	US-09-199-637A-75
2	34	58.6	204	1	US-08-591-989-4
3	34	58.6	213	2	US-08-655-821-16
4	34	58.6	231	3	US-08-926-842B-20
5	34	58.6	231	4	US-09-172-952-32
6	34	58.6	231	4	US-09-172-952-33
7	34	58.6	238	4	US-09-172-952-18
8	34	58.6	240	3	US-08-926-842B-21
9	34	58.6	349	1	US-08-872-784-4
10	34	58.6	349	2	US-09-100-851-4
11	34	58.6	349	4	US-09-265-294-4
12	34	58.6	536	2	US-08-551-211-3
13	33	56.9	178	4	US-09-134-001C-5564
14	33	56.9	180	4	US-09-134-001C-5294
15	32	55.2	36	1	US-08-053-131-84
16	32	55.2	36	1	US-08-645-641-84
17	32	55.2	36	1	US-07-853-408B-84
18	32	55.2	36	2	US-08-096-762-84
19	32	55.2	36	2	US-08-308-855-84
20	32	55.2	36	4	US-09-042-353-281
21	32	55.2	36	4	US-08-758-417A-129
22	32	55.2	36	5	PCT-US92-10983-84
23	32	55.2	103	2	US-08-596-319-31
24	32	55.2	123	2	US-08-652-816A-8
25	32	55.2	384	1	US-08-707-793A-5
26	32	55.2	384	1	US-08-707-792A-5
27	32	55.2	443	1	US-07-940-245-2

28	32	55.2	443	1	US-08-226-486-2	Sequence 2, Appl
29	32	55.2	630	2	US-08-394-177-5	Sequence 5, Appl
30	32	55.2	630	2	US-08-596-319-2	Sequence 2, Appl
31	32	55.2	630	3	US-08-394-912A-5	Sequence 5, Appl
32	32	55.2	630	4	US-09-333-636-5	Sequence 5, Appl
33	32	55.2	907	3	US-08-938-830-26	Sequence 26, Appl
34	32	55.2	907	3	US-09-020-222-26	Sequence 26, Appl
35	32	55.2	3033	1	US-07-925-695-8	Sequence 8, Appl
36	32	55.2	3033	1	US-07-925-695-9	Sequence 9, Appl
37	31	53.4	14	3	US-08-956-307B-3	Sequence 3, Appl
38	31	53.4	94	3	US-09-147-550-14	Sequence 14, Appl
39	31	53.4	94	3	US-09-147-550-45	Sequence 45, Appl
40	31	53.4	94	3	US-09-147-550-48	Sequence 48, Appl
41	31	53.4	94	3	US-09-147-550-77	Sequence 77, Appl
42	31	53.4	94	3	US-09-147-550-84	Sequence 84, Appl
43	31	53.4	94	3	US-09-147-550-90	Sequence 90, Appl
44	31	53.4	94	3	US-09-147-550-101	Sequence 101, Appl
45	31	53.4	94	4	US-09-557-917-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1

US-09-199-637A-75

; Sequence 75, Application US/09199637A

; Patent No. 6355411

; GENERAL INFORMATION:

; APPLICANT: Ausubel, Frederick

; APPLICANT: Goodman, Howard M.

; APPLICANT: Rahme, Laurence G.

; APPLICANT: Mahajan-Miklos, Shalina

; APPLICANT: Tan, Man-Wah

; APPLICANT: Cao, Hui

; APPLICANT: Drenkard, Eliana

; APPLICANT: Tsongalis, John

; TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID

; FILE REFERENCE: 00786/361002

; CURRENT FILING DATE: 1998-11-25

; PRIOR APPLICATION NUMBER: 60/066,517

; PRIOR FILING DATE: 1997-11-25

; NUMBER OF SEQ ID NOS: 437

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 75

; LENGTH: 99

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-199-637A-75

Query Match

Best Local Similarity

Matches

5; Conservative

1; Mismatches

1; Indels

0; Gaps

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0;

; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.40 MB
; MEDIUM TYPE: storage
; COMPUTER: IBM COMPATIBLE
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/591,989
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX 49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 204
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-591-989-4

Query Match 58.6%; Score 34; DB 1; Length 204;
Best Local Similarity 75.0%; Pred. No. 80;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ARNHGSF 8
Db 137 APHGHSF 144

RESULT 3
US-08-655-821-16
; Sequence 16, Application US/08655821
; Patent No. 5846718
; GENERAL INFORMATION:
; APPLICANT: Zhang, Ying
; NAME: Scorpio, Angelo
; TITLE OF INVENTION: IDENTIFICATION OF PYRAZINAMIDE-RESISTANT
; TITLE OF INVENTION: MYCOBACTERIA AND METHODS FOR TREATING
; TITLE OF INVENTION: MYCOBACTERIAL INFECTIONS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/655,821
; FILING DATE: 31-MAY-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ellison, Eldora L.
; REGISTRATION NUMBER: 39,967
; REFERENCE/DOCKET NUMBER: 07662/003001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 16:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 213 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-655-821-16

Query Match 58.6%; Score 34; DB 2; Length 213;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 NHGSFA 9
Db 57 NHGSFA 62

RESULT 4
US-08-926-842B-20
; Sequence 20, Application US/08926842B
; Patent No. 6030807
; GENERAL INFORMATION:
; APPLICANT: Sa-No. 6030807ueira, Isabel
; APPLICANT: de Lencastre, Herminia
; TITLE OF INVENTION: HIGHLY REGULABLE PROMOTER FOR HETEROLOGOUS GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/926,842B
; FILING DATE: 10-SEP-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-089 N
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 231 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Escherichia coli
; US-08-926-842B-20

Query Match 58.6%; Score 34; DB 3; Length 231;
Best Local Similarity 62.5%; Pred. No. 90;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 HNHGSFA 10
Db 169 HSHGPF 176

RESULT 5

US-09-172-952-32
; Sequence 32, Application US/09172952
; Patent No. 6368793
; GENERAL INFORMATION:
; APPLICANT: Hoch, James
; APPLICANT: Dartois, Veronique
; TITLE OF INVENTION: METABOLIC SELECTION METHODS
; FILE REFERENCE: 234/191
; CURRENT APPLICATION NUMBER: US/09/172,952
; CURRENT FILING DATE: 1998-10-14
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Yias-Ec
US-09-172-952-32

Query Match 58.6%; Score 34; DB 4; Length 231;
Best Local Similarity 62.5%; Pred. No. 90;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNHGSFAY 10
|:|:|:
Db 169 HSHGPFAY 176

RESULT 6
US-09-172-952-33
; Sequence 33, Application US/09172952
; Patent No. 6368793
; GENERAL INFORMATION:
; APPLICANT: Hoch, James
; APPLICANT: Dartois, Veronique
; TITLE OF INVENTION: METABOLIC SELECTION METHODS
; FILE REFERENCE: 234/191
; CURRENT APPLICATION NUMBER: US/09/172,952
; CURRENT FILING DATE: 1998-10-14
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Yias-Hi
US-09-172-952-33

Query Match 58.6%; Score 34; DB 4; Length 231;
Best Local Similarity 62.5%; Pred. No. 90;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNHGSFAY 10
|:|:|:
Db 169 HSHGPFAY 176

RESULT 7
US-09-172-952-18
; Sequence 18, Application US/09172952
; Patent No. 6368793
; GENERAL INFORMATION:
; APPLICANT: Hoch, James
; APPLICANT: Dartois, Veronique
; TITLE OF INVENTION: METABOLIC SELECTION METHODS
; FILE REFERENCE: 234/191
; CURRENT APPLICATION NUMBER: US/09/172,952
; CURRENT FILING DATE: 1998-10-14
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Yias-Ko
US-09-172-952-18

Query Match 58.6%; Score 34; DB 4; Length 238;
Best Local Similarity 62.5%; Pred. No. 93;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNHGSFAY 10
|:|:|:
Db 169 HSHGPFAY 176

RESULT 8
US-08-926-842B-21
; Sequence 21, Application US/08926842B
; Patent No. 6030807
; GENERAL INFORMATION:
; APPLICANT: Sa-No. 6030807ueira, Isabel
; APPLICANT: de Lencastre, Herminia
; TITLE OF INVENTION: HIGHLY REGULABLE PROMOTER FOR HETEROLOGOUS GENE
; TITLE OF INVENTION: HIGHLY REGULABLE PROMOTER FOR HETEROLOGOUS GENE
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/926,842B
; FILING DATE: 10-SEP-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-089 N
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 240 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Salmonella typhimurium
US-08-926-842B-21

Query Match 58.6%; Score 34; DB 3; Length 240;
Best Local Similarity 62.5%; Pred. No. 94;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNHGSFAY 10
|:|:|:
Db 169 HSHGPFAY 176

RESULT 9
US-08-872-784-4
; Sequence 4, Application US/08872784
; Patent No. 5776753
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.

```
; TITLE OF INVENTION: HUMAN PEROXISOMAL THIOESTERASE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/872,784
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0293 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 349 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 854594
; US-08-872-784-4

Query Match 58.6%; Score 34; DB 1; Length 349;
Best Local Similarity 60.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARNHGSEAY 10
||:|: |||
Db 247 ARYNYVAFY 256

RESULT 10
US-09-100-851-4
; Sequence 4, Application US/09100851
; Patent No. 5911984
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: HUMAN PEROXISOMAL THIOESTERASE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/100,851
; FILING DATE:
; PRIOR APPLICATION DATA:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0293 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 349 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 854594
; US-08-872-784-4
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; APPLICATION NUMBER: US/08/872,784
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0293 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 349 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 854594
; US-09-100-851-4

Query Match 58.6%; Score 34; DB 2; Length 349;
Best Local Similarity 60.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARNHGSEAY 10
||:|: |||
Db 247 ARYNYVAFY 256

RESULT 11
US-09-265-294-4
; Sequence 4, Application US/09265294
; Patent No. 6210890
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: HUMAN PEROXISOMAL THIOESTERASE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/265,294
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/100,851
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0293 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 349 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 854594
```


US-09-265-294-4

Query Match 58.6%; Score 34; DB 4; Length 349;
Best Local Similarity 60.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARNHGSFAY 10
|||:||||
Db 247 ARYNYVAFAY 256

RESULT 12

US-08-551-211-3
; Sequence 3, Application US/08551211

; Patent No. 5843735

; GENERAL INFORMATION:

; APPLICANT: LEE, Jung Joon

; APPLICANT: KIM, Young Ho

; APPLICANT: HONG, Soon Kwang

; APPLICANT: HONG, Young Soo

; APPLICANT: HWANG, Cheol Kyu

; APPLICANT: KIM, Hang Sub

; TITLE OF INVENTION: AKLAVINONE C-11 HYDROXYLASE, GENE CODING

; TITLE OF INVENTION: FOR SAME, EXPRESSION VECTOR THEREFOR, AND

; TITLE OF INVENTION: PROCESS FOR PREPARING HYBRID ANTIBIOTICS

; TITLE OF INVENTION: BY USING SAID VECTOR

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LEE, Jung Joon

; STREET: Hanbit Apt. 132-201, Oeun-dong, Youseong-ku

; CITY: Daejeon

; STATE: Daejeon

; COUNTRY: Republic of Korea

; ZIP: 305-333

; ADDRESSEE: KIM, Young Ho

; STREET: Hanbit Apt. 125-1504, Oeun-dong, Youseong-ku

; CITY: Daejeon

; STATE: Daejeon

; COUNTRY: Republic of Korea

; ZIP: 305-333

; ADDRESSEE: HONG, Soon Kwang

; STREET: #231-32 Mochung-dong

; CITY: Cheongju-si

; STATE: Chungcheongbuk-do

; COUNTRY: Republic of Korea

; ZIP: 360-140

; ADDRESSEE: HONG, Young Soo

; STREET: #San-1, Oeun-dong, Youseong-ku

; CITY: Daejeon

; STATE: Daejeon

; COUNTRY: Republic of Korea

; ZIP: 305-333

; ADDRESSEE: HWANG, Cheol Kyu

; STREET: #San-1, Oeun-dong, Youseong-ku

; CITY: Daejeon

; STATE: Daejeon

; COUNTRY: Republic of Korea

; ZIP: 305-333

; ADDRESSEE: KIM, Hang Sub

; STREET: Sindonga Apt. 11-1403, Yongjeon-dong, Dong-ku

; CITY: Daejeon

; STATE: Daejeon

; COUNTRY: Republic of Korea

; ZIP: 300-200

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage

; COMPUTER: IBM PC/AT

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: Word Perfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/551,211

; FILING DATE: 31-OCT-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: KR 95-1950

; FILING DATE: 2-MAR-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Shahan Islam

; REGISTRATION NUMBER: 32,507

; REFERENCE/DOCKET NUMBER: DT-1421

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 278-1000

; TELEFAX: (212) 953-7249

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 536 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-551-211-3

Query Match

Best Local Similarity 58.6%; Score 34; DB 2; Length 536;

Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNHGSFAY 10

Db 193 RHGGTGLAH 201

RESULT 13

US-09-134-001C-5564

; Sequence 5564, Application US/09134001C

; Patent No. 6380370

; GENERAL INFORMATION:

; APPLICANT: Lynn Doucette-Stamm et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC

; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: GTC-007

; CURRENT APPLICATION NUMBER: US/09/134,001C

; CURRENT FILING DATE: 1998-08-13

; PRIOR APPLICATION NUMBER: US 60/064,964

; PRIOR FILING DATE: 1997-11-08

; PRIOR APPLICATION NUMBER: US 60/055,779

; PRIOR FILING DATE: 1997-08-14

; NUMBER OF SEQ ID NOS: 5674

; SEQ ID NO 5564

; LENGTH: 178

; TYPE: PRT

; ORGANISM: Staphylococcus epidermidis

US-09-134-001C-5564

Query Match

Best Local Similarity 56.9%; Score 33; DB 4; Length 178;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 NHGSFAY 10

Db 63 NHTSPAY 69

RESULT 14

US-09-134-001C-5294

; Sequence 5294, Application US/09134001C

; Patent No. 6380370

; GENERAL INFORMATION:

; APPLICANT: Lynn Doucette-Stamm et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC

; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: GTC-007

; CURRENT APPLICATION NUMBER: US/09/134,001C

; CURRENT FILING DATE: 1998-08-13

; PRIOR APPLICATION NUMBER: US 60/064,964

; PRIOR FILING DATE: 1997-11-08

; PRIOR APPLICATION NUMBER: US 60/055,779

; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 5294
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5294

Query Match 56.9%; Score 33; DB 4; Length 180;
Best Local Similarity 71.4%; Pred. No. 1e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 NHGSFAY 10
:11:111
Db 104 HGTTFAY 110

RESULT 15

US-08-053-131-84
; Sequence 84, Application US/08053131
; Patent No. 5661016
; GENERAL INFORMATION:
; APPLICANT: Lonberg; Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 197
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 200
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/053,131
; FILING DATE: 26-APR-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,860
; FILING DATE: 16-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/810,279
; FILING DATE: 17-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/853,408
; FILING DATE: 18-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14643-9-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-053-131-84

Query Match 55.2%; Score 32; DB 1; Length 36;
Best Local Similarity 60.0%; Pred. No. 32;
Matches 1.6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARNHGGSFAY 10

Db 3 ARHYGGSY 12

Search completed: November 18, 2002, 17:43:35
Job time : 4.2402 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:01 ; Search time 4.90196 Seconds
(without alignments)
196.114 Million cell updates/sec

Title: US-09-016-061-62

Perfect score: 58

Sequence: 1 ARHNYGSYAY 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR-73:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	77.6	108	2	S26316
2	45	77.6	110	2	S26317
3	42	72.4	446	2	T19625
4	40	69.0	316	2	T15395
5	38	65.5	236	2	T27233
6	38	65.5	428	2	T03934
7	38	65.5	482	2	T01932
8	37	63.8	289	2	T34688
9	37	63.8	420	2	I51088
10	37	63.8	1144	2	A36968
11	36	62.1	9	2	S36850
12	36	62.1	113	2	S26458
13	36	62.1	143	1	HSURB2
14	36	62.1	301	2	JW0079
15	36	62.1	349	1	S52763
16	36	62.1	349	2	T33263
17	36	62.1	626	2	T18733
18	35	60.3	119	2	C30562
19	35	60.3	119	2	C30562
20	35	60.3	119	2	D30562
21	35	60.3	150	2	D69081
22	35	60.3	155	2	T03042
23	35	60.3	241	2	T16802
24	35	60.3	246	1	C64705
25	35	60.3	246	2	C71815
26	35	60.3	257	2	B81155
27	35	60.3	257	2	C81949
28	35	60.3	281	2	S71251
29	35	60.3	293	2	F64969

transcription regu
site-specific DNA-
cysteine proteinas
hypothetical prote
conserved hypothet
probable phenylala
UL47h protein - Ma
amelogenin TRAP -
conserved hypothet
hypothetical prote
hypothetical prote
hypothetical prote
probable membrane
dehydrin - barley
amelogenin I precu
dehydrin 18 - barl

ALIGNMENTS

RESULT 1

S26316

Ig heavy chain V region - mouse

C:Species: Mus musculus (house mouse)

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000

C:Accession: S26316

R:Stark, S.E.; Caton, A.J.

J. Exp. Med. 174, 613-624, 1991

A:Title: Antibodies that are specific for a single amino acid interchange in a protei

A:Reference number: S26309; MUID:91341421; PMID:1908510

A:Accession: S26316

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-108 <STA>

A:Cross-references: EMBL:X59190; NID:g52066; PIDN:CAA41900.1; PID:g1334035

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:2-85/Domain: immunoglobulin homology <IMM>

Query Match 77.6%; Score 45; DB 2; Length 108;

Best Local Similarity 80.0%; Pred. No. 0.54;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSYAY 10

|| |||:||||

Db 84 ARGNYGNAY 93

RESULT 2

S26317

Ig heavy chain V region - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 21-Jan-2000

C:Accession: S26317

R:Stark, S.E.; Caton, A.J.

J. Exp. Med. 174, 613-624, 1991

A:Title: Antibodies that are specific for a single amino acid interchange in a protei

A:Reference number: S26309; MUID:91341421; PMID:1908510

A:Accession: S26317

A:Molecule type: mRNA

A:Residues: 1-110 <STA>

A:Cross-references: EMBL:X59186

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:4-87/Domain: immunoglobulin homology <IMM>

Query Match 77.6%; Score 45; DB 2;

Best Local Similarity 80.0%; Pred. No. 0.55;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSYAY 10

|| |||:||||

Db 86 ARGNVGNVAY 95

RESULT 3

T19625

hypothetical protein C31H5.6 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000

C:Accession: T19625

R:Kershaw, J.

submitted to the EMBL Data Library, April 1997

A:Reference number: Z19153

A:Accession: T19625

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-446 <WIL>

A:Cross-references: EMBL:Z93778; PIDN:CAB07846.1; GSPDB:GN00019; CESP:C31H5.6

A:Experimental source: clone C31H5

C:Genetics:

A:Gene: CESP:C31H5.6

A:Map position: 1

A:Introns: 49/2; 85/1; 120/2; 183/3; 218/3; 255/3; 285/2; 331/3; 360/3

C:Superfamily: Caenorhabditis elegans hypothetical protein W03D8.8

Query Match 72.4%; Score 42; DB 2; Length 446;

Best Local Similarity 87.5%; Pred. No. 7.3;

Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHNYGSYA 9

|||||:

Db 51 RHNYGSHA 58

RESULT 4

T15395

hypothetical protein C03F11.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C:Accession: T15395

R:Bentley, D.

submitted to the EMBL Data Library, October 1995

A:Description: The sequence of C. elegans cosmid C03F11.

A:Reference number: Z18342

A:Accession: T15395

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-316 <BEN>

A:Cross-references: EMBL:U39744; NID:g1049465; PID:g1049467; PIDN:AAA80440.1; CESP:C03F11

C:Genetics:

A:Gene: CESP:C03F11.2

A:Introns: 90/3; 133/2; 171/1; 227/1; 262/1; 309/2

Query Match 69.0%; Score 40; DB 2; Length 316;

Best Local Similarity 70.0%; Pred. No. 12;

Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSYAY 10

|||:||||

Db 69 ARHFFGSY 78

RESULT 5

T27233

hypothetical protein Y57G11C.21 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T27233

R:McMurray, A.

submitted to the EMBL Data Library, September 1997

A:Reference number: Z20330

A:Accession: T27233

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-236 <WIL>

A:Cross-references: EMBL:Z99281; PIDN:CAB16522.1; GSPDB:GN00022; CESP:Y57G11C.21

A:Experimental source: clone Y57G11C

C:Genetics:

A:Gene: CESP:Y57G11C.21

A:Map position: 4

Query Match 65.5%; Score 38; DB 2; Length 236;

Best Local Similarity 60.0%; Pred. No. 20;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSYAY 10

||||:||||

Db 118 AYHNFNVAY 127

RESULT 6

T03934

DNA binding protein ACBF - common tobacco

C:Species: Nicotiana tabacum (common tobacco)

C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000

C:Accession: T03934

R:Seguin, A.; Laible, G.; Leyva, A.; Dixon, R.A.; Lamb, C.J.

Plant Mol. Biol. 35, 281-291, 1997

A:Title: Characterization of a gene encoding a DNA-binding protein that interacts in

A:Reference number: Z15144; MUID:98009965; PMID:9349252

A:Accession: T03934

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-428 <SEG>

A:Cross-references: EMBL:U90212; NID:g1899187; PIDN:AAC49850.1; PID:g1899188

A:Experimental source: tissue-type stem

A>Note: interacts in vitro with vascular-specific cis-elements of the phenylalanine a

C:Superfamily: unassigned ribonucleoprotein repeat-containing proteins; ribonucleopro

Query Match 65.5%; Score 38; DB 2; Length 428;

Best Local Similarity 66.7%; Pred. No. 36;

Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 RHNYGSYAY 10

|||||:

Db 387 RQNYGGYGY 395

RESULT 7

T01932

RNA binding protein homolog - common tobacco (fragment)

C:Species: Nicotiana tabacum (common tobacco)

C>Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 26-May-2000

C:Accession: T01932

R:Deslandes, L.; Manevski, A.; Lescure, B.; Marco, Y.; Tremousaygue, D.

submitted to the EMBL Data Library, October 1997

A:Reference number: Z14459

A:Accession: T01932

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-482 <DES>

A:Cross-references: EMBL:AF029351; NID:g2708531; PID:g2708532

C:Genetics:

A:Gene: ORRBP-1

C:Superfamily: unassigned ribonucleoprotein repeat-containing proteins; ribonucleopro

Query Match 65.5%; Score 38; DB 2; Length 482;

Best Local Similarity 66.7%; Pred. No. 41;

Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 RHNYGSYAY 10

|||||:

Db 442 RQNYGGYGY 450

RESULT 8

T34688

probable lipoprotein - Streptomyces coelicolor
 C:Species: Streptomyces coelicolor
 C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
 C:Accession: F34688
 R:Harris, D.; Taylor, K.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
 submitted to the EMBL Data Library, May 1998
 A:Reference number: Z21553
 A:Accession: T34688
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-289 <HAR>
 A:Cross-references: EMBL:AL023517; PIDN:CAA18984.1; GSPDB:GN00070; SCOEDB:SC1B5.10c
 A:Experimental source: strain A3(2)
 C:Genetics:
 A:Gene: SCOEDB:SC1B5.10c

Query Match 63.8%; Score 37; DB 2; Length 289;
 Best Local Similarity 60.0%; Pred. No. 37;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ARHNYGSYAY 10
 | : | : | : | : |
 Db 144 ANHSYSHYAY 153

RESULT 9
 I51088
 L-SF precursor - Japanese medaka
 C:Species: Oryzias latipes (Japanese medaka)
 C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 20-Aug-1999
 C:Accession: I51088
 R:Murata, K.; Sasaki, T.; Yasumasu, S.; Tuchi, I.; Enami, J.; Yasumasu, I.; Yamagami, K.
 Dev. Biol. 167, 9-17, 1995
 A:Title: Cloning of cDNAs for the precursor protein of a low-molecular-weight subunit of
 A:Reference number: I51088; MUID:95154588; PMID:7851666
 A:Accession: I51088
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-420 <MUR>
 A:Cross-references: GB:D38630; NID:g1060937; PIDN:BAA07610.1; PID:g1060938
 C:Genetics:
 A:Gene: l-sf
 C:Superfamily: sperm-binding glycoprotein ZP3; ZP domain homology
 F:84-338/Domain: ZP domain homology <ZPH>

Query Match 63.8%; Score 37; DB 2; Length 420;
 Best Local Similarity 60.0%; Pred. No. 54;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ARHNYGSYAY 10
 | : | : | : | : |
 Db 21 AQHNYGKPSY 30

RESULT 10
 A36968
 P1-like adhesin precursor - Mycoplasma pirum
 C:Species: Mycoplasma pirum
 C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 07-Dec-1999
 C:Accession: A36968
 R:Tham, T.N.; Ferris, S.; Bahrsooi, E.; Canarelli, S.; Montagnier, L.; Blanchard, A.
 J. Bacteriol. 176, 781-788, 1994
 A:Title: Molecular characterization of the P1-like adhesin gene from Mycoplasma pirum.
 A:Reference number: A36968; MUID:94131957; PMID:8300531
 A:Accession: A36968
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1144 <FHA>
 A:Cross-references: GB:L19685; NID:g404770; PIDN:AAC36866.1; PID:g404771
 C:Genetics:
 A:Genetic code: SCC3

Query Match 63.8%; Score 37; DB 2; Length 1144;

Best Local Similarity 66.7%; Pred. No. 1.4e+02;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 RHNYGSYAY 10
 : | | | | |
 Db 885 KQNYGSYFY 893
 RESULT 11
 S36850
 Ig heavy chain V region - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 06-Jan-1994 #sequence_revision 01-Dec-1995 #text_change 05-Nov-1999
 C:Accession: S36850
 R:Jacob, J.; Kelsoe, G.
 submitted to the EMBL Data Library, July 1992
 A:Description: In situ studies on the primary immune response to (4-hydroxy-3-nitroph
 A:Reference number: S25024
 A:Accession: S36850
 A:Status: preliminary
 A:Molecule type: nucleic acid
 A:Residues: 1-9 <JAC>
 A:Cross-references: EMBL:X67387; NID:g50113; PIDN:CAA47799.1; PID:e51594; PID:g133387
 C:Keywords: heterotetramer; immunoglobulin

Query Match 62.1%; Score 36; DB 2; Length 9;
 Best Local Similarity 75.0%; Pred. No. 2.8e+05;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSY 8
 | : | : | : | : |
 Db 1 ARYDYSY 8

RESULT 12
 S26468
 Ig heavy chain V region - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
 C:Accession: S26468
 R:Kavaler, J.
 submitted to the EMBL Data Library, April 1991
 A:Reference number: S26459
 A:Accession: S26468
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-113 <KAV>
 A:Cross-references: EMBL:X59107; NID:g51944; PIDN:CAA41833.1; PID:g51945
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:11-94/Domain: immunoglobulin homology <IMM>

Query Match 62.1%; Score 36; DB 2; Length 113;
 Best Local Similarity 75.0%; Pred. No. 23;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ARHNYGSY 8
 | : | : | : | : |
 Db 93 ARHPYGNV 100

RESULT 13
 HSURB2
 histone H2B.2, sperm - sea urchin (Lytechinus pictus)
 C:Species: Lytechinus pictus (painted urchin)
 C:Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 22-Jun-1999
 C:Accession: A24329; B25381
 R:Lai, Z.C.; Childs, G.
 Nucleic Acids Res. 14, 6845-6856, 1986
 A:Title: Isolation and characterization of the gene encoding the testis specific hist
 A:Reference number: A93637; MUID:87016329; PMID:3763394
 A:Accession: A24329
 A:Molecule type: DNA

A;Residues: 1-143 <LAI>
A;Cross-references: GB:X04384; NID:g9618; PIDN:CAA27971.1; PID:g9619
A;Experimental source: testis
R;Lieber, T.; Weissner, K.; Childs, G.
Mol. Cell. Biol. 6, 2602-2612, 1986
A;Title: Analysis of histone gene expression in adult tissues of the sea urchins Strongylocentrotus purpuratus
A;Reference number: A93078; MUID:87084560; PMID:3785204
A;Accession: B25381
A;Molecule type: mRNA
A;Residues: 59-75, 'A', '77-137, 'N', '139-143 <LIE>
A;Cross-references: GB:M13635; NID:g161315; PIDN:AAA30001.1; PID:g161316
A;Experimental source: testis
A;Note: this sequence most likely represents an alternative allele of the same gene
C;Superfamily: histone H2B
C;Keywords: chromosomal protein; DNA binding; nucleosome core
F;2-143/Product: histone H2B.2, sperm #status predicted <MAT>

Query Match 62.1%; Score 36; DB 1; Length 143;
Best Local Similarity 66.7%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSYAY 10
| :||| |
Db 52 RESIGSYIY 60

RESULT 14
JW0079
heterogeneous nuclear ribonucleoprotein homolog JKTBP [imported] - human
N;Alternate names: JKTBP
C;Species: Homo sapiens (man)
C;Date: 17-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 02-Sep-2000
C;Accession: JW0079
R;Tsuchiya, N.; Kamei, D.; Takano, A.; Matsui, T.; Yamada, M.
J. Biochem. 123, 499-507, 1998
A;Title: Cloning and characterization of a cDNA encoding a novel heterogeneous nuclear ribonucleoprotein
A;Reference number: JW0079; MUID:98207031; PMID:9538234
A;Accession: JW0079
A;Molecule type: mRNA
A;Residues: 1-301 <TSU>
A;Cross-references: DBJ:D89092; NID:g2780747; PIDN:BAA24361.1; PID:d1025273; PID:g2780747
C;Superfamily: unassigned ribonucleoprotein repeat-containing proteins; ribonucleoprotein repeat-containing proteins
F;28-101,113-187/Domain: RNA-binding #status predicted <RNA>
F;30-96/Domain: ribonucleoprotein repeat homology <RRM1>

Query Match 62.1%; Score 36; DB 2; Length 301;
Best Local Similarity 62.5%; Pred. No. 58;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSYAY 10
| :||| |
Db 263 YNYGNVGY 270

RESULT 15
S52763
hypothetical protein YJR019c - yeast (Saccharomyces cerevisiae)
N;Alternate names: Hypothetical protein J1456
C;Species: Saccharomyces cerevisiae
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C;Accession: S52763; S55209; S57034; S65928
R;Hani, J.; Stumpf, G.; Dondey, H.
submitted to the EMBL Data Library, March 1995
A;Description: PFI1 encodes an essential protein in Saccharomyces cerevisiae, which shows a role in the cell cycle
A;Reference number: S52762
A;Accession: S52763
A;Molecule type: DNA
A;Residues: 1-349 <HAN>
A;Cross-references: EMBL:X85972; NID:g758283; PID:g758285
R;de Haan, M.; Smits, P.H.M.; Grivell, L.A.
submitted to the EMBL Data Library, May 1995
A;Reference number: S55183
A;Accession: S55209

A;Molecule type: DNA
A;Residues: 1-349 <DEH>
A;Cross-references: EMBL:X87611; NID:g854567; PID:g854594
R;de Haan, M.; Grivell, L.A.; Smits, P.H.M.
submitted to the Protein Sequence Database, September 1995
A;Reference number: S56771
A;Accession: S57034
A;Molecule type: DNA
A;Residues: 1-349 <ZAG>
A;Cross-references: EMBL:Z49519; NID:g1015654; PID:g1015655; GSPDB:GNO0010; MIPS:YJRO
R;Hani, J.; Stumpf, G.; Dondey, H.
FEBS Lett. 365, 198-202, 1995
A;Title: PFI1 encodes an essential protein in Saccharomyces cerevisiae, which shows a role in the cell cycle
A;Reference number: S65927; MUID:95300974; PMID:7781779
A;Accession: S65928
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-349 <HAW>
A;Cross-references: EMBL:X85972; NID:g758283; PIDN:CAA59960.1; PID:g758285
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1995
C;Genetics:
A;Gene: SGD:TSL1; MIPS:YJR019c
A;Cross-references: SGD:S0003780; MIPS:YJR019c
A;Map position: 10R
C;Superfamily: acyl-CoA thioesterase II

Query Match 62.1%; Score 36; DB 1; Length 349;
Best Local Similarity 60.0%; Pred. No. 67;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSYAY 10
| :||| |
Db 247 ARYNYVAFAY 256

Search completed: November 18, 2002, 17:47:03
Job time : 5.90196 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:00 ; Search time 2.45098 Seconds
(without alignments)
169.223 Million cell updates/sec

Title: US-09-016-061-62
Perfect score: 58
Sequence: 1 ARHNYGSYAY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	41	70.7		909	1	HEX_ADEM1	P48308 mouse adeno
2	40	69.0		316	1	YX12_CAEEL	Q11123 caenorhabdi
3	36	62.1		142	1	H2B2_LYTP1	P06146 lytechinus
4	36	62.1		202	1	AMEL_MONDO	Q28462 monodelphis
5	36	62.1		349	1	PTEL_YEAST	P41903 saccharomyc
6	35	60.3		293	1	RBA1_ECOLI	P37744 escherichia
7	35	60.3		544	1	SYFB_SULSO	P95960 sulfolobus
8	34	58.6		150	1	Y109_CHLMU	O9plj0 chlamydia m
9	34	58.6		150	1	Y736_CHLTR	O84741 chlamydia t
10	34	58.6		189	1	AMEL_PIG	P45561 sus scrofa
11	34	58.6		213	1	AMEX_BOVIN	P02817 bos taurus
12	34	58.6		218	1	Y4VH_RHIN	Q53216 rhizobium s
13	34	58.6		225	1	DH4_HORVU	P12949 hordeum vul
14	34	58.6		323	1	CCSA_LOTJA	Q9bbp4 lotus japon
15	34	58.6		448	1	ASTB_PSEAE	O50175 pseudomonas
16	34	58.6		456	1	KICH_SCHPO	Q10276 schizosacch
17	34	58.6		576	1	PEX5_PICPA	P32922 pichia past
18	34	58.6		719	1	PAK7_HUMAN	Q9p286 homo sapien
19	34	58.6		1150	1	C9EA_BACTA	Q9zn19 bacillus th
20	34	58.6		1156	1	C9AA_BACTG	Q99031 bacillus th
21	34	58.6		1157	1	C9CA_BACTO	Q45733 bacillus th
22	34	58.6		1169	1	C9DA_BACTP	O05014 bacillus th
23	33	56.9		180	1	CH19_DROSU	P13428 drosophila
24	33	56.9		317	1	Y640_AQUAE	O66883 aquifex aeo
25	33	56.9		405	1	VGLM_EBV	P03215 epstein-bar
26	33	56.9		419	1	YMD2_CAEEL	P34456 caenorhabdi
27	33	56.9		425	1	PURA_FUSNU	P58793 fusobacteri
28	33	56.9		425	1	PURA_FUSNU	O68581 fusobacteri
29	33	56.9		520	1	PAX7_HUMAN	P23759 homo sapien
30	33	56.9		629	1	KSYK_MOUSE	P48025 mus musculu
31	33	56.9		635	1	KSYK_HUMAN	P43405 homo sapien
32	33	56.9		649	1	GPDM_SCHPO	O14400 schizosacch
33	33	56.9		786	1	EXOP_RHINE	P33698 rhizobium m

34	33	56.9	809	1	UBPL_YEAST	P25037 saccharomyc
35	33	56.9	1569	1	GLI3_XENLA	Q91660 xenopus lae
36	33	56.9	1596	1	GLI3_HUMAN	P10071 homo sapien
37	33	56.9	1596	1	GLI3_MOUSE	Q61602 mus musculu
38	32	55.2	79	1	CYB_DIPCA	P16359 dipodomys c
39	32	55.2	79	1	CYB_DIPPE	P16358 dipodomys h
40	32	55.2	79	1	CYB_DIPPA	P16357 dipodomys p
41	32	55.2	81	1	IRX2_HUMAN	Q9B211 homo sapien
42	32	55.2	129	1	YPS6_MYCTU	Q50742 mycobacteri
43	32	55.2	134	1	CYB_DRYNI	O03713 dryomys nit
44	32	55.2	198	1	HB2G_HUMAN	P01911 homo sapien
45	32	55.2	202	1	DHSC_BACSU	P08064 bacillus su

ALIGNMENTS

RESULT 1
HEX_ADEM1
ID HEX_ADEM1 STANDARD; PRT; 909 AA.
AC P48308; O11839;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Hexon protein (Late protein 2).
DE PII.
GN Mouse adenovirus type 1 (MAV-1).
OS Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=10530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FL;
RX MEDLINE=94157453; PubMed=7509368;
RA Weber J.M., Cai F., Murali R., Burnett R.M.;
RT "Sequence and structural analysis of murine adenovirus type 1 hexon.";
RL J. Gen. Virol. 75:141-147(1994).
RN [2]
RP REVISIONS TO 443.
RA Weber J.M.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC !- FUNCTION: THIS PROTEIN IS ONE OF THE STRUCTURAL PROTEINS IN THE
CC !- VIRAL COAT AND IS SYNTHESIZED DURING LATE INFECTION.
CC !- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC -----
CC EMBL; M81889; AAB48187.1; -.
DR HSP; P03277; IDHX.
DR InterPro; IPR000736; Adeno_hexon.
DR Pfam; PF01065; Adeno_hexon; 1.
DR Pfam; PF03678; Adeno_hexon.C; 1.
DR ProDom; PD002815; Adeno_hexon; 1.
KW Coat protein; Hexon protein; Late protein.
SQ SEQUENCE 909 AA; 102368 MW; 7E1C17DF7F0E95A0 CRC64;

Query Match 70.7%; Score 41; DB 1; Length 909;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 NYGSYAY 10
Db 210 NYGSYAY 216
|||||

RESULT 2
YX12_CAEEL
ID YX12_CAEEL STANDARD; PRT; 316 AA.

```

AC Q1123;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 35.1 kDa protein C03F11.2 in chromosome X.
GN C03F11.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Bentley D.;
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: WEAK, IN THE N-TERMINUS, TO C.ELEGANS F53B1.5.
CC -----
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CC -----
DR EMBL; U39744; AAK1883.1; -.
DR WormPep; C03F11.2; CE03914.
KW Hypothetical protein.
SQ SEQUENCE 316 AA; 35107 MW; 6A725FCAC21CF676 CRC64;

Query Match 69.0%; Score 40; DB 1; Length 316;
Best Local Similarity 70.0%; Pred. No. 7.1;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNGSYAY 10
   III :III I
DB 69 ARHFGSYEY 78

RESULT 3
H2B2_LYTPI
ID H2B2_LYTPI STANDARD; PRT; 142 AA.
AC P06146;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Histone H2B.2, sperm.
OS Lytechinus pictus (Painted sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Echinacea; Temnopleuroidea; Toxopneustidae;
OC Lytechinus.
OX NCBI_TaxID=7653;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=87016329; PubMed=3763394;
RA Lai Z.-C., Childs G.J.;
RT "Isolation and characterization of the gene encoding the testis
RT specific histone protein H2B-2 from the sea urchin Lytechinus
RT pictus."
RL Nucleic Acids Res. 14:6845-6856(1986).
RN [2]
RP SEQUENCE OF 58-142 FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=87064560; PubMed=3785204;
RA Lieber T., Weisser K., Childs G.;
RT "Analysis of histone gene expression in adult tissues of the sea
RT urchins Strongylocentrotus purpuratus and Lytechinus pictus:
RT tissue-specific expression of sperm histone genes."
RL Mol. Cell. Biol. 6:2602-2612(1986).
CC -!- SUBUNIT: THE NUCLEOSOME IS AN OCTAMER CONTAINING TWO MOLECULES OF
CC H2A, H2B, H3, AND H4; WHICH WRAP APPROXIMATELY 146 BP OF DNA.
CC -!- SUBCELLULAR LOCATION: Nuclear.

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CC -!- SIMILARITY: BELONGS TO THE HISTONE H2B FAMILY.
CC -----
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CC -----
DR EMBL; X04384; CAA27971.1; -.
DR EMBL; M13635; AAA30001.1; -.
DR PIR; A24329; HSURB2.
DR InterPro; IPR000558; Histone_H2B.
DR InterPro; IPR004822; Histone_core.
DR Pfam; PF00125; histone; 1.
DR PRINTS; PR00621; HISTONEH2B.
DR ProDom; PD000497; Histone_H2B; 1.
DR SMART; SM00427; H2B; 1.
DR PROSITE; PS00357; HISTONE_H2B; 1.
KW Chromosomal protein; Nucleosome core; Nuclear protein; DNA-binding;
KW Multigene family.
FT INIT_MET 0
FT VARIANT 75 75 G -> A.
FT VARIANT 137 137 K -> N.
SQ SEQUENCE 142 AA; 15805 MW; 8BF47E2C5EE878D5 CRC64;

Query Match 62.1%; Score 36; DB 1; Length 142;
Best Local Similarity 66.7%; Pred. No. 16;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNGSYAY 10
   I :III I
DB 51 RESYGSYIY 59

RESULT 4
AMEL_MONDO
ID AMEL_MONDO STANDARD; PRT; 202 AA.
AC Q28462;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Amelogenin.
GN AMEL.
OS Monodelphis domestica (Short-tailed grey opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Monodelphis.
OX NCBI_TaxID=13616;
RN [1]
RP SEQUENCE FROM N.A.; SEQUENCE OF 1-42, AND ALTERNATIVE SPLICING.
RX MEDLINE=97113826; PubMed=8955666;
RA Hu C.C., Zhang C., Qian Q., Ryu O.H., Moradian-Oldak J., Fincham A.G.,
RA Simmer J.P.;
RT "Cloning, DNA sequence, and alternative splicing of opossum
RT amelogenin mRNAs."
RL J. Dent. Res. 75:1728-1734(1996).
CC -!- FUNCTION: PLAYS A ROLE IN THE BIOMINERALIZATION OF TEETH. SEEMS
CC STAGE OF TOOTH ENAMEL DEVELOPMENT. THOUGHT TO PLAY A MAJOR ROLE IN
CC THE STRUCTURAL ORGANIZATION AND MINERALIZATION OF DEVELOPING
CC ENAMEL.
CC -!- SUBCELLULAR LOCATION: Extracellular matrix.
CC -!- ALTERNATIVE PRODUCTS: A number of isoforms are produced by
CC alternative splicing.
CC -!- SIMILARITY: BELONGS TO THE AMELOGENIN FAMILY.
CC -----
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CC -----
DR EMBL: U43407; ABA41109.1; -.
DR InterPro: IPR004116; Amelogenin.
DR Pfam: PF02948; Amelogenin; 1.
KW Extracellular matrix; Phosphorylation; Enamel; Repeat;
KW Alternative splicing.
FT MOD_RES 16 16 PHOSPHORYLATION (BY SIMILARITY).
FT CONFLICT 32 33 HE -> QQ (IN REF 1; AA SEQUENCE).
SQ SEQUENCE 202 AA; 22996 MW; 277FD2935211A6C6 CRC64;

Query Match 62.1%; Score 36; DB 1; Length 202;
Best Local Similarity 66.7%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 RHNYGSYAY 10
Db 31 RHEYPYGY 39
II III

RESULT 5
PTEI_YEAST STANDARD; PRT; 349 AA.
AC P41903;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Peroxisomal acyl-coenzyme A thioester hydrolase 1 (EC 3.1.2.2)
DE (Peroxisomal long-chain acyl-CoA thioesterase 1).
GN TES1 OR PTE1 OR YJR019C OR J1456.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DH484;
RA Hani J., Stumpf G., Domdey H.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c / FY1679;
RA de Haan M., Smits P.H.M., Grivell L.A.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RX MEDLINE=99194760; PubMed=10092594;
RA Jones J.M., Nau K., Geraghty M.T., Erdmann R., Gould S.J.;
RT "Identification of peroxisomal acyl-CoA thioesterases in yeast and humans.";
RL J. Biol. Chem. 274:9216-9223(1999).
CC -1- FUNCTION: MAY PLAY A ROLE IN FATTY ACID OXIDATION RATHER THAN
CC FORMATION OF FATTY ACIDS.
CC -1- CATALYTIC ACTIVITY: Palmitoyl-CoA + H(2)O = CoA + palmitate.
CC -1- SUBCELLULAR LOCATION: Peroxisomal.
CC -1- SIMILARITY: BELONGS TO THE C/M/P THIOESTER HYDROLASE FAMILY.
CC -----
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CC -----
DR EMBL: X85972; CAA59960.1; -.
DR EMBL: X87611; CAA60943.1; -.
DR EMBL: Z49519; CAA89543.1; -.
DR EMBL: AF124265; AAD27617.1; -.
DR SGD: S0003780; TES1.
DR InterPro: IPR003703; Acyl_CoA_thio.
DR Pfam: PF02551; Acyl_CoA_thio; 2.
DR TIGRFAMS; TIGR00189; tesB; 1.

KW Hydrolase; Serine esterase; Peroxisome.
FT ACT_SITE 259 259 BY SIMILARITY.
FT SITE 347 349 MICROBODY TARGETING SIGNAL (POTENTIAL).
SQ SEQUENCE 349 AA; 40259 MW; F1B5A51C9A46783E CRC64;

Query Match 62.1%; Score 36; DB 1; Length 349;
Best Local Similarity 60.0%; Pred. No. 37;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSYAY 10
Db 247 ARNYVAFAY 256
II III

RESULT 6
RBAL_ECOLI STANDARD; PRT; 293 AA.
AC P37744; P78081;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Glucose-1-phosphate thymidyltransferase (EC 2.7.7.24) (dTDP-glucose
DE synthase) (dTDP-glucose pyrophosphorylase).
GN RFBA OR RMLA OR B2039.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / WGI;
RX MEDLINE=94292435; PubMed=7517391;
RA Stevenson G., Neal B., Liu D., Hobbs M., Packer N.H., Batley M.,
RA Redmond J.W., Lindquist L., Reeves P.R.;
RT "Structure of the O antigen of Escherichia coli K-12 and the sequence
RT of its rfb gene cluster.";
RL J. Bacteriol. 176:4144-4156(1994).
RN [2]
RP REVISION TO 288.
RC STRAIN=K12 / WGI;
RA Stevenson G.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97251358; PubMed=9097040;
RA Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T.,
RA Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T.,
RA Saito N., Sampei G., Seki Y., Sivasubramanian S., Tagami H.,
RA Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiiuchi T.;
RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 40.1-50.0 min region on the linkage map.";
RL DNA Res. 3:379-392(1996).
RN [5]
RP SEQUENCE OF 247-293 FROM N.A.
RC STRAIN=K12 / W3110;
RX MEDLINE=94292434; PubMed=7517390;
RA Yao Z., Valvano M.A.;
RT "Genetic analysis of the O-specific lipopolysaccharide biosynthesis
RT region (rfb) of Escherichia coli K-12 W3110: identification of genes
RT that confer group 6 specificity to Shigella flexneri serotypes Y and
```

RT 4a.;

CC J. Bacteriol. 176:4133-4143(1994).

CC -I- CATALYTIC ACTIVITY: dTTP + alpha-D-glucose 1-phosphate =

CC diphosphate + dTDP-glucose.

CC -I- PATHWAY: dTDP-L-RHAMNOSE BIOSYNTHESIS WITHIN THE O ANTIGEN

CC BIOSYNTHESIS PATHWAY OF LIPOPOLYSACCHARIDE BIOSYNTHESIS.

CC -I- SIMILARITY: BELONGS TO THE GLUCOSE-1-PHOSPHATE

CC THYMIDYLTRANSFERASE FAMILY.

CC -----

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CC -----

DR EMBL; U09876; AAB88400.1; -.

DR EMBL; AE000294; AAC75100.1; -.

DR EMBL; D90841; BAA15881.1; -.

DR EMBL; D90842; BAA15893.1; -.

DR EMBL; U03041; AAC31629.1; -.

DR EcoGene; EGI1978; rfba.

DR InterPro; IPR001825; NTP_transferase.

DR Pfam; PF00483; NTP_transferase; 1.

DR TIGRFAMs; TIGR01207; rmlA; 1.

DR Lipopolysaccharide biosynthesis; Transferase; Kinase;

KW Nucleotidyltransferase; Complete proteome.

FT CONFLICT 247 247 Q -> P (IN REF. 5).

SQ SEQUENCE 293 AA; 32693 MW; BA895362D1C5CA55_CRC64;

Query Match 60.3%; Score 35; DB 1; Length 293;

Best Local Similarity 55.6%; Pred. No. 47;

Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSYAY 10

Db :||| |

278 KNNYGVLY 286

RESULT 7

SYFB_SULSO

ID SYFB_SULSO STANDARD; PRT; 544 AA.

AC P95960;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Phenylalanine-tRNA synthetase beta chain (EC 6.1.1.20) (Phenylalanine--

DE tRNA ligase beta chain) (Phers).

GN PHET OR SSO0101 OR C04_021.

OS Sulfolobus solfataricus.

OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;

OC Sulfolobus.

OX NCBI_TaxID=2287;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 35092 / DSM 1617 / P2;

RX MEDLINE=97055432; PubMed=8899719;

RA Sengen C.W., Klenk H.-P., Singh R.K., Allard G., Chan C.C.-Y.,

RA Liu Q.Y., Penny S.L., Young F., Schenk M.E., Gaasterland T.,

RA Doolittle W.F., Ragan M.A., Charlebois R.L.;

RT "Organizational characteristics and information content of an archaeal

RT genome: 156 kb of sequence from Sulfolobus solfataricus P2.;"

RL Mol. Microbiol. 22:175-191(1996).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 35092 / DSM 1617 / P2;

RX MEDLINE=21322296; PubMed=11427726;

RA She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,

RA Awqeyez M.J., Chan-Welner C.C.-Y., Clausen I.G., Curtis B.A.,

RA De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,

RA Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,

RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,

RA Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,

RA Garrett R.A., Ragan M.A., Sengen C.W., Van der Oost J.;

RT "The complete genome of the crenarchaeon Sulfolobus solfataricus P2.;"

RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).

CC -I- CATALYTIC ACTIVITY: ATP + L-phenylalanine + tRNA(Phe) = AMP +

CC diphosphate + L-phenylalanyl-tRNA(Phe).

CC -I- SUBUNIT: Tetramer of two alpha and two beta chains (by

CC similarity).

CC -I- SUBCELLULAR LOCATION: Cytoplasmic.

CC -I- SIMILARITY: BELONGS TO THE PHENYLALANYL-TRNA SYNTHETASE BETA

CC CHAIN FAMILY. SUBFAMILY 2.

CC -----

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CC -----

DR EMBL; Y08257; CAA69550.1; -.

DR EMBL; AE006649; AAK40457.1; -.

DR InterPro; IPR005146; B3_4.

DR InterPro; IPR005147; B5.

DR InterPro; IPR004531; Phet_arch.

DR Pfam; PF03483; B3_4; 1.

DR Pfam; PF03484; B5; 1.

DR TIGRFAMs; TIGR00471; phet_arch; 1.

DR Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;

KW Complete proteome.

SQ SEQUENCE 544 AA; 61815 MW; 4B1A2234BA8ABDE_CRC64;

Query Match 60.3%; Score 35; DB 1; Length 544;

Best Local Similarity 85.7%; Pred. No. 83;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 NYGSYAY 10

Db :||| |

350 NYGSVDY 356

RESULT 8

Y109_CHLMU

ID Y109_CHLMU STANDARD; PRT; 150 AA.

AC Q9PLJ0;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Hypothetical protein TC0109.

GN TC0109.

OS Chlamydia muridarum.

OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.

OX NCBI_TaxID=83560;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=MOpn / Nigg.

RX MEDLINE=20150255; PubMed=10684935;

RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,

RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,

RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,

RA Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,

RA Eisen J., Fraser C.M.;

RT "Genome sequences of Chlamydia trachomatis MOpn and Chlamydia

RT pneumoniae AK39.;"

RL Nucleic Acids Res. 28:1397-1406(2000).

CC -I- SIMILARITY: BELONGS TO THE PF0098 FAMILY.

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CC -----
DR EMBL; AE002278; AAF3988.1; -.
DR HSSP; P77368; IFUX.
DR TIGR; TC0109; -.
DR InterPro; IPR005247; Cons_hypoth481.
DR TIGRFAMs; TIGR00481; TIGR00481.1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 150 AA; 16478 MW; C093FFI42BB8928 CRC64;

Query Match      58.6%; Score 34; DB 1; Length 150;
Best Local Similarity 60.0%; Pred. No. 37;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARHNYGSYAY 10
   | | | | |
Db 103 AKHRYFFAY 112

RESULT 9
Y736_CHLTR
ID Y736_CHLTR STANDARD; PRT; 150 AA.
AC O84741;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein CT736.
GN CT736.
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D/UW-3/Cx;
RX MEDLINE=99000809; PubMed=9784136;
RA Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
RA Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
RA Davis R.W.;
RT "Genome sequence of an obligate intracellular pathogen of humans:
RT Chlamydia trachomatis.";
RL Science 282:754-759(1998).
CC -!- SIMILARITY: BELONGS TO THE UPF0098 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AE001344; AAC68331.1; -.
DR HSSP; P77368; IFUX.
DR InterPro; IPR005247; Cons_hypoth481.
DR TIGRFAMs; TIGR00481; TIGR00481.1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 150 AA; 16508 MW; E480FE4899354C67 CRC64;

Query Match      58.6%; Score 34; DB 1; Length 150;
Best Local Similarity 60.0%; Pred. No. 37;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARHNYGSYAY 10
   | | | | |
Db 103 AKHRYFFAY 112

RESULT 10
AMEL_PIG
ID AMEL_PIG STANDARD; PRT; 189 AA.
AC P45561;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
```

```
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Amelogenin precursor (Amelogenin 173A/173B) [Contains: Leucine-rich
DE amelogenin peptide (LRAP)].
GN AMEL.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX MEDLINE=97113827; PubMed=8955667;
RA Hu C.C., Bartlett J.D., Zhang C.H., Qian Q., Ryu O.H., Simmer J.P.;
RT "Cloning, cDNA sequence, and alternative splicing of porcine
RT amelogenin mRNAs.";
RL J. Dent. Res. 75:1735-1741(1996).
RN [2]
RP SEQUENCE OF 17-61 AND 78-181.
RC TISSUE=Tooth;
RX MEDLINE=94071951; PubMed=8250931;
RA Fincham A.G., Moradian-Oldak J.;
RT "Amelogenin post-translational modifications: carboxy-terminal
RT processing and the phosphorylation of bovine and porcine 'TRAP' and
RT 'LRAP' amelogenins.";
RL Biochem. Biophys. Res. Commun. 197:248-255(1993).
CC -!- FUNCTION: PLAYS A ROLE IN THE BIOMINERALIZATION OF TEETH. SEEMS
CC TO REGULATE THE FORMATION OF CRYSTALLITES DURING THE SECRETORY
CC STAGE OF TOOTH ENAMEL DEVELOPMENT. THOUGHT TO PLAY A MAJOR ROLE IN
CC THE STRUCTURAL ORGANIZATION AND MINERALIZATION OF DEVELOPING
CC ENAMEL.
CC -!- SUBCELLULAR LOCATION: Extracellular matrix.
CC -!- ALTERNATIVE PRODUCTS: A number of isoforms are produced by
CC alternative splicing. One of these forms, LRAP, lacks the central
CC section of amelogenin. Additional isoforms may be produced by the
CC use of alternative promoters.
CC -!- SIMILARITY: BELONGS TO THE AMELOGENIN FAMILY.
CC -----
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CC -----
DR EMBL; U43405; AAB41110.1; -.
DR EMBL; U43406; AAB41111.1; -.
DR PIR; PC2006; PC2006.
DR PIR; PC2008; PC2008.
DR InterPro; IPR004116; Amelogenin.
DR Pfam; PF02948; Amelogenin; 1.
KW Extracellular matrix; Phosphorylation; Enamel; Repeat; Signal;
KW Alternative splicing.
FT SIGNAL 1 16
FT CHAIN 17 189 AMELOGENIN.
FT MOD_RES 32 32 PHOSPHORYLATION.
FT VARSPPLIC 34 45 MISSING (IN ISOFORM LRAP).
FT VARSPPLIC 6 6 L -> F (IN ISOFORM 173B).
FT VARSPPLIC 14 16 AFS -> SLA (IN ISOFORM 173B).
SQ SEQUENCE 189 AA; 21387 MW; 6392212E0A31D00C CRC64;

Query Match      58.6%; Score 34; DB 1; Length 189;
Best Local Similarity 66.7%; Pred. No. 46;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 RHNYGSYAY 10
   | | | | |
Db 47 RHPYTSYG 55

RESULT 11
AMEX_BOVIN
ID AMEX_BOVIN STANDARD; PRT; 213 AA.
AC P02817;
```

DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Amelogenin, class I precursor.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91113686; PubMed=1989679;
 RA Gibson C., Golub E., Herold R., Risser M., Ding W., Shimokawa H.,
 RA Young M., Termine J., Rosenbloom J.;
 RT "Structure and expression of the bovine amelogenin gene.";
 RL Biochemistry 30:1075-1079(1991).
 RN [2]
 RP PRELIMINARY SEQUENCE OF 17-201.
 RX MEDLINE=84231410; PubMed=6732825;
 RA Takagi T., Suzuki M., Baba T., Minegishi K., Sasaki S.;
 RT "Complete amino acid sequence of amelogenin in developing bovine
 RT enamel.";
 RL Biochem. Biophys. Res. Commun. 121:592-597(1984).
 RN [3]
 RP ALTERNATIVE SPLICING (ISOFORM LRAP).
 RC TISSUE=Tooth;
 RX MEDLINE=91144612; PubMed=1996994;
 RA Gibson C.W., Golub E., Ding W., Shimokawa H., Young M., Termine J.,
 RA Rosenbloom J.;
 RT "Identification of the leucine-rich amelogenin peptide (LRAP) as the
 RT translation product of an alternatively spliced transcript.";
 RL Biochem. Biophys. Res. Commun. 174:1306-1312(1991).
 RN [4]
 RP SEQUENCE OF 17-49 AND 188-213.
 RX MEDLINE=94071951; PubMed=8250931;
 RA Fincham A.G., Moradian-Oldak J.;
 RT "Amelogenin post-translational modifications: carboxy-terminal
 RT processing and the phosphorylation of bovine and porcine 'TRAP' and
 RT 'LRAP' amelogenins.";
 RL Biochem. Biophys. Res. Commun. 197:248-255(1993).
 RN [5]
 RP STRUCTURE BY NMR.
 RX MEDLINE=90091473; PubMed=2598664;
 RA Renuopalakrishnan V., Prabhakaran M., Huang S.G., Balasubramanian A.,
 RA Strawich E., Glimcher M.J.;
 RT "Secondary structure and limited three-dimensional structure of
 RT bovine amelogenin.";
 RL Connect. Tissue Res. 22:131-138(1989).
 CC -!- FUNCTION: PLAYS A ROLE IN THE BIOMINERALIZATION OF TEETH. SEEMS
 CC TO REGULATE THE FORMATION OF CRYSTALLITES DURING THE SECRETORY
 CC STAGE OF TOOTH ENAMEL DEVELOPMENT. THOUGHT TO PLAY A MAJOR ROLE IN
 CC THE STRUCTURAL ORGANIZATION AND MINERALIZATION OF DEVELOPING
 CC ENAMEL.
 CC -!- SUBCELLULAR LOCATION: Extracellular matrix.
 CC -!- ALTERNATIVE PRODUCTS: A number of isoforms are produced by
 CC alternative splicing. One of these forms, LRAP, lacks the central
 CC section of amelogenin.
 CC -!- MISCELLANEOUS: AMELOGENIN IS THE PREDOMINANT PROTEIN IN DEVELOPING
 CC DENTAL ENAMEL.
 CC -!- MISCELLANEOUS: CLASS I AMELOGENINS LOCATED ON X CHROMOSOME.
 CC -!- SIMILARITY: BELONGS TO THE AMELOGENIN FAMILY.
 CC
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 CC
 CC EMBL: M63499; AAA30372.1; -;
 CC EMBL: M63631; AAA30625.1; -;
 CC PIR: A03300; JMB0.

DR PIR: JN0123; JN0123.
 DR PIR: PC2007; PC2007.
 DR InterPro: IPR004116; Amelogenin.
 DR Pfam: PF02948; Amelogenin; 1.
 KW Extracellular matrix; Phosphorylation; Enamel; Repeat; Signal;
 KW Alternative splicing.
 FT SIGNAL 1 16
 FT CHAIN 17 213 AMELOGENIN, CLASS I.
 FT MOD_RES 32 32 PHOSPHORYLATION.
 FT VARSPLIC 50 187 MISSING (IN ISOFORM LRAP).
 SQ SEQUENCE 213 AA; 24119 MW; 163BD538806366DF CRC64;

 Query Match 58.6%; Score 34; DB 1; Length 213;
 Best Local Similarity 66.7%; Pred. No. 51;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

 QY 2 RHNYGSYAY 10
 Db 47 RHPYPSYGY 55

 RESULT 12
 Y4VH_RHISN STANDARD; PRT; 218 AA.
 ID Y4VH_RHISN AC Q53216;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Hypothetical 24.6 kDa protein Y4VH.
 GN Y4VH.
 OS Rhizobium sp. (strain NGR234).
 OG Plasmid sym pNGR234a.
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae-group;
 OC Rhizobiaceae; Rhizobium.
 OX NCBI_TaxID=394;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97305956; PubMed=9163424;
 RA Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
 RA Perret X.;
 RT "Molecular basis of symbiosis between Rhizobium and legumes.";
 RL Nature 387:394-401(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96389014; PubMed=8796346;
 RA Freiberg C., Perret X., Broughton W.J., Rosenthal A.;
 RT "Sequencing the 500-kb GC-rich symbiotic replicon of Rhizobium sp.
 RT NGR234 using dye terminators and a thermostable 'sequenase'; a
 RT beginning.";
 RL Genome Res. 6:590-600(1996).
 CC -!- SIMILARITY: NONE OBVIOUS.
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 CC
 CC EMBL: Z68203; CAA92423.1; -;
 DR EMBL: AE000101; AAB91896.1; -;
 KW Hypothetical protein; Plasmid.
 SQ SEQUENCE 218 AA; 24594 MW; 501C6C3B8A09A2E5 CRC64;

 Query Match 58.6%; Score 34; DB 1; Length 218;
 Best Local Similarity 66.7%; Pred. No. 52;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

 QY 1 ARHNYGSYA 9
 Db 68 ARDNHGSYS 76

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RESULT 13
DH4_HORVU          STANDARD;          PRT;    225 AA.
AC P12949;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DE 01-AUG-1991 (Rel. 19, Last annotation update)
DE Dehydrin DHN4 (B18).
GN DHN4.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Himalaya; TISSUE=Seedling;
RX MEDLINE=93357436; PubMed=2562763;
RA Close T.J., Kortt A.A., Chandler P.M.;
RT "A cDNA-based comparison of dehydration-induced proteins (dehydrins)
RT in barley and corn."
RL Plant Mol. Biol. 13:95-108(1989).
CC -1- INDUCTION: BY ABSICISIC ACID AND WATER STRESS.
CC -1- SIMILARITY: STRONG TO BARLEY DHN1 AND DHN2, MAIZE DHN1, AND
CC ESPECIALLY TO BARLEY DHN3. TWO EXTREMELY CONSERVED BLOCKS WERE
CC IDENTIFIED, WITH A LESS CONSERVED REPEATING UNIT POSITIONED
CC BETWEEN THEM. DEHYDRIN DHN4 HAS FIVE SUCH SEMI-CONSERVED TANDEM
CC REPEATING UNITS.
CC -1- SIMILARITY: BELONGS TO THE PLANT DEHYDRIN FAMILY.
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DR EMBL; X15287; CAA33361.1; -.
DR PIR; S05546; S05546.
DR InterPro; IPR000167; Dehydrin.
DR Pfam; PF00257; dehydrin; 1.
DR PROSITE; PS00315; DEHYDRIN_1; 1.
DR PROSITE; PS00823; DEHYDRIN_2; 2.
KW Dehydrin; Repeat.
FT DOMAIN 60 68 POLY-SER.
FT DOMAIN 105 199 5 X APPROXIMATE TANDEM REPEATS.
FT REPEAT 105 118 1.
FT REPEAT 119 136 2.
FT REPEAT 137 159 3.
FT REPEAT 160 178 4.
FT REPEAT 179 199 5.
SQ SEQUENCE 225 AA; 22574 MW; F0636B368CE5FF6C CRC64;

Query Match 58.6%; Score 34; DB 1; Length 225;
Best Local Similarity 55.6%; Pred. No. 54;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSVAY 10
DB 97 OHNAGTYGY 105

RESULT 14
CCSA_LOTJA
ID CCSA_LOTJA          STANDARD;          PRT;    323 AA.
AC Q9BBP4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cytochrome c biogenesis protein ccSA.
GN CCSA.

Lotus japonicus.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Lotaeae; Lotus.
OX NCBI_TaxID=34305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Accession MG-20;
RX MEDLINE=21082929; PubMed=11214967;
RA Kato T., Kaneko T., Sato S., Nakamura Y., Tabata S.;
RT "Complete structure of the chloroplast genome of a legume, Lotus
RT japonicus."
RL DNA Res. 7:323-330(2000).
CC -1- FUNCTION: REQUIRED DURING CYTOCHROME BIOGENESIS AT THE STEP OF
CC HEME ATTACHMENT (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CCMF/CYCK/CCL1/NRFE/CCSA FAMILY.
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DR EMBL; AP002983; BAB33244.1; -.
DR InterPro; IPR002541; Cytc_asm.
DR Pfam; PF01578; Cytc_asm; 1.
KW Cytochrome c-type biogenesis; Chloroplast.
SQ SEQUENCE 323 AA; 37185 MW; 5A034E3E2829FE35 CRC64;

Query Match 58.6%; Score 34; DB 1; Length 323;
Best Local Similarity 83.3%; Pred. No. 75;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSV 8
DB 315 HNYGSF 320

RESULT 15
ASTB_PSEAE
ID ASTB_PSEAE          STANDARD;          PRT;    448 AA.
AC O50175;
DT 15-DEC-1998 (Rel. 37, Created)
DT 16-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Succinylarginine dihydrolase (EC 3.5.1.15).
GN ASTB OR ARUB OR PA0899.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=98053840; PubMed=9393691;
RA Itoh Y.;
RT "Cloning and characterization of the aru genes encoding enzymes of
RT the catabolic arginine succinyltransferase pathway in Pseudomonas
RT aeruginosa."
RL J. Bacteriol. 179:7280-7290(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;

```

RT "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
RL opportunistic pathogen.";
CC Nature 406:959-964(2000).
CC -!- FUNCTION: CATALYZES THE HYDROLYSIS OF N(2)-SUCCINYLRARGININE INTO
CC N(2)-SUCCINYLRNITHINE, AMMONIA AND CO(2).
CC -!- PATHWAY: SECOND STEP IN ARGININE CATABOLISM BY THE ARGININE
CC SUCCINYLTRANSFERASE PATHWAY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF011922; AAC46013.1; -;
DR EMBL; AE004524; AAG04288.1; -;
DR Arginine metabolism; Hydrolase; Complete proteome.
KW SEQUENCE 448 AA; 48875 MW; 39F9F379CCC16196 CRC64;
SQ

Query Match 58.6%; Score 34; DB 1; Length 448;
Best Local Similarity 62.5%; Pred. No. 1e+02; 2; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 HNYGSYAY 10
||| :|
Db 16 HNYGGLSY 23

Search completed: November 18, 2002, 17:33:24
Job time : 3.45098 secs

GenCore version 5.1.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:01 : Search time 10.4412 Seconds
(without alignments)
197.341 Million cell updates/sec

Title: US-09-016-061-62
Perfect score: 58
Sequence: 1 ARHNGSVAY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 segs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database :
- 1: sp_archaea.*
 - 2: sp_bacteria.*
 - 3: sp_fungi.*
 - 4: sp_human.*
 - 5: sp_invertebrate.*
 - 6: sp_mammal.*
 - 7: sp_mhc.*
 - 8: sp_organelle.*
 - 9: sp_phage.*
 - 10: sp_plant.*
 - 11: sp_rodent.*
 - 12: sp_virus.*
 - 13: sp_vertebrate.*
 - 14: sp_unclassified.*
 - 15: sp_rvrius.*
 - 16: sp_bacteriap.*
 - 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	42	72.4	446	5	O62086	O62086 caenorhabdi
2	40	69.0	839	10	Q9LIE5	Q9LIE5 arabidopsis
3	39	67.2	91	10	Q94KW7	Q94KW7 brassica na
4	39	67.2	91	10	Q94KW6	Q94KW6 brassica ca
5	39	67.2	224	10	Q9FUZ3	Q9FUZ3 brassica ni
6	39	67.2	576	9	O64311	O64311 enterobacte
7	39	67.2	3115	5	O9QV01	O9QV01 drosophila
8	38	65.5	236	5	O18245	O18245 caenorhabdi
9	38	65.5	238	10	Q943R5	Q943R5 oryza sativ
10	38	65.5	271	10	Q9XEI2	Q9XEI2 nicotiana t
11	38	65.5	271	10	Q9XT29	Q9XT29 nicotiana t
12	38	65.5	428	10	P93843	P93843 nicotiana t
13	38	65.5	428	10	Q9LEB3	Q9LEB3 nicotiana t
14	38	65.5	482	10	O48955	O48955 nicotiana t
15	37	63.8	276	7	Q9GJN0	Q9GJN0 calman croc
16	37	63.8	289	16	O69838	O69838 streptomyce

17	37	63.8	338	5	O9GS14	Q9GS14 caenorhabdi
18	37	63.8	381	16	Q8RF69	Q8RF69 fusobacteri
19	37	63.8	420	13	Q91184	Q91184 oryzias lat
20	37	63.8	1144	2	Q50371	Q50371 mycoplasma
21	37	63.8	5317	5	Q8TA74	Q8TA74 hemimentrot
22	36	62.1	76	8	Q94ZM6	Q94ZM6 struthio ca
23	36	62.1	94	8	Q9T882	Q9T882 otus longic
24	36	62.1	166	2	Q9AET2	Q9AET2 pasteurella
25	36	62.1	254	17	Q8TPI2	Q8TPI2 methanosarc
26	36	62.1	301	4	Q96IM0	Q96IM0 homo sapien
27	36	62.1	301	11	Q92130	Q92130 mus musculu
28	36	62.1	349	5	O76436	O76436 caenorhabdi
29	36	62.1	349	5	O965U4	O965U4 caenorhabdi
30	36	62.1	420	4	O14979	O14979 homo sapien
31	36	62.1	593	5	Q8T5L2	Q8T5L2 anopheles g
32	36	62.1	626	5	O62017	O62017 caenorhabdi
33	36	62.1	1049	12	O83611	O83611 ectromelia
34	35	60.3	65	7	Q9BCZ6	Q9BCZ6 rattus norv
35	35	60.3	69	7	Q9BD01	Q9BD01 rattus norv
36	35	60.3	69	7	Q9BCZ9	Q9BCZ9 rattus norv
37	35	60.3	89	7	O19495	O19495 gallus gall
38	35	60.3	111	8	Q9MEJ5	Q9MEJ5 pronolagus
39	35	60.3	114	7	Q9TNU3	Q9TNU3 rattus norv
40	35	60.3	115	7	Q9TNU4	Q9TNU4 rattus norv
41	35	60.3	116	7	Q9TNU5	Q9TNU5 rattus norv
42	35	60.3	120	7	Q98183	Q98183 rattus norv
43	35	60.3	120	7	Q98186	Q98186 rattus norv
44	35	60.3	134	8	Q9G2W4	Q9G2W4 manis penta
45	35	60.3	135	7	Q9BCL8	Q9BCL8 rattus norv

ALIGNMENTS

RESULT 1
O62086 PRELIMINARY; PRT; 446 AA.
ID O62086
AC O62086;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE C3IH5.6 protein.
GN C3IH5.6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Kershaw J.K.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RL Science 282:2012-2018(1998).
DR EMBL; Z93778; CAB07846.1; -.
DR InterPro; IPR000379; Ser_estrs_site.
SQ SEQUENCE 446 AA; 50763 MW; 82AD969CDAD753DE CRC64;

Query Match 72.4%; Score 42; DB 5; Length 446;
Best Local Similarity 87.5%; Pred. No. 16;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHNYGSVA 9
| | | | |
Db 51 RHNYGSVA 58

RESULT 2
Q9LIE5

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ID Q9LIE5 PRELIMINARY; PRT; 839 AA.
AC Q9LIE5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Far-red impaired response protein, mutator-like transposase-like
DE protein, phytochrome A signaling protein-like.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=20363099; PubMed=10907853;
RA Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.
RT Sequence features of the regions of 4,251,695 bp covered by ninety P1,
RT TAC and BAC clones.";
RL DNA Res. 7:217-221(2000).
DR EMBL; AP001306; BAB03065.1; -.
DR InterPro; IPR004330; FARI.
DR InterPro; IPR001000; Glyco_hydro_10.
DR Pfam; PF03101; FARI; 1.
DR PROSITE; PS00591; GLYCOSYL_HYDROL_F10; UNKNOWN_1.
SQ SEQUENCE 839 AA; 95996 MW; CBBF60DF8B6797F8 CRC64;

Query Match 59.0%; Score 40; DB 10; Length 839;
Best Local Similarity 75.0%; Pred. No. 76;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNGSY 8
Db :|||||
Db 274 SRHNGSF 281

RESULT 3
Q94KW7 PRELIMINARY; PRT; 91 AA.
AC Q94KW7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE COL2-like protein (Fragment).
GN COL2-LIKE-BN-3.
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3708;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=CV. YUDAL;
RX Fourmann M., Froger N., Brunel D.;
RT "Amplified consensus gene markers: Tools designing for a genetic map
RT of Arabidopsis-known-function genes in Brassica.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF258300; AAK49092.1; -.
FT NON_TER 1
FT NON_TER 91
SQ SEQUENCE 91 AA; 10544 MW; 951CEBF31F36C093 CRC64;

Query Match 67.2%; Score 39; DB 10; Length 91;
Best Local Similarity 60.0%; Pred. No. 9;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARHNGSY 10
Db :|||||
Db 95 SHHNGHY 104

RESULT 6
O64311 PRELIMINARY; PRT; 576 AA.
ID O64311

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Db 13 SHHNGHY 22

RESULT 4
Q94KW6 PRELIMINARY; PRT; 91 AA.
AC Q94KW6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE COL2-like protein (Fragment).
GN COL2-LIKE-BR-2.
OS Brassica campestris (Field mustard).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3711;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=CV. R500;
RX Fourmann M., Froger N., Brunel D.;
RT "Amplified consensus gene markers: Tools designing for a genetic map
RT of Arabidopsis-known-function genes in Brassica.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF258301; AAK49093.1; -.
FT NON_TER 1
FT NON_TER 91
SQ SEQUENCE 91 AA; 10505 MW; 956BEBFF82C78CE CRC64;

Query Match 67.2%; Score 39; DB 10; Length 91;
Best Local Similarity 60.0%; Pred. No. 9.6;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARHNGSY 10
Db :|||||
Db 13 SHHNGHY 22

RESULT 5
Q9FUZ3 PRELIMINARY; PRT; 224 AA.
AC Q9FUZ3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE COL2-like protein.
OS Brassica nigra (black mustard).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3710;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=20473001; PubMed=11018156;
RA Lagercrantz U., Axelsson T.;
RT "Rapid evolution of the family of CONSTANS LIKE genes in plants.";
RL Mol. Biol. Evol. 17:1499-1507(2000).
DR EMBL; AF269129; AAG27548.1; -.
SQ SEQUENCE 224 AA; 25552 MW; 718E52925FDC0CFD CRC64;

Query Match 67.2%; Score 39; DB 10; Length 224;
Best Local Similarity 60.0%; Pred. No. 26;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARHNGSY 10
Db :|||||
Db 95 SHHNGHY 104

RESULT 6
O64311 PRELIMINARY; PRT; 576 AA.
ID O64311

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AC 064311;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Replicase.
OS Enterobacteria phage NL95.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC serungroup IV.
OX NCBI_TaxID=75725;
ON [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=95239761; PubMed=7723040;
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RT "Secondary structure model for the last two domains of single-stranded
RT RNA phage Q beta.";
RL J. Mol. Biol. 247:903-917(1995).
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=96190948; PubMed=8609616;
RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
RT "Secondary structure model for the first three domains of Q beta RNA.
RT Control of A-protein synthesis.";
RL J. Mol. Biol. 256:8-19(1996).
RN [3]
RN SEQUENCE FROM N.A.
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF059243; AAC14705.1; -
DR InterPro; IPR005093; RNAtrep_beta.
DR Pfam; PF03431; RNA_replicase_B; 1.
SQ SEQUENCE 576 AA; 65012 MW; 6075160795D366FD CRC64;

Query Match 67.2%; Score 39; DB 9; Length 576;
Best Local Similarity 66.7%; Pred. No. 76;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSVAY 10
DB 503 RHEFGSTLY 511

RESULT 7
QYQV1 PRELIMINARY; PRT; 3115 AA.
ID QYQV1
AC QYQV1
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE CG3921 protein.
GN CG3921.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
ON [1]
RN SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnikier S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandal M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Baldwin D.,
RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busan M.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo S., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

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RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J.J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
CC 1- SIMILARITY: CONTAINS 1 CUB DOMAIN.
DR EMBL; AE003578; AAF51061.1; -
DR FlyBase; FBgn0031571; CG3921.
DR InterPro; IPR000859; CUB_domain.
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR001190; Strc_receptor.
DR Pfam; PF00059; lectin_c; 1.
DR Pfam; PF00530; SRCR; 3.
DR PRINTS; PR00258; SPERACTRCPTR.
DR SMART; SM00034; CLECT; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00202; SR; 3.
DR PROSITE; PS50287; SRCR_2; 3.
SQ SEQUENCE 3115 AA; 349451 MW; A17EA222A4718112 CRC64;

Query Match 67.2%; Score 39; DB 5; Length 3115;
Best Local Similarity 87.5%; Pred. No. 5e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSY 8
DB 2550 ARHNYWSY 2557

RESULT 8
ID 018245
AC 018245 PRELIMINARY; PRT; 236 AA.
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Y57G11C.21 protein.
GN Y57G11C.21.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
ON [1]
RN SEQUENCE FROM N.A.
RA McMurray A.A.;
EL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; Z99281; CAB16522.1; -

```

SQ SEQUENCE 236 AA; 26579 MW; 8E92144E065E7D30 CRC64;

Query Match 65.5%; Score 38; DB 5; Length 236;
Best Local Similarity 60.0%; Pred. No. 42;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNGSYAY 10

Db 118 AVHFNYSYAY 127

RESULT 9

Q943R5 ID Q943R5 PRELIMINARY; PRT; 238 AA.
AC Q943R5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Putative sterol-C5(6)-desaturase.
GN OSJNBA0083M16.22.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, BAC
RT clone:OSJNBA0083M16.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AP003214; BAB64621.1; -.
DR InterPro: IPR001541; Sterol_desat.
DR Pfam: PF01598; Sterol_desat; 1.
SQ SEQUENCE 238 AA; 28320 MW; 6D4BCE1D51EE0964 CRC64;

Query Match 65.5%; Score 38; DB 10; Length 238;
Best Local Similarity 85.7%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNGSY 8

Db 211 RHNGHY 217

RESULT 10

Q9XE12 ID Q9XE12 PRELIMINARY; PRT; 271 AA.
AC Q9XE12;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Sterol-C5(6)-desaturase homolog.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. XANTHI SH6; TISSUE=LEAF;
RX MEDLINE=99273992; PubMed=10344195;
RA Husselstein T., Schaller H., Gachotte D., Benveniste P.;
RT "Delta7-sterol-C5-desaturase: molecular characterization and
RT functional expression of wild-type and mutant alleles.";
RL Plant Mol. Biol. 39:891-906(1993).
DR EMBL: AF099969; AAD20458.1; -.
DR InterPro: IPR001541; Sterol_desat.
DR Pfam: PF01598; Sterol_desat; 1.
SQ SEQUENCE 271 AA; 32036 MW; 1E705A0B69C320D4 CRC64;

Query Match 65.5%; Score 38; DB 10; Length 271;

Best Local Similarity 85.7%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNGSY 8

Db 243 RHNGHY 249

RESULT 11

Q92T29 ID Q92T29 PRELIMINARY; PRT; 271 AA.
AC Q92T29;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Sterol-C5(6)-desaturase.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. XANTHI SH6; TISSUE=CALLI DERIVED;
RX MEDLINE=99273992; PubMed=10344195;
RA Husselstein T., Schaller H., Gachotte D., Benveniste P.;
RT "Delta7-sterol-C5-desaturase: molecular characterization and
RT functional expression of wild-type and mutant alleles.";
RL Plant Mol. Biol. 39:891-906(1993).
DR EMBL: AF081794; AAD04034.1; -.
DR InterPro: IPR001541; Sterol_desat.
DR Pfam: PF01598; Sterol_desat; 1.
SQ SEQUENCE 271 AA; 31842 MW; 361520EAAAB56D86F CRC64;

Query Match 65.5%; Score 38; DB 10; Length 271;
Best Local Similarity 85.7%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNGSY 8

Db 243 RHNGHY 249

RESULT 12

P93843 ID P93843 PRELIMINARY; PRT; 428 AA.
AC P93843;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE DNA binding protein ACPF.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=STEM;
RX MEDLINE=98009965; PubMed=9349252;
RA Sequin A., Laible G., Leyva A., Dixon R.A., Lamb C.J.;
RT "Characterization of a gene encoding a DNA-binding protein that
RT interacts in vitro with vascular specific cis elements of the
RT phenylalanine ammonia-lyase promoter.";
RL Plant Mol. Biol. 35:281-291(1997).
DR EMBL: U90212; AAC49850.1; -.
DR HSP; P11940; 1CVJ.
DR InterPro: IPR000504; RNA_rec_mot.
DR Pfam: PF00076; rrm; 3.
DR SMART; SMO0360; RRM; 3.
DR PROSITE; PS50102; RRM; 3.
DR PROSITE; PS00030; RRM_RNP_1; 1.
SQ SEQUENCE 428 AA; 46981 MW; 0E7DB8A517705E5B CRC64;

Query Match 65.5%; Score 38; DB 10; Length 428;
 Best Local Similarity 66.7%; Pred. No. 83;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 RHNYGSYAY 10
 I I I I I
 Db 387 RQNYGGYGY 395

RESULT 13

Q9LEB3 PRELIMINARY; PRT; 428 AA.
 AC Q9LEB3;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE RNA binding protein 47.
 GN RBP47.
 OS Nicotiana plumbaginifolia (Leadwort-leaved tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
 OX NCBI_TaxID=4092;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20555308; PubMed=11105760;
 RA Lorkovic Z.J., Wiecezorek Kirk D.A., Klahre U., Hemmings-Mieszczak M.,
 RA Filipowicz W.;
 RT "RBP45 and RBP47, two oligouridylylate-specific hnRNP-like proteins
 interacting with poly(A)+ RNA in nuclei of plant cells.";
 RL RNA 6:1610-1624(2000).
 DR EMBL: AJ292768; CAC01238.1; -.
 DR HSSP: P11940; 1CVJ.
 DR InterPro: IPR000504; RNA_rec_mot.
 DR Pfam: PF00076; rrm; 3.
 DR SMART: SM00360; RRM; 3.
 DR PROSITE: PS0102; RRM; 3.
 DR PROSITE; PS00030; RRM_RNP_1; UNKNOWN_1.
 SQ SEQUENCE 428 AA; 47374 MW; E5579F481C40523D CRC64;

Query Match 65.5%; Score 38; DB 10; Length 428;
 Best Local Similarity 66.7%; Pred. No. 83;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 RHNYGSYAY 10
 I I I I I
 Db 388 RQNYGGYGY 396

RESULT 14

O48955 PRELIMINARY; PRT; 482 AA.
 AC O48955;
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Putative RNA binding protein (Fragment).
 GN ORBP-1.
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
 OX NCBI_TaxID=4097;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Deslandes L., Manevski A., Lescure B., Marco Y., Tremousaygue D.;
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF029351; AAB92518.1; -.
 DR HSSP: P11940; 1CVJ.
 DR InterPro: IPR000504; RNA_rec_mot.
 DR Pfam: PF00076; rrm; 3.
 DR SMART: SM00360; RRM; 3.

DR PROSITE; PS0102; RRM; 3.
 DR PROSITE; PS00030; RRM_RNP_1; 1.
 FT NON_TER 1
 SQ SEQUENCE 482 AA; 53582 MW; B7BFB3AFCFCA98EE CRC64;

Query Match 65.5%; Score 38; DB 10; Length 482;
 Best Local Similarity 66.7%; Pred. No. 94;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 RHNYGSYAY 10
 I I I I I
 Db 442 RQNYGGYGY 450

RESULT 15

Q9GJN0 PRELIMINARY; PRT; 276 AA.
 AC Q9GJN0;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE MHC class II beta chain.
 GN H2IIBETA.
 OS Calman crocodilus (Spectacled calman) (Calman sclerops).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Crocodylidae; Alligatorinae; Calman.
 OX NCBI_TaxID=8499;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Voldby J., Vitved L., Due M., Gronlund J., Holmskov U., Teisner B.,
 RA Salomonsen J., Brusgaard K., Skjoldt K.;
 RT "Cloning, sequence and genomic structure of MHC class II antigens from
 the spectacled calman, Calman crocodilus.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF256651; AAF99283.1; -.
 DR HSSP: P13760; 2SEB.
 DR InterPro: IPR003597; Ig_cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR000353; MHC_II_beta.
 DR Pfam: PF00047; Ig; 1.
 DR Pfam: PF00969; MHC_II_beta; 1.
 DR PRODOM: PD000328; MHC_II_beta; 1.
 DR SMART: SM00407; IG_c1; 1.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 KW Glycoprotein; MHC II; Transmembrane.
 SQ SEQUENCE 276 AA; 30366 MW; EA8A4684986AEA6A CRC64;

Query Match 63.8%; Score 37; DB 7; Length 276;
 Best Local Similarity 75.0%; Pred. No. 76;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSYA 9
 I I I I I
 Db 108 RQNYGVFA 115

Search completed: November 18, 2002, 17:40:44
 Job time : 12.4912 secs

GenCore version 5.1.3
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OM protein.- protein search, using sw model

Run on: November 18, 2002, 17:21:57 ; Search time 13.8235 Seconds
(without alignments)
96.394 Million cell updates/sec

Title: US-09-016-061-62
Perfect score: 58
Sequence: 1 ARHNYGSYAY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	58	100.0	10	AAW76021	LM609 grafted anti
2	58	100.0	10	AAW76021	Mutant VH CDR3 pep
3	54	93.1	10	AAW76010	LM609 grafted anti
4	54	93.1	10	AAW76010	LM609 VH CDR3 pep
5	54	93.1	117	AAW76001	Vitaxin antibody h
6	54	93.1	117	AAW76003	LM609 antibody hea
7	54	93.1	117	AAW76003	Murine monoclonal
8	54	93.1	117	AAW76003	Humanised LM609 an
9	54	93.1	117	AAW76003	A heavy chain vari
10	54	93.1	117	AAW76003	A heavy chain vari

11	54	93.1	117	22	AAW76021	Vitaxin heavy chain
12	54	93.1	117	22	AAW76021	Antibody LM609 hea
13	54	93.1	118	20	AAW76038	Humanised LM609 an
14	54	93.1	118	20	AAW76038	Humanised LM609 an
15	54	93.1	118	20	AAW76038	Humanised LM609 an
16	54	93.1	118	20	AAW76038	Humanised LM609 an
17	54	93.1	130	20	AAW76039	Murine monoclonal
18	49	84.5	10	19	AAW76020	LM609 grafted anti
19	49	84.5	10	22	AAW76020	Mutant VH CDR3 pep
20	48	82.8	10	19	AAW76022	LM609 grafted anti
21	48	82.8	10	19	AAW76023	LM609 grafted anti
22	48	82.8	10	22	AAW76023	Mutant VH CDR3 pep
23	48	82.8	10	22	AAW76024	Mutant VH CDR3 pep
24	47	81.0	10	19	AAW76024	LM609 grafted anti
25	47	81.0	10	19	AAW76025	LM609 grafted anti
26	47	81.0	10	19	AAW76026	LM609 grafted anti
27	47	81.0	10	19	AAW76027	LM609 grafted anti
28	47	81.0	10	19	AAW76028	LM609 grafted anti
29	47	81.0	10	19	AAW76029	LM609 grafted anti
30	47	81.0	10	19	AAW76030	LM609 grafted anti
31	47	81.0	10	22	AAW76030	Mutant VH CDR3 pep
32	47	81.0	10	22	AAW76031	Mutant VH CDR3 pep
33	47	81.0	10	22	AAW76032	Mutant VH CDR3 pep
34	47	81.0	10	22	AAW76033	Mutant VH CDR3 pep
35	47	81.0	10	22	AAW76034	Mutant VH CDR3 pep
36	47	81.0	10	22	AAW76035	Mutant VH CDR3 pep
37	47	81.0	10	22	AAW76036	Mutant VH CDR3 pep
38	46	79.3	110	20	AAW84099	Murine vitronectin alpha
39	46	79.3	117	20	AAW84093	Vitronectin alpha
40	46	79.3	117	20	AAW84097	Humanised anti-alp
41	45	77.6	8	20	AAW08371	Murine monoclonal
42	43	74.1	10	19	AAW76039	LM609 grafted anti
43	43	74.1	10	19	AAW76040	LM609 grafted anti
44	43	74.1	10	22	AAW76040	Multiple mutant VH
45	43	74.1	10	22	AAW76040	Multiple mutant VH

ALIGNMENTS

RESULT 1
AAW76021
ID AAW76021 standard; Protein; 10 AA.
XX
AC AAW76021;
XX
DT 02-NOV-1998 (first entry)
XX
DE LM609 grafted antibody V-H region CDR3 protein fragment #3.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
XX LM609; inhibitor; integrin-mediated signal transduction; treatment;
XX diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
XX neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
XX macular degeneration; osteoporosis; primer; V-H region; CDR;
XX complementarity determining region.

OS Mus sp.

PN WO9833919-A2.

XX 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

PI Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

DR N-PSDB; AAW49858.

XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
XX Claim 62; Page 41; 129pp; English.
PS
XX AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
CC antibodies contain non-murine framework regions so are suitable for use
CC in humans. Enhanced types of LM609 have affinity more than 90 times
CC greater than that of parent the parent antibody.
XX
XX Sequence 10 AA;
SQ
Query Match 100.0%; Score 58; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0026;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ARHNYGSYAY 10
DB 1 ARHNYGSYAY 10
|||||
RESULT 2
AAB61379
ID AAB61379 standard; peptide; 10 AA.
XX
AC AAB61379;
XX
XX 03-APR-2001 (first entry)
DT
XX
DE Mutant VH CDR3 peptide #2.
XX
XX LM609; grafted antibody; alphaVbeta_3 integrin; angiogenesis;
KW inflammatory; cancer; retina; restenosis; osteoporosis.
KW
XX Unidentified.
OS
XX WO200078815-A1.
PN
XX 28-DEC-2000.
PD
XX 23-JUN-2000; 2000WO-US17454.
XX
XX 24-JUN-1999; 99US-0339922.
PR
XX (MOLE-) APPLIED MOLECULAR EVOLUTION.
PA
XX Huse WD, Wu H;
PI
XX WPI; 2001-050110/06.
DR
XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
XX to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
PT osteoporosis -
XX
XX Disclosure; Page 41; 132pp; English.
PS
XX The present invention relates to enhanced LM609 grafted antibodies
CC exhibiting selective binding affinity to alphaVbeta_3 integrin or
CC their functional fragments. The antibodies or their functional
CC fragments can be used in the diagnosis and treatment of
CC alphaVbeta_3-mediated diseases such as angiogenesis, inflammatory

CC diseases (such as psoriasis and chronic articular rheumatism),
CC disorders associated with inappropriate or inopportune invasion of
CC vessels (such as diabetic retinopathy, neovascular glaucoma and
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
CC diseases (such as macular degeneration), restenosis and
CC osteoporosis.
XX
XX Sequence 10 AA;
SQ
Query Match 100.0%; Score 58; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0026;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ARHNYGSYAY 10
DB 1 ARHNYGSYAY 10
|||||
RESULT 3
AAW76010
ID AAW76010 standard; Protein; 10 AA.
XX
AC AAW76010;
XX
XX 02-NOV-1998 (first entry)
DT
XX
DE LM609 grafted antibody V-H region CDR3 protein fragment #1.
XX
XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
XX
XX Mus sp.
XX
XX WO9833919-A2.
PN
XX 06-AUG-1998.
PD
XX 30-JAN-1998; 98WO-US01826.
PF
XX 30-JAN-1997; 97US-0791391.
PR
XX (IXSY-) IXSYS INC.
PA
XX Glaser SM, Huse WD;
PI
XX WPI; 1998-437472/37.
DR
XX N-PSDB; AAV49847.
XX
XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
XX Disclosure; Page 40; 129pp; English.
PS
XX
XX AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
CC antibodies contain non-murine framework regions so are suitable for use
CC in humans. Enhanced types of LM609 have affinity more than 90 times
CC greater than that of parent the parent antibody.
XX
XX Sequence 10 AA;
SQ

Query Match 93.1%; Score 54; DB 19; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.012; Mismatches 1; Conservative 9; Gaps 0;

QY 1 ARHNYGSYAY 10
 |||||:|
 Db 1 ARHNYGSFAY 10

RESULT 4

AAB61368
 ID AAB61368 standard; peptide; 10 AA.

XX
 AC AAB61368;

DT 03-APR-2001 (first entry)

XX LM609 VH CDR3 peptide.

XX LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis.

XX Unidentified.

OS WO200078815-A1.

PN 28-DEC-2000.

XX 23-JUN-2000; 2000WO-US17454.

PF 24-JUN-1999; 99US-0339922.

PR (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX Huse WD, Wu H;

PI WPI; 2001-050110/06.

XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 osteoporosis -

PS Disclosure; Page 39; 132pp; English.

XX The present invention relates to enhanced LM609 grafted antibodies
 exhibiting selective binding affinity to alphaVbeta_3 integrin or
 their functional fragments. The antibodies or their functional
 fragments can be used in the diagnosis and treatment of
 CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.

XX Sequence 10 AA;

Query Match 93.1%; Score 54; DB 22; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.012; Mismatches 9; Conservative 1; Gaps 0;

QY 1 ARHNYGSYAY 10
 |||||:|
 Db 1 ARHNYGSFAY 10

RESULT 5

AAW76001

ID AAW76001 standard; Protein; 117 AA.

XX

AC AAW76001;
 DT 02-NOV-1998 (first entry)
 DE Vitaxin antibody heavy chain variable region protein fragment.

XX Vitaxin; antibody; variable region; heavy chain; light chain; Integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.

OS Mus sp.

PN WO9833919-A2.

XX 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

PA (IXSY-) IXSYS INC.

PI Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

DR N-PSDB; AAV49820.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 integrin - and related grafted antibodies based on murine monoclonal
 LM609, also related nucleic acid, used to treat, prevent or diagnose
 angiogenesis or restenosis

PS Claim 1; Fig 1a; 129pp; English.

XX This sequence represents a fragment of the vitaxin antibody variable
 heavy chain region. Vitaxin and the antibody LM609 bind selectively to
 CC integrin alphavbeta3 and can be used to inhibit binding of alphavbeta3
 CC to a ligand and thus block integrin-mediated signal transduction. This is
 CC useful in the treatment, prevention and diagnosis of alphavbeta3-mediated
 CC disease, specifically angiogenesis and restenosis (but also e.g.
 CC (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,
 CC cancer, psoriasis, rheumatoid arthritis, macular degeneration,
 CC osteoporosis etc.). The antibodies contain non-murine framework regions
 CC so are suitable for use in humans. Enhanced types of LM609 have affinity
 CC more than 90 times greater than that of parent the parent antibody.

XX Sequence 117 AA;

Query Match 93.1%; Score 54; DB 19; Length 117;
 Best Local Similarity 90.0%; Pred. No. 0.15; Mismatches 9; Conservative 1; Gaps 0;

QY 1 ARHNYGSYAY 10
 |||||:|
 Db 97 ARHNYGSFAY 106

RESULT 6

AAW76003

ID AAW76003 standard; Protein; 117 AA.

XX AAW76003;

XX 02-NOV-1998 (first entry)

DE LM609 antibody heavy chain variable region protein fragment.

XX Vitaxin; antibody; variable region; heavy chain; light chain; Integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;

KW macular degeneration; osteoporosis.

OS Mus sp.

XX WO9833919-A2.

XX 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

XX Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

XX N-PSDB; AAV49822.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3 integrin - and related grafted antibodies based on murine monoclonal LM609, also related nucleic acid, used to treat, prevent or diagnose angiogenesis or restenosis

PS Claim 43; Fig 2a; 129pp; English.

XX This sequence represents the LM609 antibody variable heavy chain region. LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3 and can be used to inhibit binding of alphavbeta3 to a ligand and thus block integrin-mediated signal transduction. This is useful in the treatment, prevention and diagnosis of alphavbeta3-mediated disease, specifically angiogenesis and restenosis (but also e.g. (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis etc.). The antibodies contain non-murine framework regions so are suitable for use in humans. Enhanced types of LM609 have affinity more than 90 times greater than that of parent the parent antibody.

XX Sequence 117 AA;

Query Match 93.1%; Score 54; DB 19; Length 117;

Best Local Similarity 90.0%; Pred. No. 0.15;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSYAY 10

Db 97 ARHNYGSFAY 106

RESULT 7

AAV06381

ID AAY06381 standard; Protein; 117 AA.

XX AC AAY06381;

XX 06-SEP-1999 (first entry)

XX Murine monoclonal antibody LM609 VH region.

XX Humanised antibody; antibody humanisation; antibody engineering; LM609; monoclonal antibody; complementarity determining region; CDR grafting; mouse; human; integrin; apoptosis; angiogenesis; cancer; therapy; diagnosis.

XX Mus musculus.

XX WO9929888-A1.

XX 17-JUN-1999.

XX 04-DEC-1998; 98WO-US25828.

XX 05-DEC-1997; 97US-0986016.

PR

XX (SCRI) SCRIPPS RES INST.

XX Barbas CF, Rader C;

XX WPI; 1999-394979/33.

XX Production of humanized mouse monoclonal antibodies

XX Disclosure; Page 52-53; 55pp; English.

XX This sequence represents the heavy chain variable region of murine monoclonal antibody LM609. LM609 is directed to integrin alpha-v beta-3. It selectively promotes apoptosis of vascular cells that have been stimulated to undergo angiogenesis, making it a tool for cancer diagnosis and therapy. The invention provides humanised antibodies, especially humanised LM609. In such humanized antibodies, a light chain CDR from a mouse antibody such as LM609 is grafted onto a human light chain, and a heavy chain CDR from a mouse antibody is grafted onto a human antibody heavy chain to produce a library from which a humanised murine antibody having the desired specificity is selected. By preserving the original CDR sequences such as the HCDR3 and LCDR3 sequences of LM609 (see AAY06371-72), the humanisation strategy ensures epitope conservation.

XX Sequence 117 AA;

Query Match 93.1%; Score 54; DB 20; Length 117;

Best Local Similarity 90.0%; Pred. No. 0.15;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSYAY 10

Db 97 ARHNYGSFAY 106

RESULT 8

AAV06387

ID AAY06387 standard; Protein; 117 AA.

XX AC AAY06387;

XX 06-SEP-1999 (first entry)

XX Humanised LM609 antibody VH domain.

XX Humanised antibody; antibody humanisation; antibody engineering; LM609; monoclonal antibody; complementarity determining region; CDR grafting; mouse; human; integrin; apoptosis; angiogenesis; cancer; therapy; diagnosis.

XX Homo sapiens.

XX Synthetic.

XX Key Location/Qualifiers

XX Peptide 1..2 /note= "vector-encoded residues"

XX Region 31..35 /note= "CDR1"

XX Region 50..66 /note= "CDR2"

XX Region 107..117 /note= "CDR3"

XX WO9929888-A1.

XX 17-JUN-1999.

XX 04-DEC-1998; 98WO-US25828.

XX 05-DEC-1997; 97US-0986016.

XX (SCRI) SCRIPPS RES INST.

XX Barbas CF, Rader C;
 XX WPI; 1999-394979/33.
 XX Production of humanized mouse monoclonal antibodies
 XX Disclosure; Page 52; 55pp; English.
 XX This sequence represents the heavy chain variable region of a
 CC humanised LM609 antibody. LM609 is directed to human integrin
 CC alpha-v beta-3. It selectively promotes apoptosis of vascular
 CC cells that have been stimulated to undergo angiogenesis, making it
 CC a tool for cancer diagnosis and therapy. The invention provides
 CC humanised antibodies, especially humanised LM609. In such humanized
 CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
 CC grafted onto a human light chain, and a heavy chain CDR from a mouse
 CC antibody is grafted onto a human antibody heavy chain to produce
 CC libraries from which a humanised murine antibody having the desired
 CC specificity is selected. By preserving the original CDR sequences
 CC such as the HCDR3 and LCDR3 sequences of LM609 (see AA06371-72), the
 CC humanisation strategy ensures epitope conservation.
 XX Sequence 117 AA;
 SQ Query Match 93.1%; Score 54; DB 20; Length 117;
 Best Local Similarity 90.0%; Pred. No. 0.15;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSYAY 10
 DB 97 ARHNYGSFAY 106
 |||||:|

RESULT 9
 AAG63587
 ID AAG63587 standard; Protein; 117 AA.
 XX AC AAG63587;
 XX DT 15-OCT-2001 (first entry)
 XX DE A heavy chain variable region of LM609 grafted antibody.
 XX KW Grafted antibody; LM609; integrin; alphavbeta3; inflammatory disorder;
 KW chronic articular rheumatism; psoriasis; diabetic retinopathy;
 KW neovascular glaucoma; capillary proliferation; atherosclerotic plaque;
 KW cancer.
 XX OS Synthetic.
 XX Mus sp.
 XX PN US2001011125-A1.
 XX PD 02-AUG-2001.
 XX PF 30-JAN-1997; 97US-0790540.
 XX PR 30-JAN-1997; 97US-0790540.
 XX PA (HUSE/) HUSE W D.
 XX PI Huse WD;
 XX WPI; 2001-496171/54.
 XX N-PSDB; AAH74623.
 XX New LM609 grafted antibody exhibiting selective binding affinity to
 PT alphavbeta3, comprising at least one LM609 grafted heavy and light
 PT chain polypeptide, useful for diagnosing and treating e.g. inflammatory
 PT disorders or cancer -
 XX Claim 1; Fig 1A; 25pp; English.

XX The present sequence represents the heavy chain variable region of the
 CC grafted monoclonal antibody LM609. LM609 is a murine antibody which
 CC specifically recognises the integrin alphavbeta3, and inhibits its
 CC functional activity. The LM609 grafted antibody has the
 CC complementarity determining regions (CDRs) substituted into a non-murine
 CC framework. Nucleic acids encoding LM609 grafted heavy and light chain
 CC polypeptides and fragments are useful in diagnostic and therapeutic
 CC purposes, such as in the production of LM609 grafted antibodies and
 CC fragments having binding specificity and inhibitory activity against
 CC the integrin alphavbeta3. The antibody can be used for the diagnosis
 CC or treatment of alphavbeta3-mediated diseases (e.g. inflammatory
 CC disorders, chronic articular rheumatism, psoriasis, disorders
 CC associated with inappropriate or inopportune invasion of vessels such
 CC as diabetic retinopathy, neovascular glaucoma and capillary
 CC proliferation in atherosclerotic plaques, or cancers), and to inhibit
 CC binding activity of alphavbeta3 that are necessary for progression of
 CC an alphavbeta3-mediated disease.
 XX Sequence 117 AA;
 SQ Query Match 93.1%; Score 54; DB 22; Length 117;
 Best Local Similarity 90.0%; Pred. No. 0.15;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSYAY 10
 DB 97 ARHNYGSFAY 106
 |||||:|

RESULT 10
 AAG63589
 ID AAG63589 standard; Protein; 117 AA.
 XX AC AAG63589;
 XX DT 15-OCT-2001 (first entry)
 XX DE A heavy chain variable region of LM609 antibody.
 XX KW Grafted antibody; LM609; integrin; alphavbeta3; inflammatory disorder;
 KW chronic articular rheumatism; psoriasis; diabetic retinopathy;
 KW neovascular glaucoma; capillary proliferation; atherosclerotic plaque;
 KW cancer.
 XX OS Mus sp.
 XX PN US2001011125-A1.
 XX PD 02-AUG-2001.
 XX PF 30-JAN-1997; 97US-0790540.
 XX PR 30-JAN-1997; 97US-0790540.
 XX PA (HUSE/) HUSE W D.
 XX PI Huse WD;
 XX WPI; 2001-496171/54.
 XX N-PSDB; AAH74625.
 XX New LM609 grafted antibody exhibiting selective binding affinity to
 PT alphavbeta3, comprising at least one LM609 grafted heavy and light
 PT chain polypeptide, useful for diagnosing and treating e.g. inflammatory
 PT disorders or cancer -
 XX Disclosure; Fig 2A; 25pp; English.
 XX The present sequence represents the heavy chain variable region of the
 CC monoclonal antibody LM609. LM609 is a murine antibody which specifically
 CC recognises the integrin alphavbeta3, and inhibits its functional activity.
 CC The specification describes a LM609 grafted antibody which has the

CC complementarity determining regions (CDRs) substituted into a non-murine
 CC framework. Nucleic acids encoding LM609 grafted heavy and light chain
 CC polypeptides and fragments are useful in diagnostic and therapeutic
 CC purposes, such as in the production of LM609 grafted antibodies and
 CC fragments having binding specificity and inhibitory activity against
 CC the integrin alphavbeta3. The antibody can be used for the diagnosis
 CC or treatment of alphavbeta3-mediated diseases (e.g. inflammatory
 CC disorders, chronic articular rheumatism, psoriasis, disorders
 CC associated with inappropriate or inopportune invasion of vessels such
 CC as diabetic retinopathy, neovascular glaucoma and capillary
 CC proliferation in atherosclerotic plaques, or cancers), and to inhibit
 CC binding activity of alphavbeta3 that are necessary for progression of
 CC an alphavbeta3-mediated disease.

XX
 XX
 SQ Sequence 117 AA;

Query Match 93.1%; Score 54; DB 22; Length 117;
 Best Local Similarity 90.0%; Pred. No. 0.15;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSYAY 10
 |||||:|
 Db 97 ARHNYGSFAY 106

RESULT 11
 AAB61359
 ID AAB61359 standard; protein; 117 AA.

XX
 AC AAB61359;

XX
 DT 03-APR-2001 (first entry)

XX
 DE Vitaxin heavy chain variable region protein.

XX LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis.
 XX
 OS Unidentified.

XX
 PN WO200078815-A1.
 XX
 PD 28-DEC-2000.

XX
 PF 23-JUN-2000; 2000WO-US17454.

XX
 PR 24-JUN-1999; 99US-0339922.

XX
 PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
 XX
 PI Huse WD, Wu H;

XX
 DR WPI; 2001-050110/06.

XX
 PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -

XX
 PS Disclosure; Fig 1; 132pp; English.

XX
 CC The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphavbeta_3 integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.

XX

SQ Sequence 117 AA;

Query Match 93.1%; Score 54; DB 22; Length 117;
 Best Local Similarity 90.0%; Pred. No. 0.15;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSYAY 10
 |||||:|
 Db 97 ARHNYGSFAY 106

RESULT 12
 AAB61361
 ID AAB61361 standard; protein; 117 AA.

XX
 AC AAB61361;

XX
 DT 03-APR-2001 (first entry)

XX
 DE Antibody LM609 heavy chain variable region protein.

XX LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis.
 XX
 OS Unidentified.

XX
 PN WO200078815-A1.
 XX
 PD 28-DEC-2000.

XX
 PF 23-JUN-2000; 2000WO-US17454.

XX
 PR 24-JUN-1999; 99US-0339922.

XX
 PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
 XX
 PI Huse WD, Wu H;

XX
 DR WPI; 2001-050110/06.

XX
 PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -

XX
 PS Disclosure; Fig 2; 132pp; English.

XX
 CC The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphavbeta_3 integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.

SQ Sequence 117 AA;

Query Match 93.1%; Score 54; DB 22; Length 117;
 Best Local Similarity 90.0%; Pred. No. 0.15;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSYAY 10
 |||||:|
 Db 97 ARHNYGSFAY 106

RESULT 13
 AAY06384
 ID AAY06384 standard; Protein; 118 AA.

```

XX AC AAY06384;
XX DT
XX DE
XX DE 06-SEP-1999 (first entry)
XX DE Humanised LM609 antibody VH domain.
XX KW Humanised antibody; antibody humanisation; antibody engineering;
XX KW LM609; monoclonal antibody; complementarity determining region;
XX KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
XX KW cancer; therapy; diagnosis.
XX OS Homo sapiens.
XX OS Synthetic.
XX FH
XX FT Key Location/Qualifiers
XX FT Peptide 1..2
XX FT /note= "vector-encoded residues"
XX FT Region 31..37
XX FT /note= "CDR1"
XX FT Region 52..67
XX FT /note= "CDR2"
XX FT Region 100..107
XX FT /note= "CDR3"
XX PN WO9929888-A1.
XX PD 17-JUN-1999.
XX PF 04-DEC-1998; 98WO-US25828.
XX PR 05-DEC-1997; 97US-0986016.
XX PA (SCRI ) SCRIPPS RES INST.
XX PI Barbas CF, Rader C;
XX PI WPI; 1999-394979/33.
XX PT Production of humanized mouse monoclonal antibodies
XX PS Disclosure; Page 51; 55pp; English.
XX CC This sequence represents the heavy chain variable region of a
XX CC humanised LM609 antibody. LM609 is directed to human integrin
XX CC alpha-v beta-3. It selectively promotes apoptosis of vascular
XX CC cells that have been stimulated to undergo angiogenesis, making it
XX CC a tool for cancer diagnosis and therapy. The invention provides
XX CC humanised antibodies, especially humanised LM609. In such humanized
XX CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
XX CC grafted onto a human light chain, and a heavy chain CDR from a mouse
XX CC antibody is grafted onto a human antibody heavy chain to produce
XX CC libraries from which a humanised murine antibody having the desired
XX CC specificity is selected. By preserving the original CDR sequences
XX CC such as the HCDR3 and LCDR3 sequences of LM609 (see AAY06371-72), the
XX CC humanisation strategy ensures epitope conservation.
XX SQ Sequence 118 AA;
XX Query Match 93.18; Score 54; DB 20; Length 118;
XX Best Local Similarity 90.0%; Pred. No. 0.16;
XX Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 ARHNYGSYAY 10
XX | | | | | | | |
XX Db 98 ARHNYGSFAY 107
XX RESULT 14
XX AAY06385
XX ID AAY06385 standard; Protein; 118 AA.
XX AC AAY06385;

```

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XX DT
XX DE 06-SEP-1999 (first entry)
XX DE Humanised LM609 antibody VH domain.
XX KW Humanised antibody; antibody humanisation; antibody engineering;
XX KW LM609; monoclonal antibody; complementarity determining region;
XX KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
XX KW cancer; therapy; diagnosis.
XX OS Homo sapiens.
XX OS Synthetic.
XX FH
XX FT Key Location/Qualifiers
XX FT Peptide 1..2
XX FT /note= "vector-encoded residues"
XX FT Region 31..37
XX FT /note= "CDR1"
XX FT Region 52..67
XX FT /note= "CDR2"
XX FT Region 100..107
XX FT /note= "CDR3"
XX PN WO9929888-A1.
XX PD 17-JUN-1999.
XX PF 04-DEC-1998; 98WO-US25828.
XX PR 05-DEC-1997; 97US-0986016.
XX PA (SCRI ) SCRIPPS RES INST.
XX PI Barbas CF, Rader C;
XX PI WPI; 1999-394979/33.
XX PT Production of humanized mouse monoclonal antibodies
XX PS Disclosure; Page 51; 55pp; English.
XX CC This sequence represents the heavy chain variable region of a
XX CC humanised LM609 antibody. LM609 is directed to human integrin
XX CC alpha-v beta-3. It selectively promotes apoptosis of vascular
XX CC cells that have been stimulated to undergo angiogenesis, making it
XX CC a tool for cancer diagnosis and therapy. The invention provides
XX CC humanised antibodies, especially humanised LM609. In such humanized
XX CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
XX CC grafted onto a human light chain, and a heavy chain CDR from a mouse
XX CC antibody is grafted onto a human antibody heavy chain to produce
XX CC libraries from which a humanised murine antibody having the desired
XX CC specificity is selected. By preserving the original CDR sequences
XX CC such as the HCDR3 and LCDR3 sequences of LM609 (see AAY06371-72), the
XX CC humanisation strategy ensures epitope conservation.
XX SQ Sequence 118 AA;
XX Query Match 93.1%; Score 54; DB 20; Length 118;
XX Best Local Similarity 90.0%; Pred. No. 0.16;
XX Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 ARHNYGSYAY 10
XX | | | | | | | |
XX Db 98 ARHNYGSFAY 107
XX RESULT 15
XX AAY06386
XX ID AAY06386 standard; Protein; 118 AA.
XX AC AAY06386;
XX DT 06-SEP-1999 (first entry)

```

```
XX DE Humanised LM609 antibody VH domain.
XX DE
XX KW Humanised antibody; antibody humanisation; antibody engineering;
KW LM609; monoclonal antibody; complementarity determining region;
KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
KW cancer; therapy; diagnosis.
XX OS Homo sapiens.
OS Synthetic.
XX OS
XX FH Key Location/Qualifiers
XX FT Peptide 1..2
XX FT Region 31..37 /note= "vector-encoded residues"
XX FT Region 52..67 /note= "CDR1"
XX FT Region 100..107 /note= "CDR2"
XX FT Region /note= "CDR3"
XX PN WO9929888-A1.
XX XX
XX PD 17-JUN-1999.
XX XX
XX PF 04-DEC-1998; 98WO-US25828.
XX XX
XX PR 05-DEC-1997; 97US-0986016.
XX XX
XX PA (SCRI ) SCRIPPS RES INST.
XX XX
XX PI Barbas CF, Rader C;
XX XX
XX DR WPI; 1999-394979/33.
XX XX
XX PT Production of humanized mouse monoclonal antibodies
XX XX
XX PS Disclosure; Page 51-52; 55pp; English.
XX XX
CC This sequence represents the heavy chain variable region of a
CC humanised LM609 antibody. LM609 is directed to human integrin
CC alpha-v beta-3. It selectively promotes apoptosis of vascular
CC cells that have been stimulated to undergo angiogenesis, making it
CC a tool for cancer diagnosis and therapy. The invention provides
CC humanised antibodies, especially humanised LM609. In such humanized
CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
CC grafted onto a human light chain, and a heavy chain CDR from a mouse
CC antibody is grafted onto a human antibody heavy chain to produce
CC libraries from which a humanised murine antibody having the desired
CC specificity is selected. By preserving the original CDR sequences
CC such as the HCDR3 and LCDR3 sequences of LM609 (see AAY06371-72), the
CC humanisation strategy ensures epitope conservation.
XX XX
SQ Sequence 118 AA;
Query Match 93.1%; Score 54; DB 20; Length 118;
Best Local Similarity 90.0%; Pred. No. 0.16;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 ARHNYGSYAY 10
Db 98 ARHNYGSFAY 107
|||||:|:|
|||||:|:|

Search completed: November 18, 2002, 17:31:37
Job time : 14.8235 secs
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:54:45 ; Search time 1.96078 Seconds
(without alignments)
76.811 Million cell updates/sec

Title: US-09-016-061-62

Perfect score: 58

Sequence: 1 ARHNYGSYAY 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 97044 seqs, 15060890 residues

Total number of hits satisfying chosen parameters: 97044

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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- 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
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- 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	54	93.1	117	8	US-08-791-391A-2
4	54	93.1	117	8	US-08-791-391A-6
5	38	65.5	428	12	US-10-062-254-372
6	36	62.1	14	1	US-08-677-599B-22
7	36	62.1	301	10	US-09-799-777-64
8	36	62.1	349	10	US-09-766-366-4
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10	35	60.3	279	10	US-09-775-879-23
11	35	60.3	281	10	US-09-775-879-18
12	35	60.3	281	10	US-09-775-879-21
13	34	58.6	28	10	US-09-864-761-41603
14	34	58.6	41	10	US-09-864-761-46620
15	34	58.6	123	9	US-09-144-886-60
16	34	58.6	123	9	US-09-144-886-61
17	33	56.9	14	1	US-08-677-599B-21
18	33	56.9	87	10	US-09-965-602-48
19	33	56.9	101	10	US-09-764-853-432
					Sequence 2, Appl
					Sequence 6, Appl
					Sequence 2, Appl
					Sequence 6, Appl
					Sequence 372, App
					Sequence 22, Appl
					Sequence 64, Appl
					Sequence 4, Appl
					Sequence 11611, A
					Sequence 23, Appl
					Sequence 18, Appl
					Sequence 21, Appl
					Sequence 41603, A
					Sequence 46620, A
					Sequence 60, Appl
					Sequence 61, Appl
					Sequence 21, Appl
					Sequence 48, Appl
					Sequence 432, App

Query Match 93.1%; Score 54; DB 8; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.006;

20	32	55.2	14	1	US-08-677-599B-11	Sequence 11, Appl
21	32	55.2	14	1	US-08-677-599B-12	Sequence 12, Appl
22	32	55.2	14	1	US-08-677-599B-13	Sequence 13, Appl
23	32	55.2	14	1	US-08-677-599B-14	Sequence 14, Appl
24	32	55.2	14	1	US-08-677-599B-15	Sequence 15, Appl
25	32	55.2	14	1	US-08-677-599B-16	Sequence 16, Appl
26	32	55.2	14	1	US-08-677-599B-17	Sequence 17, Appl
27	32	55.2	14	1	US-08-677-599B-18	Sequence 18, Appl
28	32	55.2	14	1	US-08-677-599B-19	Sequence 19, Appl
29	32	55.2	14	1	US-08-677-599B-20	Sequence 20, Appl
30	32	55.2	14	1	US-08-677-599B-23	Sequence 23, Appl
31	32	55.2	15	10	US-09-756-983-11	Sequence 11, Appl
32	32	55.2	25	1	US-08-677-599B-8	Sequence 8, Appl
33	32	55.2	93	12	US-10-081-281-121	Sequence 121, App
34	32	55.2	94	10	US-09-766-378A-37	Sequence 37, Appl
35	32	55.2	150	10	US-09-893-737-2	Sequence 2, Appl
36	32	55.2	181	10	US-09-815-837-103	Sequence 103, Appl
37	32	55.2	183	10	US-09-815-837-16	Sequence 16, Appl
38	32	55.2	184	10	US-09-815-837-15	Sequence 15, Appl
39	32	55.2	185	10	US-09-815-837-13	Sequence 13, Appl
40	32	55.2	185	10	US-09-815-837-14	Sequence 14, Appl
41	32	55.2	186	10	US-09-815-837-17	Sequence 17, Appl
42	32	55.2	186	10	US-09-815-837-19	Sequence 19, Appl
43	32	55.2	186	10	US-09-815-837-20	Sequence 20, Appl
44	32	55.2	187	10	US-09-815-837-18	Sequence 18, Appl
45	32	55.2	189	10	US-09-815-837-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-08-790-540A-2
; Sequence 2, Application US/08790540A
; Patent No. US20010011125A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,540A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-790-540A-2

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Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSYAY 10
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Db 97 ARHNYGSFAY 106

RESULT 2
US-08-790-540A-6
; Sequence 6, Application US/08790540A
; Patent No. US2001001125A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TELECOMMUNICATION INFORMATION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,540A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-790-540A-6

Query Match 93.1%; Score 54; DB 8; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.006;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSYAY 10
   |||||:|
Db 97 ARHNYGSFAY 106

RESULT 3
US-08-791-391A-2
; Sequence 2, Application US/08791391A
; Patent No. US20010016645A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TELECOMMUNICATION INFORMATION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122

Query Match 93.1%; Score 54; DB 8; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.006;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSYAY 10
   |||||:|
Db 97 ARHNYGSFAY 106

RESULT 4
US-08-791-391A-6
; Sequence 6, Application US/08791391A
; Patent No. US20010016645A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TELECOMMUNICATION INFORMATION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,391A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-791-391A-6
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,391A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-791-391A-2

Query Match 93.1%; Score 54; DB 8; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.006;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSYAY 10
   |||||:|
Db 97 ARHNYGSFAY 106

RESULT 4
US-08-791-391A-6
; Sequence 6, Application US/08791391A
; Patent No. US20010016645A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TELECOMMUNICATION INFORMATION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,391A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-791-391A-6
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Query Match          93.1%  Score 54;  DB 8;  Length 117;
Best Local Similarity 90.0%  Pred. No. 0.006;
Matches 9;  Conservative 1;  Mismatches 0;  Indels 0;  Gaps 0;

Qy 1 ARHNYGSVAY 10
Db 97 ARHNYGSFAY 106

RESULT 5
US-10-062-254-372
; Sequence 372, Application US/100622254
; Patent No. US20020138882A1
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Edgar B
; APPLICANT: Cahoon, Rebecca E
; APPLICANT: Falco, Saverio Carl
; APPLICANT: Fang, Yiwen
; APPLICANT: Hantke, Sabine S.
; APPLICANT: Lee, Jian-Ming
; APPLICANT: Li, Zhongsen
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Morgante, Michele
; APPLICANT: Niu, Xiping
; APPLICANT: Odell, Joan
; APPLICANT: Rafalski, Antoni
; APPLICANT: Sakai, Hajime
; APPLICANT: Zheng, Peizhong
; APPLICANT: Zhu, Qun
; TITLE OF INVENTION: Polynucleotides Encoding Proteins Involved In Plant Metabolism
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/062,254
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 09/630,346
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/146511
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 60/156006
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/156899
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 60/157287
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/169767
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/171054
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: 60/172958
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/171515
; PRIOR FILING DATE: 1999-12-22
; PRIOR APPLICATION NUMBER: 60/173535
; PRIOR FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 372
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-10-062-254-372

Query Match          65.5%  Score 38;  DB 12;  Length 428;
Best Local Similarity 66.7%  Pred. No. 13;
Matches 6;  Conservative 0;  Mismatches 3;  Indels 0;  Gaps 0;

Qy 2 RHNYGSVAY 10
Db 387 RQNYGGYGY 395

RESULT 6
US-08-677-599B-22
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; Sequence 22, Application US/08677599B
; Patent No. US2002015117A1
; GENERAL INFORMATION:
; APPLICANT: Sucia-Foca, Nicole
; TITLE OF INVENTION: METHODS FOR DETECTING ORGAN ALLOGRAFT
; TITLE OF INVENTION: REJECTION AND USES THEREOF
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/677,599B
; FILING DATE: 08-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq., John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 50161-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212/278/0400
; TELEFAX: 212/391/0525
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-677-599B-22

Query Match          62.1%  Score 36;  DB 1;  Length 14;
Best Local Similarity 100.0%  Pred. No. 1;
Matches 6;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy 1 ARHNYG 6
Db 9 ARHNYG 14

RESULT 7
US-09-799-777-64
; Sequence 64, Application US/09799777
; Patent No. US20020091244A1
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; Hillman, Jennifer L.
; Corley, Neil C.
; Guegler, Karl J.
; Baugh, Mariah
; Sather, Susan
; Shah, Purvi
; TITLE OF INVENTION: HUMAN SIGNAL PEPTIDE-CONTAINING PROTEINS
; NUMBER OF SEQUENCES: 154
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/799,777
; FILING DATE: 06-Mar-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/002,485
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: BILLINGS, LUCY J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0459 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 301 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: UTRSTUT05
; CLONE: 2879068
; SEQUENCE DESCRIPTION: SEQ ID NO: 64 :
US-09-799-777-64

Query Match 62.1%; Score 36; DB 10; Length 301;
Best Local Similarity 62.5%; Pred. No. 20;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSYAY 10
Db 263 YNYGNYGY 270

RESULT 8
US-09-766-366-4
; Sequence 4, Application US/09766366
; Patent No. US20010024786A1
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; Shah, Purvi
; Corley, Neil C.
; TITLE OF INVENTION: HUMAN PEROXISOMAL THIOESTERASE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESS: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/766,366
; FILING DATE: 18-Jan-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/872,784
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0293 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
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;
; LENGTH: 349 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 854594
; SEQUENCE DESCRIPTION: SEQ ID NO: 4 :
US-09-766-366-4

Query Match 62.1%; Score 36; DB 10; Length 349;
Best Local Similarity 60.0%; Pred. No. 23;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSYAY 10
Db 247 ARYNYVAFAY 256

RESULT 9
US-09-815-242-11611
; Sequence 11611, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011a
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11611
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-815-242-11611

Query Match 60.3%; Score 35; DB 10; Length 246;
Best Local Similarity 71.4%; Pred. No. 24;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 NYGSYAY 10
Db 196 NYGAVSY 202

RESULT 10
US-09-775-879-23
; Sequence 23, Application US/09775879
; Patent No. US20020068822A1
; GENERAL INFORMATION:
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; APPLICANT: Choe, Sunghwa
; APPLICANT: Feldmann, Kenneth A
; TITLE OF INVENTION: Dwf7 MUTANTS
; FILE REFERENCE: 2225-0003
; CURRENT APPLICATION NUMBER: US/09/775.879
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/179,901
; PRIOR FILING DATE: 2000-02-02
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 279
; TYPE: PRT
; ORGANISM: HDEF7
US-09-775-879-23

Query Match      60.3%; Score 35; DB 10; Length 279;
Best Local Similarity 71.4%; Pred. No. 28;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 RHNYGSY 8
Db      247 KHNHYGY 253

RESULT 11
US-09-775-879-18
; Sequence 18, Application US/09775879
; Patent No. US20020068822A1
; GENERAL INFORMATION:
; APPLICANT: Choe, Sunghwa
; APPLICANT: Feldmann, Kenneth A
; TITLE OF INVENTION: Dwf7 MUTANTS
; FILE REFERENCE: 2225-0003
; CURRENT APPLICATION NUMBER: US/09/775.879
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/179,901
; PRIOR FILING DATE: 2000-02-02
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 281
; TYPE: PRT
; ORGANISM: DWF7/STEL (Arabidopsis)
US-09-775-879-18

Query Match      60.3%; Score 35; DB 10; Length 281;
Best Local Similarity 71.4%; Pred. No. 28;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 RHNYGSY 8
Db      246 KHNHYGY 252

RESULT 12
US-09-775-879-21
; Sequence 21, Application US/09775879
; Patent No. US20020068822A1
; GENERAL INFORMATION:
; APPLICANT: Choe, Sunghwa
; APPLICANT: Feldmann, Kenneth A
; TITLE OF INVENTION: Dwf7 MUTANTS
; FILE REFERENCE: 2225-0003
; CURRENT APPLICATION NUMBER: US/09/775.879
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/179,901
; PRIOR FILING DATE: 2000-02-02
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC008506.4
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 20
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 22
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 17

; APPLICANT: Choe, Sunghwa
; APPLICANT: Feldmann, Kenneth A
; TITLE OF INVENTION: Dwf7 MUTANTS
; FILE REFERENCE: 2225-0003
; CURRENT APPLICATION NUMBER: US/09/775.879
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/179,901
; PRIOR FILING DATE: 2000-02-02
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 279
; TYPE: PRT
; ORGANISM: HDEF7
US-09-775-879-23

Query Match      60.3%; Score 35; DB 10; Length 281;
Best Local Similarity 71.4%; Pred. No. 28;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 RHNYGSY 8
Db      246 KHNHYGY 252

RESULT 13
US-09-864-761-41603
; Sequence 41603, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aecmca-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 41603
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC008506.4
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 20
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 22
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 17
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; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 16
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 20
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 20
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 32
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 20
US-09-864-761-41603

Query Match 58.6%; Score 34; DB 10; Length 28;
Best Local Similarity 71.4%; Pred. No. 4.4;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYSY 8
||| :|
Db 6 RHNYSY 12

RESULT 14
US-09-864-761-46620
; Sequence 46620, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Acomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 46620
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:

; OTHER INFORMATION: MAP TO AC006378.2
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.83
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.82
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.99
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN HEL100, SIGNAL = 0.92
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 0.93
; OTHER INFORMATION: EST_HUMAN HIT: BF130458.1, EVALUE 3.00e-06
US-09-864-761-46620

Query Match 58.6%; Score 34; DB 10; Length 41;
Best Local Similarity 71.4%; Pred. No. 6.3;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 NYGSYAY 10
||| :|
Db 7 NYGNYG 13

RESULT 15
US-09-144-886-60
; Sequence 60, Application US/09144886
; Patent No. US2002015114A1
; GENERAL INFORMATION:
; APPLICANT: Amersdorfer, Peter
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; FILE REFERENCE: 2500.117050
; CURRENT APPLICATION NUMBER: US/09/144,886
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone
; OTHER INFORMATION: IAL region VH epitope 2
US-09-144-886-60

Query Match 58.6%; Score 34; DB 9; Length 123;
Best Local Similarity 71.4%; Pred. No. 18;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYSY 8
||| :|
Db 98 RHGYGNY 104

Search completed: November 18, 2002, 18:45:15
Job time : 1.96078 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:01 ; Search time 4.2402 Seconds
(without alignments)
69.390 Million cell updates/sec

Title: US-09-016-061-62
Perfect score: 58
Sequence: 1 ARHNYGSYAY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA.*
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3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	69.0	119	3	US-08-767-128-6
2	38	65.5	191	4	Sequence 6, Appli
3	38	65.5	235	4	Sequence 24, Appl
4	38	65.5	260	4	Sequence 30, Appl
5	38	65.5	261	4	Sequence 10, Appl
6	38	65.5	269	4	Sequence 26, Appl
7	38	65.5	271	4	Sequence 28, Appl
8	38	65.5	271	4	Sequence 32, Appl
9	37	63.8	36	1	Sequence 33, Appl
10	37	63.8	36	1	Sequence 84, Appl
11	37	63.8	36	1	Sequence 84, Appl
12	37	63.8	36	1	Sequence 84, Appl
13	37	63.8	36	2	Sequence 84, Appl
14	37	63.8	36	4	Sequence 84, Appl
15	37	63.8	36	4	Sequence 281, App
16	37	63.8	36	5	Sequence 129, App
17	36	62.1	349	1	Sequence 84, Appl
18	36	62.1	349	2	Sequence 4, Appli
19	36	62.1	349	4	Sequence 4, Appli
20	34	58.6	120	2	Sequence 4, Appli
21	34	58.6	120	2	Sequence 1, Appli
22	34	58.6	1134	4	Sequence 1, Appli
23	34	58.6	1150	4	Sequence 76, Appl
24	34	58.6	1156	4	Sequence 74, Appl
25	34	58.6	1156	4	Sequence 10, Appl
26	34	58.6	1156	4	Sequence 70, Appl
27	34	58.6	1157	2	Sequence 72, Appl
					Sequence 5, Appli

28 34 58.6 1157 2 US-08-379-656B-5 Sequence 5, Appli
29 34 58.6 1157 3 US-08-455-838-5 Sequence 5, Appli
30 34 58.6 1157 4 US-09-019-809-5 Sequence 5, Appli
31 34 58.6 1157 4 US-09-471-177-5 Sequence 5, Appli
32 34 58.6 1169 1 US-08-542-921-2 Sequence 2, Appli
33 34 58.6 1169 2 US-08-880-685-2 Sequence 2, Appli
34 34 58.6 1169 2 US-08-880-684-2 Sequence 2, Appli
35 33 56.9 94 3 US-09-147-550-14 Sequence 14, Appl
36 33 56.9 94 3 US-09-147-550-45 Sequence 45, Appl
37 33 56.9 94 3 US-09-147-550-48 Sequence 48, Appl
38 33 56.9 94 3 US-09-147-550-77 Sequence 77, Appl
39 33 56.9 94 3 US-09-147-550-84 Sequence 84, Appl
40 33 56.9 94 3 US-09-147-550-90 Sequence 90, Appl
41 33 56.9 94 3 US-09-147-550-101 Sequence 101, App
42 33 56.9 94 4 US-09-557-917-14 Sequence 14, Appl
43 33 56.9 94 4 US-09-557-917-45 Sequence 45, Appl
44 33 56.9 94 4 US-09-557-917-48 Sequence 48, Appl
45 33 56.9 94 4 US-09-557-917-77 Sequence 77, Appl

ALIGNMENTS

RESULT 1
US-08-767-128-6
; Sequence 6, Application US/08767128
; Patent No. 611079
; GENERAL INFORMATION:
; APPLICANT: WYLIE, DWANE E.
; APPLICANT: LOPEZ, OSVALDO
; APPLICANT: MURRAY, PETER JOSEPH
; APPLICANT: GOBEL, PETER
; TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
; NUCLEOTIDES CODING THEREFORE
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
; STREET: 3100 No. 611079west Center, 90 South Seventh St
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/767,128
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE: 04-DEC-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/09258
; FILING DATE: 05-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/541,373
; FILING DATE: 10-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/462,798
; FILING DATE: 05-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G.
; REGISTRATION NUMBER: 35,093
; REFERENCE/DOCKET NUMBER: 8648.49USEF1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/371-5278
; TELEFAX: 612/332-9081
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
US-08-767-128-6

Query Match 69.0%; Score 40; DB 3; Length 119;
Best Local Similarity 77.8%; Pred. No. 6.9;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ARHNYGSYA 9
|||:| | |
Db 97 ARHYGYA 105

RESULT 2
US-09-443-041A-24
; Sequence 24, Application US/09443041A
; Patent No. 6465717
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Orozco, Buddy
; APPLICANT: Rafalski, Antoni
; APPLICANT: Shen, Jennie
; TITLE OF INVENTION: Sterol Metabolism Enzymes
; FILE REFERENCE:
; CURRENT FILING DATE: 1999-11-18
; PRIOR APPLICATION NUMBER: 60/109,283
; PRIOR FILING DATE: 1998-11-20
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 24
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Zea mays
US-09-443-041A-24

Query Match 65.5%; Score 38; DB 4; Length 191;
Best Local Similarity 85.7%; Pred. No. 23;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSY 8
|||||
Db 171 RHNYGHY 177

RESULT 3
US-09-443-041A-30
; Sequence 30, Application US/09443041A
; Patent No. 6465717
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Orozco, Buddy
; APPLICANT: Rafalski, Antoni
; APPLICANT: Shen, Jennie
; TITLE OF INVENTION: Sterol Metabolism Enzymes
; FILE REFERENCE:
; CURRENT FILING DATE: 1999-11-18
; PRIOR APPLICATION NUMBER: 60/109,283
; PRIOR FILING DATE: 1998-11-20
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 30
; LENGTH: 236
; TYPE: PRT

; ORGANISM: Triticum aestivum
US-09-443-041A-30

Query Match 65.5%; Score 38; DB 4; Length 236;
Best Local Similarity 85.7%; Pred. No. 29;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSY 8
|||||
Db 216 RHNYGHY 222

RESULT 4
US-09-443-041A-10
; Sequence 10, Application US/09443041A
; Patent No. 6465717
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Orozco, Buddy
; APPLICANT: Rafalski, Antoni
; APPLICANT: Shen, Jennie
; TITLE OF INVENTION: Sterol Metabolism Enzymes
; FILE REFERENCE:
; CURRENT FILING DATE: 1999-11-18
; PRIOR APPLICATION NUMBER: 60/109,283
; PRIOR FILING DATE: 1998-11-20
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 10
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Zea mays
; NAME/KEY: UNSURE
; LOCATION: (233)
; OTHER INFORMATION: ANY AMINO ACID
; NAME/KEY: UNSURE
; LOCATION: (254)
; OTHER INFORMATION: ANY AMINO ACID
US-09-443-041A-10

Query Match 65.5%; Score 38; DB 4; Length 260;
Best Local Similarity 85.7%; Pred. No. 31;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSY 8
|||||
Db 240 RHNYGHY 246

RESULT 5
US-09-443-041A-26
; Sequence 26, Application US/09443041A
; Patent No. 6465717
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Orozco, Buddy
; APPLICANT: Rafalski, Antoni
; APPLICANT: Shen, Jennie
; TITLE OF INVENTION: Sterol Metabolism Enzymes
; FILE REFERENCE:
; CURRENT FILING DATE: 1999-11-18
; PRIOR APPLICATION NUMBER: 60/109,283
; PRIOR FILING DATE: 1998-11-20
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 26
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Oryza sativa
US-09-443-041A-26

Query Match 65.5%; Score 38; DB 4; Length 261;
Best Local Similarity 85.7%; Pred. No. 32;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSY 8
Db 241 RHNYGHY 247
|||||

RESULT 6
US-09-443-041A-28
; Sequence 28, Application US/09443041A
; Patent No. 6465717
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Orozco, Buddy
; APPLICANT: Rafalski, Antoni
; APPLICANT: Shen, Jennie
; TITLE OF INVENTION: Sterol Metabolism Enzymes
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/443, 041A
; CURRENT FILING DATE: 1999-11-18
; PRIOR APPLICATION NUMBER: 60/109,283
; PRIOR FILING DATE: 1998-11-20
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 28
; LENGTH: 269
; TYPE: PRT
; ORGANISM: Glycine max
US-09-443-041A-28

Query Match 65.5%; Score 38; DB 4; Length 269;
Best Local Similarity 85.7%; Pred. No. 32;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSY 8
Db 241 RHNYGHY 247
|||||

RESULT 7
US-09-443-041A-32
; Sequence 32, Application US/09443041A
; Patent No. 6465717
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Orozco, Buddy
; APPLICANT: Rafalski, Antoni
; APPLICANT: Shen, Jennie
; TITLE OF INVENTION: Sterol Metabolism Enzymes
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/443, 041A
; CURRENT FILING DATE: 1999-11-18
; PRIOR APPLICATION NUMBER: 60/109,283
; PRIOR FILING DATE: 1998-11-20
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 32
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-443-041A-32

Query Match 65.5%; Score 38; DB 4; Length 271;
Best Local Similarity 85.7%; Pred. No. 33;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSY 8
Db 243 RHNYGHY 249
|||||

RESULT 8
US-09-443-041A-33
; Sequence 33, Application US/09443041A
; Patent No. 6465717
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Orozco, Buddy
; APPLICANT: Rafalski, Antoni
; APPLICANT: Shen, Jennie
; TITLE OF INVENTION: Sterol Metabolism Enzymes
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/443, 041A
; CURRENT FILING DATE: 1999-11-18
; PRIOR APPLICATION NUMBER: 60/109,283
; PRIOR FILING DATE: 1998-11-20
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 33
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-443-041A-33

Query Match 65.5%; Score 38; DB 4; Length 271;
Best Local Similarity 85.7%; Pred. No. 33;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSY 8
Db 243 RHNYGHY 249
|||||

RESULT 9
US-08-053-131-84
; Sequence 84, Application US/08053131
; Patent No. 5661016
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 197
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 200
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/053,131
; FILING DATE: 26-APR-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,860
; FILING DATE: 16-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/810,279
; FILING DATE: 17-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/853,408
; FILING DATE: 18-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14643-9-3
; TELECOMMUNICATION INFORMATION:

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; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-053-131-84

Query Match 63.8%; Score 37; DB 1; Length 36;
Best Local Similarity 70.0%; Pred. No. 6.8;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSYAY 10
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Db 3 ARHYGSGSY 12

RESULT 10
US-08-645-641-84
; Sequence 84, Application US/08645641
; Patent No. 5719032
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 5719032-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 150
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/645,641
; FILING DATE: 20-MAY-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/904,068
; FILING DATE: 23-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14643-000913
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-645-641-84

Query Match 63.8%; Score 37; DB 1; Length 36;
Best Local Similarity 70.0%; Pred. No. 6.8;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSYAY 10
   ||| ||| :|
Db 3 ARHYGSGSY 12

RESULT 11
US-07-853-408B-84
; Sequence 84, Application US/07853408B
; Patent No. 5789650
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 5789650-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 150
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/853,408B
; FILING DATE: 19920318
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14643-9
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-853-408B-84

Query Match 63.8%; Score 37; DB 1; Length 36;
Best Local Similarity 70.0%; Pred. No. 6.8;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSYAY 10
   ||| ||| :|
Db 3 ARHYGSGSY 12

RESULT 12
US-08-096-762-84
; Sequence 84, Application US/08096762
; Patent No. 5814318
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 5814318-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 210
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 200
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/096,762
FILING DATE: 22-JUL-1993
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
APPLICATION NUMBER: US 07/904,068
FILING DATE: 23-JUN-1992
APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14643-9-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-096-762-84

Query Match 63.8%; Score 37; DB 2; Length 36;
Best Local Similarity 70.0%; Pred. No. 6.8;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSYAY 10
||| ||| :|
Db 3 ARHYGSGSY 12

RESULT 13
US-08-308-865-84
Sequence 84, Application US/08308865
Patent No. 5877397
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
TITLE OF INVENTION: Transgenic No. 5877397-Human Animals for
Producing Heterologous Antibodies
TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 150
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/308,865
FILING DATE: 800
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/145,707

FILING DATE:
APPLICATION NUMBER: US 07/904,068
FILING DATE: 23-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14643-9-1-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-308-865-84

Query Match 63.8%; Score 37; DB 2; Length 36;
Best Local Similarity 70.0%; Pred. No. 6.8;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSYAY 10
||| ||| :|
Db 3 ARHYGSGSY 12

RESULT 14
US-09-042-353-281
Sequence 281, Application US/09042353
Patent No. 6255458
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for
Producing Heterologous Antibodies
TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 421
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,353
FILING DATE: 13-MAR-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
APPLICATION NUMBER: US 07/904,068
FILING DATE: 23-JUN-1992
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
APPLICATION NUMBER: US 08/096,762
FILING DATE: 22-JUL-1993
APPLICATION NUMBER: 800

APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US96/16433
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/758,417
FILING DATE: 02-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/21803
FILING DATE: 01-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 014643-0090400S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 281:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-042-353-281

Query Match 63.8%; Score 37; DB 4; Length 36;
Best Local Similarity 70.0%; Pred. No. 6.8;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSYAY 10
||| ||| :|
Db 3 ARHYGSGSY 12

RESULT 15
US-08-758-417A-129
Sequence 129, Application US/08758417A
Patent No. 6300129
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for
Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 417
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/758,417A
FILING DATE: 02-DEC-1996
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
APPLICATION NUMBER: US 08/096,762
FILING DATE: 22-JUL-1993
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Serafini, Andrew T.
REGISTRATION NUMBER: 41,303
REFERENCE/DOCKET NUMBER: 014643-0090300S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 129:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 129:
US-08-758-417A-129

Query Match 63.8%; Score 37; DB 4; Length 36;
Best Local Similarity 70.0%; Pred. No. 6.8;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSYAY 10
||| ||| :|
Db 3 ARHYGSGSY 12

Search completed: November 18, 2002, 17:43:36
Job time : 5.2402 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:01 ; Search time 4.90196 Seconds
(without alignments)
196.114 Million cell updates/sec

Title: US-09-016-061-64

Perfect score: 59

Sequence: 1 ARHNYGSFDY 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_73.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	67.8	812	2 D98149	hypothetical prote
2	40	67.8	812	2 AG3138	fimbrial usher pro
3	39.5	66.9	137	2 H32513	Ig heavy chain pre
4	39	66.1	316	2 T15395	hypothetical prote
5	39	66.1	544	2 S75388	probable phenylala
6	38	64.4	82	2 I51106	Major Histocompati
7	38	64.4	89	2 S38688	MHC class II histo
8	38	64.4	89	2 S38683	MHC class II histo
9	38	64.4	89	2 S38684	Ig heavy chain v r
10	38	64.4	117	2 S17586	MHC class II OVAR-
11	38	64.4	225	2 T47095	probable GTP-bind
12	38	64.4	605	2 E71314	hypothetical prote
13	37.5	63.6	369	2 T04947	hypothetical prote
14	37	62.7	123	2 G90878	hypothetical prote
15	37	62.7	123	2 C85740	partial probable o
16	37	62.7	315	2 T46993	hypothetical prote
17	37	62.7	377	2 D64888	outer membrane por
18	37	62.7	383	2 AE0690	outer membrane pro
19	37	62.7	453	2 G89045	protein B0238.2 [i
20	36.5	61.9	139	2 S01158	Ig heavy chain pre
21	36	61.0	86	2 D33989	Ig heavy chain v-4
22	36	61.0	369	2 S70847	outer membrane por
23	36	61.0	394	2 S34263	outer membrane por
24	36	61.0	394	2 AC0755	outer membrane por
25	36	61.0	446	2 T19625	hypothetical prote
26	36	61.0	553	2 D96884	hypothetical prote
27	36	61.0	602	2 B71561	probable GTPase -
28	36	61.0	602	2 B72088	GTP-binding protei
29	36	61.0	602	2 E86535	GTPase [imported]

30	36	61.0	602	2 B81714	GTP-binding protei
31	36	61.0	783	1 S02755	outer membrane ush
32	36	61.0	922	2 T03854	hypothetical prote
33	36	61.0	1116	2 I54378	gene X104 protein
34	35	59.3	32	2 PHI735	Ig heavy chain v r
35	35	59.3	81	2 S2731	hypothetical prote
36	35	59.3	108	2 S26316	Ig heavy chain v r
37	35	59.3	110	2 S26317	Ig heavy chain v r
38	35	59.3	195	2 G86742	conserved hypothet
39	35	59.3	304	2 B83032	probable permease
40	35	59.3	371	2 T24853	hypothetical prote
41	35	59.3	420	2 I51088	L-SF precursor - J
42	35	59.3	458	2 T34574	hypothetical prote
43	35	59.3	536	2 T24218	hypothetical prote
44	35	59.3	587	1 E69171	phosphoesterase-re
45	35	59.3	641	2 AI2524	hypothetical prote

ALIGNMENTS

RESULT 1

D98149

hypothetical protein AGR_L_299 [imported] - Agrobacterium tumefaciens (strain C58, Ce
C:Species: Agrobacterium tumefaciens

C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 11-Jan-2002

C:Accession: D98149

R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldm

A.; Liu, F.; Wollam, C.; Allinger, M.; Doughy, D.; Scott, C.; Lappas, C.; Markelz,

Science 294, 2323-2328, 2001

A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium

A:Reference number: A97359; PMID:11743194

A:Accession: D98149

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-812 <KUR>

A:Cross-references: GB:AE007870; PIDN:AAK88718.1; PID:g15158455; GSPDB:GN00170

C:Genetics:

A:Gene: AGR_L_299

A:Map position: linear chromosome

Query Match 67.8%; Score 40; DB 2; Length 812;

Best Local Similarity 75.0%; Pred. No. 30;

Matches 9; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

QY 1 ARHNYG--SFDY 10

DB 353 ARHNYGTSSFDY 364

RESULT 2

AG3138

fimbrial usher protein [imported] - Agrobacterium tumefaciens (strain C58, Dupont)

C:Species: Agrobacterium tumefaciens

C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002

C:Accession: AG3138

R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo

erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; MCCL

; Karp, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001

A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam

ster, E.W.

A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A:Reference number: AB2577; PMID:11743193

A:Accession: AG3138

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-812 <KUR>

A:Cross-references: GB:AE008689; PIDN:AAL45525.1; PID:g17743236; GSPDB:GN00187

C:Experimental source: strain C58 (Dupont)

C:Genetics:

A:Gene: Atu4731

A:Map position: linear chromosome

Query Match 67.8%; Score 40; DB 2; Length 812;
 Best Local Similarity 75.0%; Pred. No. 30;
 Matches 9; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

QY 1 ARHNYG--SFYD 10
 || ||| ||||
 Db 353 ARNYGTSSFDY 364

RESULT 3

H32513
 Ig heavy chain precursor V region (BXW16) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jan-2000
 C:Accession: H32513
 R:Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.;
 J. Clin. Invest. 82, 852-860, 1988
 A:Title: Immunoglobulin kappa light chain variable region gene complex organization and
 A:Reference number: A94689; MUID:88331394; PMID:3138286
 A:Accession: H32513
 A:Molecule type: DNA
 A:Residues: 1-137 <KOF>
 A:Cross-references: GB:M20831; NID:gl96949; PIDN:AAA38848.1; PID:gl96950
 C:Superfamily: Immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 66.9%; Score 39.5; DB 2; Length 137;
 Best Local Similarity 81.8%; Pred. No. 6.2;
 Matches 9; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 ARHNYG-SFDY 10
 || ||| ||||
 Db 116 ARKNGSSFDY 126

RESULT 4

T15395
 hypothetical protein C03F11.2 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
 C:Accession: T15395
 R:Bentley, D.
 submitted to the EMBL Data Library, October 1995
 A:Description: The sequence of C. elegans cosmid C03F11.
 A:Reference number: Z18342
 A:Accession: T15395
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-316 <BEN>
 A:Cross-references: EMBL:U39744; NID:g1049465; PID:g1049467; PIDN:AAA80440.1; CESP:C03F11
 C:Genetics:
 A:Gene: CESP:C03F11.2
 A:Introns: 90/3; 133/2; 171/1; 227/1; 262/1; 309/2

Query Match 66.1%; Score 39; DB 2; Length 316;
 Best Local Similarity 60.0%; Pred. No. 18;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFDY 10
 ||| :||:|
 Db 69 ARHFFGSFYEY 78

RESULT 5

S75388
 probable phenylalanine-tRNA ligase (EC 6.1.1.20) beta chain - Sulfolobus solfataricus
 N:Alternate names: phenylalanyl-tRNA synthetase beta chain; protein c04021
 C:Species: Sulfolobus solfataricus
 C:Date: 09-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 03-Jun-2002
 C:Accession: S75388
 R:Sensen, C.W.; Klenk, H.P.; Singh, R.K.; Allard, G.; Chan, C.C.Y.; Liu, Q.Y.; Penny, S.

Mol. Microbiol. 22, 175-191, 1996
 A:Title: Organizational characteristics and information content of an archaeal genome
 A:Reference number: S73076; MUID:97055432; PMID:8899719
 A:Accession: S75388
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-544 <SEN>
 A:Cross-references: EMBL:Y08257; NID:gl707772; PIDN:CAA69550.1; PID:gl707793
 A:Experimental source: strain P2
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199
 C:Superfamily: yeast cytosolic phenylalanine-tRNA ligase alpha chain
 C:Keywords: aminoacyl-tRNA synthetase; ATP; ligase; protein biosynthesis

Query Match 66.1%; Score 39; DB 2; Length 544;
 Best Local Similarity 85.7%; Pred. No. 30;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 NYGSFDY 10
 ||||:|
 Db 350 NYGSYDY 356

RESULT 6

I51106
 Major Histocompatibility Complex class IIB - ring-necked pheasant (fragment)
 C:Species: Phasianus colchicus (ring-necked pheasant)
 C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 23-Jul-1999
 C:Accession: I51106
 R:Witzell, H.; von Schantz, T.; Zoorob, R.; Auffray, C.
 Immunogenetics 39, 395-403, 1994
 A:Title: Molecular characterization of three Mhc class II B haplotypes in the ring-ne
 A:Reference number: I51103; MUID:94245280; PMID:7910588

A:Accession: I51106
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-82 <WIT>

A:Cross-references: EMBL:X75406; NID:g496926; PIDN:CAA53160.1; PID:g496927
 C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 64.4%; Score 38; DB 2; Length 82;
 Best Local Similarity 75.0%; Pred. No. 7;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFD 9
 |||||:
 Db 75 RHNYGVFE 82

RESULT 7

S38688
 MHC class II histocompatibility antigen HLA-DR-08 beta chain - northern lesser bushba
 C:Species: Galago senegalensis (northern lesser bushbaby)
 C:Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 19-May-2000
 C:Accession: S38688

R:Figueroa, F.; O'Huigin, C.; Tichy, H.; Klein, J.
 submitted to the EMBL Data Library, November 1993

A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduce
 A:Reference number: S38676

A:Accession: S38688
 A:Molecule type: DNA
 A:Residues: 1-89 <FIG>

A:Cross-references: EMBL:Z27158
 C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 64.4%; Score 38; DB 2; Length 89;
 Best Local Similarity 75.0%; Pred. No. 7.6;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFD 9
 |||||:
 Db 75 RHNYGVFE 82

RESULT 8

S38683
MHC class II histocompatibility antigen HLA-DR-03 beta chain - northern lesser bushbaby
C:Species: Galago senegalensis (northern lesser bushbaby)
C:Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 19-May-2000
C:Accession: S38683
R:Figuerola, F.; O'Huigin, C.; Tichy, H.; Klein, J.
submitted to the EMBL Data Library, November 1993
A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduced from the EMBL Data Library
A:Reference number: S38676
A:Accession: S38683
A:Molecule type: DNA
A:Residues: 1-89 <FIG>
A:Cross-references: EMBL:227153
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 64.4%; Score 38; DB 2; Length 89;
Best Local Similarity 75.0%; Pred. No. 7.6;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFD 9

|||||

Db 75 RHNYGVFE 82

RESULT 9

S38684
MHC class II histocompatibility antigen HLA-DR-04 beta chain - northern lesser bushbaby
C:Species: Galago senegalensis (northern lesser bushbaby)
C:Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 19-May-2000
C:Accession: S38684
R:Figuerola, F.; O'Huigin, C.; Tichy, H.; Klein, J.
submitted to the EMBL Data Library, November 1993
A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduced from the EMBL Data Library
A:Reference number: S38676
A:Accession: S38684
A:Molecule type: DNA
A:Residues: 1-89 <FIG>
A:Cross-references: EMBL:227154
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 64.4%; Score 38; DB 2; Length 89;
Best Local Similarity 75.0%; Pred. No. 7.6;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFD 9

|||||

Db 75 RHNYGVFE 82

RESULT 10

S17586
Ig heavy chain V region (E8) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S17586
R:Mylvaganam, S.E.; Paterson, Y.; Kaiser, K.; Bowdish, K.; Getzoff, E.D.
J. Mol. Biol. 221, 455-462, 1991
A:Title: Biochemical implications from the variable gene sequences of an anti-cytochrome forms.

A:Reference number: S17586; MUID:92015240; PMID:1656053

A:Accession: S17586

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-117 <MYL>

A:Cross-references: EMBL:X60683; NID:951820; PIDN:CAA43095.1; PID:g51821

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 64.4%; Score 38; DB 2; Length 117;
Best Local Similarity 60.0%; Pred. No. 9.9;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFDY 10

|:|:|:|:|

Db 97 AGYDYGFDI 106

RESULT 11

I47095
MHC class II OVAR-DR-beta-3 - sheep (fragment)
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 15-Oct-1996 #sequence_revision 15-Oct-1996 #text_change 21-Jan-2000
C:Accession: I47095
R:Fabb, S.A.; Maddox, J.F.; Gogolin-Ewens, K.J.; Baker, L.; Wu, M.J.; Brandon, M.R.
Anim. Genet. 24, 249-255, 1993
A:Title: Isolation, characterization and evolution of ovine major histocompatibility antigen (MHC) class II OVAR-DRB3
A:Reference number: I47095; MUID:94057592; PMID:7902039
A:Accession: I47095
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-225 <FAB>
A:Cross-references: GB:L04790; NID:9458880; PIDN:AAA16562.1; PID:g458881
C:Genetics:
C:Gene: OVAR-DRB3
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology
F:98-163/Domain: immunoglobulin homology <IMM>

Query Match 64.4%; Score 38; DB 2; Length 225;
Best Local Similarity 75.0%; Pred. No. 19;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFD 9

|||||

Db 68 RHNYGVFE 75

RESULT 12

E71314
probable GTP-binding membrane protein (lepA) - syphilis spirochete
C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 02-Feb-2001
C:Accession: E71314
R:Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gerson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; Mthey, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.

A:Reference number: A71250; MUID:98332770; PMID:9665876

A:Accession: E71314

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-605 <COL>

A:Cross-references: GB:AE001227; GB:AE000520; NID:g3322797; PIDN:AAAC65498.1; PID:g332

A:Experimental source: strain Nichols

C:Genetics:

C:Gene: TP0510

C:Superfamily: GTP-binding membrane protein lepA; translation elongation factor Tu ho

F:11-140/Domain: translation elongation factor Tu homology <ETU>

F:17-24/Region: nucleotide-binding motif A (P-loop)

F:137-140/Region: GTP-binding NKXD motif

F:168-170/Region: GTP-binding SAK/L motif

F:23,24,59,137,138,140,168/Binding site: Mg-GTP (Lys, Ser, Thr, Asp, Lys, Asp, Ser) #

Query Match 64.4%; Score 38; DB 2; Length 605;
Best Local Similarity 75.0%; Pred. No. 51;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 HNYGSFDY 10

|:|:|:|:|

Db 470 HGYASFDY 477

RESULT 13

T04947
hypothetical protein F7J7.100 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-Jun-1999
C:Accession: T04947
R:Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.
submitted to the Protein Sequence Database, July 1998
A:Reference number: Z15391
A:Accession: T04947
A:Molecule type: DNA
A:Residues: 1-369 <BEV>
A:Cross-references: EMBL:AL021960
A:Experimental source: cultivar Columbia; BAC clone F7J7
C:Genetics:
A:Map position: 4
A:Introns: 14/1; 41/2; 98/3; 153/2; 203/3; 244/3; 276/3
A:Note: F7J7.100

Query Match 63.6%; Score 37.5; DB 2; Length 369;
Best Local Similarity 61.5%; Pred. No. 38;
Matches 8; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

QY 3 HNYGS-----FDY 10
|||
Db 269 HNYGSVKLQVFDY 281

RESULT 14
G90878
hypothetical protein ECs1999 [imported] - Escherichia coli (strain O157:H7, substrain R1)
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C:Accession: G90878
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: G90878
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-123 <HAY>
A:Cross-references: GB:BA000007; PIDN:BA035422.1; PID:g13361464; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain R1MD 0509952
C:Genetics:
A:Gene: ECs1999

Query Match 62.7%; Score 37; DB 2; Length 123;
Best Local Similarity 85.7%; Pred. No. 16;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 NYGSFDY 10
:|||||
Db 106 DYGSFDY 112

RESULT 15
C85740
partial probable outer membrane protein Z2333 [imported] - Escherichia coli (strain O157
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: C85740
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Illier, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: C85740
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-123 <STO>
A:Cross-references: GB:AE005174; NID:g12515326; PIDN:AAG56383.1; GSPDB:GN00145; UWGP:Z23
A:Experimental source: strain O157:H7, substrain EDL933

C:Genetics:
A:Gene: Z2333

Query Match 62.7%; Score 37; DB 2; Length 123;
Best Local Similarity 85.7%; Pred. No. 16;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 NYGSFDY 10
:|||||
Db 106 DYGSFDY 112

Search completed: November 18, 2002, 17:47:04
Job time : 5.90196 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:00 ; Search time 2.45098 Seconds
(without alignments)
169.223 Million cell updates/sec

Title: US-09-016-061-64
Perfect score: 59
Sequence: 1 ARHNGSFYD 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	ID	Description
1	42	71.2	349	1	PHOE_KLEOX	Q01606 klebsiella
2	42	71.2	351	1	PHOE_KLEPN	P30704 klebsiella
3	39	66.1	316	1	YX12-CAEEL	Q11123 caenorhabdi
4	39	66.1	544	1	SYFB-SULSO	P95960 sulfolobus
5	38	64.4	605	1	LEPA-TREPA	O83523 treponema p
6	37	62.7	323	1	CCSA-LOTJA	Q9bbp4 lotus japon
7	37	62.7	362	1	OMPD-SALTY	P37592 salmonella
8	37	62.7	374	1	OMPF-SERMA	O33980 serratia ma
9	37	62.7	376	1	OMPC-SERMA	Q54471 serratia ma
10	37	62.7	377	1	OMPN-ECOLI	P77747 escherichia
11	37	62.7	383	1	OMS2-SALTI	Q56111 salmonella
12	37	62.7	789	1	LP1A-DROME	P11995 drosophila
13	37	62.7	789	1	LP1B-DROME	P11996 drosophila
14	36	61.0	369	1	OMPF-XENNE	Q56828 xenorhabdus
15	36	61.0	394	1	OMSI-SALTI	Q56110 salmonella
16	36	61.0	602	1	LEPA-CHLMU	Q9pkx6 chlamydia m
17	36	61.0	602	1	LEPA-CHLPN	Q92814 chlamydia p
18	36	61.0	602	1	LEPA-CHLTP	O84067 chlamydia t
19	36	61.0	783	1	FAND-ECOLI	P12050 escherichia
20	36	61.0	1190	1	ZO2-HUMAN	Q9udy2 homo sapien
21	35	59.3	783	1	YNR2-CAEEL	P21988 caenorhabdi
22	35	59.3	1166	1	RPA2-EUPOC	P28365 euplotes oc
23	34.5	58.5	131	1	YRAN-ECOLI	P45465 escherichia
24	34	57.6	102	1	RNPB-PENBR	P07446 penicillium
25	34	57.6	105	1	RNF2-GIBBA	P16412 gibberella
26	34	57.6	146	1	LYC2-PIG	P12068 sus scrofa
27	34	57.6	264	1	HB24-MOUSE	P20040 mus musculu
28	34	57.6	264	1	HB21-MOUSE	P18468 mus musculu
29	34	57.6	264	1	HB2J-MOUSE	P18469 mus musculu
30	34	57.6	275	1	IF2A-PYRAB	Q9v0e4 pyrococcus
31	34	57.6	275	1	IF2A-PYRHO	O58655 pyrococcus
32	34	57.6	284	1	IPYR-PICPA	O13505 picchia past
33	34	57.6	286	1	IPYR-KLULA	P13998 kluyveromyc

34	34	57.6	286	1	IPYR-YEAST	P00817 saccharomyc
35	34	57.6	351	1	PHOE_CITFR	Q01605 citrobacter
36	34	57.6	360	1	MANB-BACSU	P55278 bacillus su
37	34	57.6	448	1	ASTB-PSEAE	O50175 pseudomonas
38	34	57.6	798	1	YLFN-CAEEL	Q20296 caenorhabdi
39	34	57.6	1323	1	RRPO-SMYEA	P28897 strawberry
40	33.5	56.8	274	1	PK1-NPVOP	O10269 orgyia pseu
41	33.5	56.8	1536	1	Y984-THEMA	Q9x079 thermotoga
42	33	55.9	65	1	CCSA-ORNEB	P31565 oenothera b
43	33	55.9	196	1	WBBJ-ECOLI	P37750 escherichia
44	33	55.9	236	1	Y139-UREPA	Q9p005 ureaplasma
45	33	55.9	250	1	Y028-RICPR	O05972 rickettsia

ALIGNMENTS

RESULT 1						
PHOE_KLEOX						
ID	PHOE_KLEOX	STANDARD;	PRT;	349	AA.	
AC	Q01606;					
DT	01-APR-1993 (Rel. 25, Created)					
DT	01-APR-1993 (Rel. 25, Last sequence update)					
DT	15-DEC-1998 (Rel. 37, Last annotation update)					
DE	Outer membrane pore protein E precursor.					
GN	PHOE.					
OS	Klebsiella oxytoca.					
OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;					
OC	Klebsiella.					
OX	NCBI_TaxID=571;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=K26;					
RX	MEDLINE=93146376; PubMed=1337052;					
RA	Spierings G., Ockhuijsen C., Hofstra H., Tommassen J.;					
RT	"Characterization of the Citrobacter freundii phoE gene and					
RT	development of C. freundii-specific oligonucleotides.";					
RL	FEMS Microbiol. Lett. 78:199-204(1992).					
CC	-!- FUNCTION: THIS IS ONE OF THE PROTEINS INDUCED WHEN CELLS ARE					
CC	GROWN UNDER PHOSPHATE LIMITATION. ITS PROTEIN PORE IS					
CC	PARTICULARLY EFFICIENT IN THE UPTAKE OF INORGANIC PHOSPHATE,					
CC	PHOSPHORYLATED COMPOUNDS, AND SOME OTHER NEGATIVELY CHARGED					
CC	SOLUTES.					
CC	-!- SUBUNIT: HOMOTRIMER.					
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.					
CC	-!- SIMILARITY: BELONGS TO THE OMPC/PHOE FAMILY OF PORINS.					
CC	-----					
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/					
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CC	-----					
CC	EMBL; X68022; CAA48163.1; -					
DR	HSSP; P02932; 1PHO.					
DR	InterPro; IPR003229; OMP_2.					
DR	InterPro; IPR001702; Porin_gram-ve.					
DR	Pfam; PF00267; Gram-ve_porins; 1.					
DR	PRINTS; PR00182; ECOLNEIPORIN.					
DR	PROSITE; PS00576; GRAM_NEG_PORIN; 1.					
KW	Outer membrane; Transmembrane; Porin; Signal.					
FT	SIGNAL 1 21					
FT	CHAIN 22 349 OUTER MEMBRANE PORE PROTEIN E.					
SQ	SEQUENCE 349 AA; 38550 MW; D0B0A5427542B3F5 CRC64;					
Query Match 71.2%; Score 42; DB 1; Length 349;						
Best Local Similarity 100.0%; Pred. No. 2;						
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
QY	4	NYGSPDY 10				

```

Db 105 NYGSFDY 111

RESULT 2
PHOE_KLEPN STANDARD; PRT; 351 AA.
AC P30704;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Outer membrane pore protein E precursor.
GN PHOE.
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Klebsiella.
OX NCBI_TaxID=573;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87190417; PubMed=3032618;
RT "A comparative study on the phoE genes of three enterobacterial
RT species. Implications for structure-function relationships in a
RT pore-forming protein of the outer membrane."
RL Eur. J. Biochem. 164:469-475(1987).
CC -!- FUNCTION: THIS IS ONE OF THE PROTEINS INDUCED WHEN CELLS ARE
CC GROWN UNDER PHOSPHATE LIMITATION. ITS PROTEIN PORE IS
CC PARTICULARLY EFFICIENT IN THE UPTAKE OF INORGANIC PHOSPHATE,
CC PHOSPHORYLATED COMPOUNDS, AND SOME OTHER NEGATIVELY CHARGED
CC SOLUTES.
CC -!- SUBUNIT: HOMOTRIMER.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
CC -!- SIMILARITY: BELONGS TO THE OMP/PHOE FAMILY OF PORINS.
CC -----
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CC -----
CC EMBL; M48295; AAA25121.1; -.
CC DR HSSP; P02932; IPHO.
CC DR InterPro; IPR003229; OMP_2.
CC DR InterPro; IPR001702; Porin_gram-ve.
CC DR Pfam; PF00267; Gram-ve_porins; 1.
CC DR PRINTS; PR00182; ECOLNEIPORIN.
CC DR PROSITE; PS00576; GRAM_NEG_PORIN; 1.
CC KW Outer membrane; Transmembrane; Porin; Signal.
CC FT SIGNAL 1 21 BY SIMILARITY.
CC FT CHAIN 22 351 OUTER MEMBRANE PORE PROTEIN E.
CC SQ SEQUENCE 351 AA; 38894 MW; 86A52866C12502EC7 CRC64;

Query Match 71.2%; Score 42; DB 1; Length 351;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NYGSFDY 10
| | | | |
Db 106 NYGSFDY 112

RESULT 3
YX12_CAEEL STANDARD; PRT; 316 AA.
AC Q11123;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 35.1 kDa protein C03F11.2 in chromosome X.
GN C03F11.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;

Db 105 NYGSFDY 111
Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Bristol N2;
RA Bentley D.;
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: WEAK, IN THE N-TERMINUS, TO C.ELEGANS F53B1.5.
CC -----
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CC -----
CC EMBL; U39744; AAK18883.1; -.
CC DR WormPep; C03F11.2; CE03914.
CC KW Hypothetical protein.
CC SQ SEQUENCE 316 AA; 35107 MW; 6A725FCAC21CF676 CRC64;

Query Match 66.1%; Score 39; DB 1; Length 316;
Best Local Similarity 60.0%; Pred. No. 6.3;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFDY 10
| | | | |
Db 69 ARHFGSYEY 78

RESULT 4
SYFB_SULSO STANDARD; PRT; 544 AA.
AC P59960;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Phenylalanyl-tRNA synthetase beta chain (EC 6.1.1.20) (Phenylalanine--
DE tRNA ligase beta chain) (PHERS).
DE PHET OR SSO0101 OR C04_021.
CN Sulfolobus solfataricus.
OS Sulfolobus solfataricus.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=2287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 35092 / DSM 1617 / P2;
RX MEDLINE=97055432; PubMed=8899719;
RA Sensen C.W., Klenk H.-P., Singh R.K., Allard G., Chan C.C.-Y.,
RA Liu Q.Y., Penny S.L., Young F., Schenk M.E., Gaasterland T.,
RA Doolittle W.F., Ragan M.A., Charlebois R.L.;
RA "Organizational characteristics and information content of an archaeal
RA genome: 156 kb of sequence from Sulfolobus solfataricus P2."
RA Mol. Microbiol. 22:175-191(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 35092 / DSM 1617 / P2;
RX MEDLINE=21332296; PubMed=11427726;
RA She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
RA Aweez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,
RA De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,
RA Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
RA Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
RA Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;
RA "The complete genome of the crenarchaeon Sulfolobus solfataricus P2."
RA Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
CC -!- CATALYTIC ACTIVITY: ATP + L-phenylalanine + tRNA(Phe) = AMP +
CC diphosphate + L-phenylalanyl-tRNA(Phe).
CC -!- SUBUNIT: Tetramer of two alpha and two beta chains (by
CC SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.

```

```
CC -!- SIMILARITY: BELONGS TO THE PHENYLALANYL-TRNA SYNTHETASE BETA
CC CHAIN FAMILY. SUBFAMILY 2.
CC -----
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CC -----
CC EMBL; Y08257; CAA69550.1; -.
CC EMBL; AE006649; AAK40457.1; -.
CC InterPro; IPR005146; B3.4.
CC InterPro; IPR005147; B5.
CC InterPro; IPR004531; PheT_arch.
CC Pfam; PF03484; B5; 1.
CC TIGRFAMS; TIGR00471; pheT_arch; 1.
CC Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
CC Complete proteome.
CC KW
CC SEQUENCE 544 AA; 61815 MW; 4B14A2234BA8ABDE CRC64;

Query Match 66.1%; Score 39; DB 1; Length 544;
Best Local Similarity 85.7%; Pred. No. 11;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 NYGSFDY 10
Db 350 NYGSYDY 356
|||||

RESULT 5
LEPA_TREPA
ID LEPA_TREPA STANDARD; PRT; 605 AA.
AC 083523;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE GTP-binding protein lepa.
GN LEPA OR TP0510.
OS Treponema pallidum.
OC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxID=160;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Nichols;
RX MEDLINE=98332770; PubMed=9665876;
RA Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
RA Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,
RA Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
RA Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,
RA McDonald L., Artlich P., Bowman C., Cotton M.D., Fujii C., Garland S.,
RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
RA Venter J.C.;
RT "Complete genome sequence of Treponema pallidum, the syphilis
RT spirochete.";
RL Science 281:375-388(1998).
CC -!- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
CC LEPA SUBFAMILY.
CC -----
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CC -----
CC EMBL; AE001227; AAC65498.1; -.
CC HSSP; P13551; 1DAR.
CC TIGR; TP0510; -.
CC InterPro; IPR004161; EFTU_D2.
```

```
DR InterPro; IPR000795; EF_GTPbind.
DR InterPro; IPR005225; Small_GTP.
DR Pfam; PF00009; GTP_EFTU_1.
DR Pfam; PF03144; GTP_EFTU_D2; 1.
DR TIGRFAMS; TIGR00231; small_GTP; 1.
DR PROSITE; PS00301; EFATOR_GTP; FALSE_NEG.
KW GTP-binding; Complete proteome.
FT NP_BIND 17 24 GTP (BY SIMILARITY).
FT NP_BIND 83 87 GTP (BY SIMILARITY).
FT NP_BIND 137 140 GTP (BY SIMILARITY).
FT SEQUENCE 605 AA; 67632 MW; BA537DEC26FD3349 CRC64;

Query Match 64.4%; Score 38; DB 1; Length 605;
Best Local Similarity 75.0%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 HNYGSFDY 10
Db 470 HGYASFDY 477
|||||

RESULT 6
CCSA_LOTJA
ID CCSA_LOTJA STANDARD; PRT; 323 AA.
AC Q9BBP4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cytochrome c biogenesis protein ccsa.
GN CCSA.
OS Lotus japonicus.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OX eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae; Lotus.
OX NCBI_TaxID=34305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Accession MG-20;
RX MEDLINE=21082929; PubMed=11214967;
RA Kato T., Kaneko T., Sato S., Nakamura Y., Tabata S.;
RT "Complete structure of the chloroplast genome of a legume, Lotus
RT japonicus";
RL DNA Res. 7:323-330(2000).
CC -!- FUNCTION: REQUIRED DURING CYTOCHROME BIOGENESIS AT THE STEP OF
CC HEME ATTACHMENT (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CCMF/CYCK/CCL1/NRFE/CCSA FAMILY.
CC -----
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CC -----
CC EMBL; AP002983; BAB33244.1; -.
CC InterPro; IPR002541; Cytc_asm.
DR Pfam; PF01578; Cytc_asm; 1.
KW Cytochrome c-type biogenesis; Chloroplast.
SQ SEQUENCE 323 AA; 37185 MW; 5A034E3E2829FE35 CRC64;

Query Match 62.7%; Score 37; DB 1; Length 323;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
Db 315 HNYGSF 320
|||||

RESULT 7
OMPD_SALT
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ID OMPD_SALTY STANDARD; PRT; 362 AA.
AC P37592;
DT 01-OCT-1994 (Rel. 30, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Outer membrane porin protein ompD precursor.
GN OMPD OR NMPC OR STM1572.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT Lt2."
RL Nature 413:852-856(2001).
RN [2]
RP SEQUENCE OF 80-362 FROM N.A.
RC STRAIN=SL1303;
RX MEDLINE=95011654; PubMed=7926834;
RA Hongo E., Morimyo M., Mita K., Machida I., Hama-Inaba H., Tsuji H.,
RA Ichimura S., Noda Y.;
RT "The methyl viologen-resistance-encoding gene smvA of Salmonella
RT typhimurium."
RL Gene 148:173-174(1994).
RN [3]
RP IDENTIFICATION AS OMPD
RA Singh S.P., Miller S., Williams Y.U., Rudd K.E., Nikaido H.;
RL Unpublished observations (FEB-1996).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
CC -!- SIMILARITY: BELONGS TO THE OMPC/PHOE FAMILY OF PORINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AE008768; AAL20490.1; -.
CC DR EMBL; D26057; BAA05056.1; -.
CC DR HSSP; P02931; LGFN.
CC DR StyGene; SG10249; ompD.
CC DR InterPro; IPR003229; OMP_2.
CC DR Pfam; PF00267; Gram-ve_porins; 2.
CC DR PROSITE; PS00576; GRAM_NEG_PORIN; 1.
CC KW Outer membrane; Transmembrane; Porin; Signal; Complete proteome.
CC FT SIGNAL 1 21 POTENTIAL.
CC FT CHAIN 157 157 OUTER MEMBRANE PORIN PROTEIN OMPD.
CC FT CONFLICT 157 157 N -> K (IN REF. 2).
CC FT CONFLICT 258 258 MISSING (IN REF. 2).
CC SQ SEQUENCE 362 AA; 9f68A9A7B948174C CRC64;

Query Match 62.7%; Score 37; DB 1; Length 362;
Best Local Similarity 85.7%; Pred. No. 17;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 NYGSFDY 10
Db 107 DYGSFDY 113

RESULT 8
OMP_F_SERMA

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ID OMPF_SERMA STANDARD; PRT; 374 AA.
AC O33980;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Outer membrane protein F precursor (Porin ompF).
GN OMPF.
OS Serratia marcescens.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Serratia.
OX NCBI_TaxID=615;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UOC-51;
RX MEDLINE=97419518; PubMed=9274033;
RA Hutsul J.A.M., Worobec E.A.;
RT "Molecular characterization of the Serratia marcescens ompF porin,
RT and analysis of S. marcescens ompF and ompC osmoregulation."
RL Microbiology 143:2797-2806(1997).
CC -!- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
CC -!- SIMILARITY: BELONGS TO THE OMPC/PHOE FAMILY OF PORINS.
CC -----
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CC -----
CC EMBL; U81967; AAB69103.1; ALT_INIT.
CC DR HSSP; Q48473; 10SM.
CC DR InterPro; IPR003229; OMP_2.
CC DR Pfam; PF00267; Gram-ve_porins; 1.
CC DR PRINTS; PR00182; ECOLNEIPORIN.
CC DR PROSITE; PS00576; GRAM_NEG_PORIN; 1.
CC KW Outer membrane; Transmembrane; Porin; Signal.
CC FT SIGNAL 1 21 POTENTIAL.
CC FT CHAIN 22 374 OUTER MEMBRANE PROTEIN F.
CC SQ SEQUENCE 374 AA; 41184 MW; BF621D385E441049 CRC64;

Query Match 62.7%; Score 37; DB 1; Length 374;
Best Local Similarity 85.7%; Pred. No. 17;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 NYGSFDY 10
Db 108 DYGSFDY 114

RESULT 9
OMP_C_SERMA
ID OMP_C_SERMA STANDARD; PRT; 376 AA.
AC Q54471;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Outer membrane protein C precursor (Porin ompC).
GN OMP_C.
OS Serratia marcescens.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Serratia.
OX NCBI_TaxID=615;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UOC-51;
RX MEDLINE=94236242; PubMed=8180703;
RA Hutsul J.A.M., Worobec E.A.;
RT "Molecular characterization of a 40 kDa OmpC-like porin from Serratia
RT marcescens."
RL Microbiology 140:379-387(1994).

```

CC -1- FUNCTION: FORM PASSIVE DIFFUSION PORES WHICH ALLOW SMALL MOLECULAR
 CC WEIGHT HYDROPHILIC MATERIALS ACROSS THE OUTER MEMBRANE.
 CC -1- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
 CC -1- SIMILARITY: BELONGS TO THE OMPC/PHOE FAMILY OF PORINS.
 CC -----
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 CC -----
 DR EMBL: L24960; AAA26562.1; -
 DR HSSP: Q48473; LOSM.
 DR InterPro: IPR003229; OMP_2.
 DR InterPro: IPR001702; Porin_gram-ve.
 DR Pfam: PF00267; Gram-ve_porins; 1.
 DR PRINTS: PR00182; ECOLNEIPORIN.
 DR PROSITE: PS00576; GRAM_NEG_PORIN; 1.
 KW Outer membrane; Transmembrane; Porin; Phage recognition; Signal.
 FT SIGNAL 1 21 BY SIMILARITY.
 FT CHAIN 22 376 OUTER MEMBRANE PROTEIN C.
 SQ SEQUENCE 376 AA; 41440 MW; 81227FE8515B568E CRC64;
 Query Match 62.7%; Score 37; DB 1; Length 376;
 Best Local Similarity 85.7%; Pred. No. 17;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 4 NYGSFDY 10 :|||||
 DB 106 DYGSFDY 112
 RESULT 10
 ID OMPN_ECOLI STANDARD; PRT; 377 AA.
 AC P77747; P76854;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Outer membrane protein N precursor (Porin ompN).
 GN OMPN OR B1377.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:1453-1474(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=97251357; PubMed=9097039;
 RA Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,
 RA Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
 RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
 RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T., Saito N.,
 RA Sampaio G., Seki Y., Sivasubraman S., Tagami H., Takeda J.,
 RA Takenoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;
 RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome
 corresponding to the 28.0-40.1 min region on the linkage map.";
 RL DNA Res. 3:363-377(1996).
 RN [3]
 RP SEQUENCE FROM N.A., SEQUENCE OF 22-33, AND CHARACTERIZATION.

RX MEDLINE=98317278; PubMed=9642192;
 RA Prilipov A., Phale P.S., Koebnik R., Widmer C., Rosenbusch J.P.;
 RT "Identification and characterization of two quiescent porin genes,
 nmpC and ompL, in Escherichia coli BE.";
 RL J. Bacteriol. 180:3388-3392(1998).
 CC -1- FUNCTION: NON-SPECIFIC PORIN.
 CC -1- SUBUNIT: HOMOTRIMER.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
 CC -1- SIMILARITY: BELONGS TO THE OMPC/PHOE FAMILY OF PORINS.
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 CC -----
 DR EMBL: AE000234; AAC74459.1; -
 DR EMBL: D90775; BAA14981.1; -
 DR EMBL: D90776; BAA14986.1; -
 DR HSSP: P02931; IGFN.
 DR EcoGene: EGI3375; ompN.
 DR InterPro: IPR003229; OMP_2.
 DR InterPro: IPR001702; Porin_gram-ve.
 DR Pfam: PF00267; Gram-ve_porins; 1.
 DR PRINTS: PR00182; ECOLNEIPORIN.
 KW Outer membrane; Transmembrane; Porin; Signal; Complete proteome.
 FT SIGNAL 1 21
 FT CHAIN 22 377 OUTER MEMBRANE PROTEIN N.
 SQ SEQUENCE 377 AA; 41220 MW; 4420D2CB9BC10F95 CRC64;
 Query Match 62.7%; Score 37; DB 1; Length 377;
 Best Local Similarity 85.7%; Pred. No. 17;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 4 NYGSFDY 10 :|||||
 DB 106 DYGSFDY 112
 RESULT 11
 ID OMS2_SALTI STANDARD; PRT; 383 AA.
 AC Q56111;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Outer membrane protein S2 precursor.
 GN OMPS2 OR STY1649.
 OS Salmonella typhi.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Salmonella.
 OX NCBI_TaxID=601;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=IMSS-1;
 RA Fernandez-Mora M., Calva E.;
 RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CT18;
 RX MEDLINE=21534947; PubMed=11677608;
 RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
 RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
 RA Baker S., Basham D., Brooks K., Chillingworth T., Conneron P.,
 RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
 RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
 RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
 RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
 RA Whitehead S., Barrall B.G.;
 RT "Complete genome sequence of a multiple drug resistant Salmonella
 enterica serovar Typhi CT18.";


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RL Nature 413:848-852(2001).
CC -1- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane
CC (by similarity).
CC -----
CC -1- SIMILARITY: BELONGS TO THE OMPK/PHOE FAMILY OF PORINS.
CC -----
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CC -----
DR EMBL: X89756; CAA61903.1; -.
DR EMBL: AL627271; CAD01894.1; -.
DR HSSP: Q48473; IOSM.
DR InterPro: IPR003229; OMP_2.
DR InterPro: IPR001702; Porin_gram-ve.
DR Pfam: PF00267; Gram-ve_porins; 1.
DR PRINTS: PR00182; ECOLNEIPORIN.
KW Outer membrane; Transmembrane; Porin; Signal; Complete proteome.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 383 OUTER MEMBRANE PROTEIN S2.
SQ SEQUENCE 383 AA; 42183 MW; 47CFB6B5F6A2370F CRC64;

Query Match 62.7%; Score 37; DB 1; Length 383;
Best Local Similarity 85.7%; Pred. No. 17;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 NYGSFDY 10
Db 106 DYGSFDY 112
:|||||

RESULT 12
LPIA_DROME
ID LPIA_DROME STANDARD; PRT; 789 AA.
AC P1195; Q9VYM4.
DT 01-OCT-1989 (Rel. 12, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Larval serum protein 1 alpha chain precursor (Hexamerin 1 alpha).
GN LSP1-ALPHA OR LSP1-A OR CG2559.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkelley.
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Randell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballwey R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Busch M.R., Butch J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos R., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodzik A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

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RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shie B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spler E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J., Yao Q.A.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RN SEQUENCE OF 1-84 FROM N.A.
RX MEDLINE=87060914; PubMed=3097321;
RA Delaney S.J., Smith D.F., McClelland A., Sunkel C., Glover D.M.;
RT "Sequence conservation around the 5' ends of the larval serum protein
RT 1 genes of Drosophila melanogaster.";
RL J. Mol. Biol. 189:1-11(1986).
RN [3]
RN SEQUENCE OF 1-52 FROM N.A.
RP Jowett T.;
RA "The regulatory domain of a larval serum protein gene in Drosophila
RT melanogaster.";
RL EMBO J. 4:3789-3795(1985).
CC -1- FUNCTION: LARVAL STORAGE PROTEIN (LSP) WHICH MAY SERVE AS A STORE
CC OF AMINO ACIDS FOR SYNTHESIS OF ADULT PROTEINS (BY SIMILARITY).
CC -1- SUBUNIT: HETEROHEXAMER, COMPOSED OF THREE SUBUNITS, ALPHA, BETA
CC AND GAMMA.
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- TISSUE SPECIFICITY: LARVAL HEMOLYMPH.
CC -1- SIMILARITY: TO ARYLPHORINS AND TO ARTHROPOD HEMOCYANINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AE003489; AAF48168.1; -.
DR EMBL: X03872; CAA27506.1; -.
DR EMBL: X03368; CAA27066.1; -.
DR PIR: A27144; A27144.
DR HSSP: P04253; ILLA.
DR FlyBase: FBgn0002562; Lsp1-alpha.
DR InterPro: IPR000896; Hemocyanin.
DR InterPro: IPR005203; hemocyanin_C.
DR InterPro: IPR005204; hemocyanin_N.
DR Pfam: PF00372; hemocyanin; 1.
DR Pfam: PF03722; hemocyanin_N; 1.
DR Pfam: PF03723; hemocyanin_C; 1.
DR PRINTS: PR00187; HAEMOCYANIN.
DR PROSITE: PS00209; HEMOCYANIN.1; FALSE_NEG.
DR PROSITE: PS00210; HEMOCYANIN2; 1.
KW Signal; Hemolymph; Storage protein; Glycoprotein; Multigene family.
FT SIGNAL 1 16 POTENTIAL.
FT CHAIN 17 789 LARVAL SERUM PROTEIN 1 ALPHA CHAIN.
SQ SEQUENCE 789 AA; 95883 MW; 47F3F21B05D53795 CRC64;

Query Match 62.7%; Score 37; DB 1; Length 789;
Best Local Similarity 85.7%; Pred. No. 36;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 NYGSFDY 10
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Db 770 NYGHFDY 776
RESULT 13
LP1B_DROME STANDARD; PRT; 789 AA.
AC P11996; Q9VPV2;
DT 01-OCT-1989 (Rel. 12, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Larval serum protein 1 beta chain precursor (Hexamerin 1 beta).
GN LSP1-BETA OR LSP1-B OR CG4178.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Canton-S;
RX MEDLINE=97274657; PubMed=9128742;
RA Massey H.C. Jr., Keizlarova-Lepesant J., Willis R.L.,
RA Castleberry A.B., Benes H.;
RT "The Drosophila Lsp-1 beta gene. A structural and phylogenetic
RL analysis.";
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Anantides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Artil J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jaisall M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RN [3]
RP SEQUENCE OF 1-100 FROM N.A.
RX MEDLINE=87060914; PubMed=1097321;
RA Delaney S.J., Smith D.F., McClelland A., Sunkel C., Glover D.M.;
RT "Sequence conservation around the 5' ends of the larval serum protein

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RT 1 genes of Drosophila melanogaster.";
RL J. Mol. Biol. 189:1-11(1986).
CC -!- FUNCTION: LARVAL STORAGE PROTEIN (LSP) WHICH MAY SERVE AS A STORE
CC OF AMINO ACIDS FOR SYNTHESIS OF ADULT PROTEINS (BY SIMILARITY).
CC -!- SUBUNIT: HETEROHEXAMER, COMPOSED OF THREE SUBUNITS, ALPHA, BETA
CC AND GAMMA.
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- TISSUE SPECIFICITY: LARVAL HEMOLYMPH.
CC -!- SIMILARITY: TO ARYLPHORINS AND TO ARTHROPOD HEMOCYANINS.
CC
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CC
CC -----
CC EMBL: U63556; AAB58821.1;
CC EMBL: AE003588; AAF51434.1;
CC EMBL: X03873; CAA27507.1;
CC PIR: B27144; B27144.
CC HSSP: P04253; IOXY.
CC FlyBase: FBgn002563; Lsp1-beta.
CC InterPro: IPR000896; Hemocyanin.
CC InterPro: IPR005203; hemocyanin_C.
CC InterPro: IPR005204; hemocyanin_N.
CC Pfam: PF00372; hemocyanin; 1.
CC Pfam: PF03723; hemocyanin_C; 1.
CC PRINTS: PR00187; HAEMOCYANIN.
CC PROSITE: PS00209; HEMOCYANIN_1; FALSE_NEG.
CC PROSITE: PS00210; HEMOCYANIN_2; 1.
CC Signal: Hemolymph; Storage protein; Glycoprotein; Multigene family.
CC SIGNAL 1 16 POTENTIAL.
CC CHAIN 17 789 LARVAL SERUM PROTEIN 1 BETA CHAIN.
CC CONFLICT 275 275 T -> N (IN REF. 1).
CC CONFLICT 725 725 S -> R (IN REF. 1).
CC SEQUENCE 789 AA; 95913 MW; AE12594515806A5B CRC64;
Query Match 62.7%; Score 37; DB 1; Length 789;
Best Local Similarity 85.7%; Pred. No. 36;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4 NYGSFDY 10
Db 770 NYGHFDY 776
RESULT 14
OMPF_XENNE STANDARD; PRT; 369 AA.
AC Q56828;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Outer membrane protein F precursor (Porin ompF) (Outer membrane
DE protein ompP).
CN OMPF OR OMP.
OS Xenorhabdus nematophilus.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Xenorhabdus.
OX NCBI_TaxID=628;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ANG/1;
RX MEDLINE=96414477; PubMed=8817498;
RA Forst S., Waukau J., Leisman G., Exner M., Hancock R.;
RT "Functional and regulatory analysis of the OmpF-like porin, OmpP, of
RT the symbiotic bacterium Xenorhabdus nematophilus.";
RL Mol. Microbiol. 18:779-789(1995).
CC -!- FUNCTION: OMPF IS A PORIN THAT PASSIVE DIFFUSION PORES WHICH ALLOW
CC SMALL MOLECULAR WEIGHT HYDROPHILIC MATERIALS ACROSS THE OUTER

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CC MEMBRANE (BY SIMILARITY).
CC -!- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
CC -!- SIMILARITY: BELONGS TO THE OMPC/PHOE FAMILY OF PORINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; L40919; AAB41114.1; -.
CC HSSP; P02932; lPHO.
CC InterPro; IPR003229; OMP_2.
CC InterPro; IPR001702; Porin_gram-ve.
CC Pfam; PF00267; Gram-ve_porins; 1.
CC PRINTS; PR00182; ECOLNEIPORIN.
CC PROSITE; PS00576; GRAM_NEG_PORIN; 1.
CC Outer membrane; Transmembrane; Porin; Signal.
CC SIGNAL 1 21 POTENTIAL.
CC CHAIN 22 369 OUTER MEMBRANE PROTEIN F.
CC SEQUENCE 369 AA; 40851 MW; 20E30CA680F8557A CRC64;
CC -----
Query Match 61.0%; Score 36; DB 1; Length 369;
Best Local Similarity 85.7%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
CC -----
QY 4 NYGSFDY 10
DB 107 NYGSLDY 113
DB -----
RESULT 15
OMSI_SALTI
ID OM51_SALTI STANDARD; PRT; 394 AA.
AC Q56110;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Outer membrane protein S1 precursor.
GN OMPS1 OR STY2203.
OS Salmonella typhi.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=601;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IMSS-1;
RX MEDLINE=95309727; PubMed=7789812;
RA Fernandez-Mora M., Oropeza R., Puente J.L., Calva E.;
RT "Isolation and characterization of ompS1, a novel Salmonella typhi
RL outer membrane protein-encoding gene.";
RL Gene 158:67-72(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrall B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18.";
RL Nature 413:848-852(2001).
CC -!- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane
CC (By similarity).

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CC -!- SIMILARITY: BELONGS TO THE OMPC/PHOE FAMILY OF PORINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X73237; CAA51710.1; -.
CC HSSP; P02931; lGFN.
CC InterPro; IPR003229; OMP_2.
CC InterPro; IPR001702; Porin_gram-ve.
CC Pfam; PF00267; Gram-ve_porins; 1.
CC PRINTS; PR00182; ECOLNEIPORIN.
CC PROSITE; PS00576; GRAM_NEG_PORIN; 1.
CC Signal; Outer membrane; Transmembrane; Porin; Complete proteome.
CC SIGNAL 1 21 POTENTIAL.
CC CHAIN 22 394 OUTER MEMBRANE PROTEIN S1.
CC SEQUENCE 394 AA; 43253 MW; E7C8FEED424931D1 CRC64;
CC -----
Query Match 61.0%; Score 36; DB 1; Length 394;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC -----
QY 5 YGSFDY 10
DB 107 YGSFDY 112
DB -----
Search completed: November 18, 2002, 17:33:25
Job time : 3.45098 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:01 : Search time 10.4412 Seconds
(without alignments)
197.341 Million cell updates/sec

Title: US-09-016-061-64
Perfect score: 59
Sequence: 1 ARHNGSFDY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mmc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	43	72.9	839	Q9LIE5	Q9LIE5 arabidopsis
2	42	71.2	78	Q9MW76	Q9mw76 leopardus p
3	42	71.2	78	Q9MW75	Q9mw75 leopardus p
4	42	71.2	78	Q9MW74	Q9mw74 leopardus p
5	42	71.2	79	Q9MX19	Q9mx19 leopardus p
6	42	71.2	79	Q9MX13	Q9mx13 leopardus p
7	42	71.2	79	Q9MX03	Q9mx03 leopardus p
8	42	71.2	79	Q9MX00	Q9mx00 leopardus p
9	42	71.2	79	Q9MW29	Q9mw29 leopardus p
10	42	71.2	79	Q9MW28	Q9mw28 leopardus p
11	42	71.2	79	Q9MW27	Q9mw27 leopardus p
12	42	71.2	79	Q9MW29	Q9mw29 leopardus p
13	42	71.2	79	Q9MW18	Q9mw18 leopardus p
14	42	71.2	79	Q9MW16	Q9mw16 leopardus p
15	42	71.2	79	Q9MW15	Q9mw15 leopardus p
16	42	71.2	79	Q9MW14	Q9mw14 leopardus p

17	42	71.2	79	Q9MWY3	Q9mwy3 leopardus p
18	42	71.2	79	Q9MWX6	Q9mwx6 leopardus p
19	42	71.2	79	Q9MWX5	Q9mwx5 leopardus p
20	42	71.2	79	Q9MWX4	Q9mwx4 leopardus p
21	42	71.2	79	Q9MWX1	Q9mwx1 leopardus p
22	42	71.2	79	Q9MWX0	Q9mwx0 leopardus p
23	42	71.2	79	Q9MWV9	Q9mwv9 leopardus p
24	42	71.2	79	Q9MWV7	Q9mwv7 leopardus p
25	42	71.2	79	Q9MWV4	Q9mwv4 leopardus p
26	42	71.2	79	Q9MWV9	Q9mwv9 leopardus p
27	42	71.2	79	Q9MWV2	Q9mwv2 leopardus p
28	42	71.2	79	Q9MWU4	Q9mwu4 leopardus p
29	42	71.2	79	Q9MWU2	Q9mwu2 leopardus p
30	42	71.2	79	Q9MWU1	Q9mwu1 leopardus p
31	42	71.2	79	Q9MWT9	Q9mwt9 leopardus p
32	42	71.2	79	Q9MWS7	Q9mws7 leopardus p
33	42	71.2	79	Q9MWS2	Q9mws2 leopardus p
34	42	71.2	79	Q9MWS0	Q9mws0 leopardus p
35	42	71.2	79	Q9MWR9	Q9mwr9 leopardus p
36	42	71.2	79	Q9MWR8	Q9mwr8 leopardus p
37	42	71.2	79	Q9MWQ4	Q9mwq4 leopardus w
38	42	71.2	79	Q9MWQ3	Q9mwq3 leopardus w
39	42	71.2	79	Q9MWQ2	Q9mwq2 leopardus w
40	42	71.2	79	Q9MWQ6	Q9mwq6 leopardus w
41	42	71.2	79	Q9MWP4	Q9mwp4 leopardus w
42	42	71.2	79	Q9MWP3	Q9mwp3 leopardus w
43	42	71.2	79	Q9MWP2	Q9mwp2 leopardus w
44	42	71.2	79	Q9MWP1	Q9mwp1 leopardus w
45	42	71.2	79	Q9MWN4	Q9mwn4 leopardus w

ALIGNMENTS

RESULT 1

Q9LIE5 PRELIMINARY: PRT; 839 AA.
AC Q9LIE5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Far-red impaired response protein, mutator-like transposase-like
DE protein, phytochrome A signaling protein-like.
OS Arabidopsis thaliana (Mouse-ear cross).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=20363099; PubMed=10907853;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.
RT Sequence features of the regions of 4,251,695 bp covered by ninety P1,
RT TAC and BAC clones.";
RL DNA Res. 7:217-221(2000).
DR EMBL; AP001306; BAB03065.1; -;
DR InterPro; IPR004330; FARI.
DR InterPro; IPR001000; Glyco_hydro_10.
DR Pfam; PF03101; FARI; 1.
DR PROSITE; PS00591; GLYCOSYL_HYDROL_F10; UNKNOWN1.
SQ SEQUENCE 839 AA; 95996 MW; CBBF60DF8B6797F8 CRC64;

Query Match 72.9%; Score 43; DB 10; Length 839;
Best Local Similarity 87.5%; Pred. No. 19;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNGSF 8
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Db 274 SRHNGSF 281

RESULT 2

Q9MWT6 PRELIMINARY; PRT; 78 AA.
ID Q9MWT6;
AC Q9MWT6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II DR antigen beta subunit (Fragment).
GN LEPA-DRB.
OS Leopardus pardalis (Ocelot).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Leopardus.
OX NCBI_TaxID=32538;
RN [1]
RP SEQUENCE FROM N.A.
RA Yuhki N., Eizirik E., Johnson W.E., O'Brien S.J.;
RT "Sequence Diversity of Major Histocompatibility Complex Class II DRB
Exon 2 Region of Two Sister Species of the Felidae, Ocelot (Leopardus
pardalis) and Margay (Leopardus wiedii).";
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF057894; AAF70946.1; -.
DR InterPro; IPR000353; MHC_II_beta.
DR Pfam; PF00969; MHC_II_beta.1.
DR ProDom; PD000328; MHC_II_beta.1.
KW Glycoprotein; MHC II; Transmembrane.
FT NON_TER 1
FT NON_TER 78
SQ SEQUENCE 78 AA; 9559 MW; 77863043708EC5B8 CRC64;

Query Match 71.2%; Score 42; DB 7; Length 78;

Best Local Similarity 87.5%; Pred. No. 2.1;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFD 9
:|||||
Db 71 RHNYGVFD 78

RESULT 3

Q9MWT5 PRELIMINARY; PRT; 78 AA.
ID Q9MWT5;
AC Q9MWT5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II DR antigen beta subunit (Fragment).
GN LEPA-DRB.
OS Leopardus pardalis (Ocelot).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Leopardus.
OX NCBI_TaxID=32538;
RN [1]
RP SEQUENCE FROM N.A.
RA Yuhki N., Eizirik E., Johnson W.E., O'Brien S.J.;
RT "Sequence Diversity of Major Histocompatibility Complex Class II DRB
Exon 2 Region of Two Sister Species of the Felidae, Ocelot (Leopardus
pardalis) and Margay (Leopardus wiedii).";
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF057895; AAF70947.1; -.
DR InterPro; IPR000353; MHC_II_beta.
DR Pfam; PF00969; MHC_II_beta.1.
DR ProDom; PD000328; MHC_II_beta.1.
KW Glycoprotein; MHC II; Transmembrane.
FT NON_TER 1
FT NON_TER 78
SQ SEQUENCE 78 AA; 9559 MW; 5076280FF45EC5A7 CRC64;

Query Match 71.2%; Score 42; DB 7; Length 78;

Best Local Similarity 87.5%; Pred. No. 2.1;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFD 9
:|||||
Db 71 RHNYGVFD 78

RESULT 4

Q9MWT4 PRELIMINARY; PRT; 78 AA.
ID Q9MWT4;
AC Q9MWT4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II DR antigen beta subunit (Fragment).
GN LEPA-DRB.
OS Leopardus pardalis (Ocelot).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Leopardus.
OX NCBI_TaxID=32538;
RN [1]
RP SEQUENCE FROM N.A.
RA Yuhki N., Eizirik E., Johnson W.E., O'Brien S.J.;
RT "Sequence Diversity of Major Histocompatibility Complex Class II DRB
Exon 2 Region of Two Sister Species of the Felidae, Ocelot (Leopardus
pardalis) and Margay (Leopardus wiedii).";
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF057896; AAF70948.1; -.
DR InterPro; IPR000353; MHC_II_beta.
DR Pfam; PF00969; MHC_II_beta.1.
DR ProDom; PD000328; MHC_II_beta.1.
KW Glycoprotein; MHC II; Transmembrane.
FT NON_TER 1
FT NON_TER 78
SQ SEQUENCE 78 AA; 9586 MW; 77863043709666B8 CRC64;

Query Match 71.2%; Score 42; DB 7; Length 78;

Best Local Similarity 87.5%; Pred. No. 2.1;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFD 9
:|||||
Db 71 RHNYGVFD 78

RESULT 5

Q9MX19 PRELIMINARY; PRT; 79 AA.
ID Q9MX19;
AC Q9MX19;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II DR antigen beta subunit (Fragment).
GN LEPA-DRB.
OS Leopardus pardalis (Ocelot).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Leopardus.
OX NCBI_TaxID=32538;
RN [1]
RP SEQUENCE FROM N.A.
RA Yuhki N., Eizirik E., Johnson W.E., O'Brien S.J.;
RT "Sequence Diversity of Major Histocompatibility Complex Class II DRB
Exon 2 Region of Two Sister Species of the Felidae, Ocelot (Leopardus
pardalis) and Margay (Leopardus wiedii).";
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF057809; AAF70863.1; -.
DR InterPro; IPR000353; MHC_II_beta.
DR Pfam; PF00969; MHC_II_beta.1.
DR ProDom; PD000328; MHC_II_beta.1.
KW Glycoprotein; MHC II; Transmembrane.
FT NON_TER 1
FT NON_TER 79

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SQ SEQUENCE 79 AA; 9609 MW; AEFDAF00716CF706 CRC64;
Query Match 71.2%; Score 42; DB 7; Length 79;
Best Local Similarity 87.5%; Pred. No. 2.1;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFD 9
    ||||| ||
Db 72 RHNYGVFD 79

RESULT 6
Q9MX13 PRELIMINARY; PRT; 79 AA.
AC Q9MX13;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II DR antigen beta subunit (Fragment).
GN LEPA-DRB.
OS Leopardus pardalis (Ocelot).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Leopardus.
OX NCBI_TaxID=32538;
RN [1]
RP SEQUENCE FROM N.A.
RA Yuhki N., Eizirik E., Johnson W.E., O'Brien S.J.;
RT "Sequence Diversity of Major Histocompatibility Complex Class II DRB
RT Exon 2 Region of Two Sister Species of the Felidae, Ocelot (Leopardus
RT pardalis) and Margay (Leopardus wiedii).";
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF057815; AAF70869.1;
DR InterPro: IPR000353; MHC_II_beta.
DR Pfam: PF00969; MHC_II_beta; 1.
DR ProDom: PD000328; MHC_II_beta; 1.
KW Glycoprotein; MHC II; Transmembrane.
FT NON_TER 1
FT NON_TER 79
SQ SEQUENCE 79 AA; 9719 MW; 142CE54986194002 CRC64;

Query Match 71.2%; Score 42; DB 7; Length 79;
Best Local Similarity 87.5%; Pred. No. 2.1;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

-QY 2 RHNYGSFD 9
    ||||| ||
Db 72 RHNYGVFD 79

RESULT 7
Q9MX03 PRELIMINARY; PRT; 79 AA.
AC Q9MX03;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II DR antigen beta subunit (Fragment).
GN LEPA-DRB.
OS Leopardus pardalis (Ocelot).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Leopardus.
OX NCBI_TaxID=32538;
RN [1]
RP SEQUENCE FROM N.A.
RA Yuhki N., Eizirik E., Johnson W.E., O'Brien S.J.;
RT "Sequence Diversity of Major Histocompatibility Complex Class II DRB
RT Exon 2 Region of Two Sister Species of the Felidae, Ocelot (Leopardus
RT pardalis) and Margay (Leopardus wiedii).";
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF057825; AAF70879.1;
DR InterPro: IPR000353; MHC_II_beta.
DR Pfam: PF00969; MHC_II_beta; 1.
DR ProDom: PD000328; MHC_II_beta; 1.

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KW Glycoprotein; MHC II; Transmembrane.
FT NON_TER 1
FT NON_TER 79
SQ SEQUENCE 79 AA; 9655 MW; 5CD326710D9302F8 CRC64;

Query Match 71.2%; Score 42; DB 7; Length 79;
Best Local Similarity 87.5%; Pred. No. 2.1;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFD 9
    ||||| ||
Db 72 RHNYGVFD 79

RESULT 8
Q9MX00 PRELIMINARY; PRT; 79 AA.
AC Q9MX00;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II DR antigen beta subunit (Fragment).
GN LEPA-DRB.
OS Leopardus pardalis (Ocelot).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Leopardus.
OX NCBI_TaxID=32538;
RN [1]
RP SEQUENCE FROM N.A.
RA Yuhki N., Eizirik E., Johnson W.E., O'Brien S.J.;
RT "Sequence Diversity of Major Histocompatibility Complex Class II DRB
RT Exon 2 Region of Two Sister Species of the Felidae, Ocelot (Leopardus
RT pardalis) and Margay (Leopardus wiedii).";
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF057828; AAF70882.1;
DR InterPro: IPR000353; MHC_II_beta.
DR Pfam: PF00969; MHC_II_beta; 1.
DR ProDom: PD000328; MHC_II_beta; 1.
KW Glycoprotein; MHC II; Transmembrane.
FT NON_TER 1
FT NON_TER 79
SQ SEQUENCE 79 AA; 9550 MW; A046AC2E31A3DEA0 CRC64;

Query Match 71.2%; Score 42; DB 7; Length 79;
Best Local Similarity 87.5%; Pred. No. 2.1;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFD 9
    ||||| ||
Db 72 RHNYGVFD 79

RESULT 9
Q9MWZ9 PRELIMINARY; PRT; 79 AA.
AC Q9MWZ9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II DR antigen beta subunit (Fragment).
GN LEPA-DRB.
OS Leopardus pardalis (Ocelot).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Leopardus.
OX NCBI_TaxID=32538;
RN [1]
RP SEQUENCE FROM N.A.
RA Yuhki N., Eizirik E., Johnson W.E., O'Brien S.J.;
RT "Sequence Diversity of Major Histocompatibility Complex Class II DRB
RT Exon 2 Region of Two Sister Species of the Felidae, Ocelot (Leopardus
RT pardalis) and Margay (Leopardus wiedii).";
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF057829; AAF70883.1;

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DR InterPro: IPR000353; MHC_II_beta.
DR Pfam: PF00969; MHC_II_beta; 1.
DR ProDom: PD000328; MHC_II_beta; 1.
KW Glycoprotein; MHC II; Transmembrane.
FT NON_TER 1 1
FT NON_TER 79 79
SQ SEQUENCE 79 AA; 9590 MW; 47B12695AF98C5A CRC64;

Query Match 71.2%; Score 42; DB 7; Length 79;
Best Local Similarity 87.5%; Pred. No. 2.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHNYGSFD 9
Db 72 RHNYGVFD 79

RESULT 10
Q9MWZ8 PRELIMINARY; PRT; 79 AA.
AC Q9MWZ8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II DR antigen beta subunit (Fragment).
GN LEPA-DRB.
OS Leopardus pardalis (Ocelot).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Leopardus.
OX NCBI_TaxID=32538;
RN [1]
RP SEQUENCE FROM N.A.
RA Yuhki N., Elzirik E., Johnson W.E., O'Brien S.J.;
RT "Sequence Diversity of Major Histocompatibility Complex Class II DRB
RT Exon 2 Region of Two Sister Species of the Felidae, Ocelot (Leopardus
RT pardalis) and Margay (Leopardus wiedii).";
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF057831; AAF70884.1; -.
DR InterPro: IPR000353; MHC_II_beta.
DR Pfam: PF00969; MHC_II_beta; 1.
DR ProDom: PD000328; MHC_II_beta; 1.
KW Glycoprotein; MHC II; Transmembrane.
FT NON_TER 1 1
FT NON_TER 79 79
SQ SEQUENCE 79 AA; 9608 MW; 2FF7C4996FE32BB CRC64;

Query Match 71.2%; Score 42; DB 7; Length 79;
Best Local Similarity 87.5%; Pred. No. 2.1;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFD 9
Db 72 RHNYGVFD 79

RESULT 11
Q9MWZ7 PRELIMINARY; PRT; 79 AA.
AC Q9MWZ7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II DR antigen beta subunit (Fragment).
GN LEPA-DRB.
OS Leopardus pardalis (Ocelot).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Leopardus.
OX NCBI_TaxID=32538;
RN [1]
RP SEQUENCE FROM N.A.
RA Yuhki N., Elzirik E., Johnson W.E., O'Brien S.J.;
RT "Sequence Diversity of Major Histocompatibility Complex Class II DRB
RT Exon 2 Region of Two Sister Species of the Felidae, Ocelot (Leopardus

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RT pardalis) and Margay (Leopardus wiedii).";
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF057832; AAF70885.1; -.
DR InterPro: IPR000353; MHC_II_beta.
DR Pfam: PF00969; MHC_II_beta; 1.
DR ProDom: PD000328; MHC_II_beta; 1.
KW Glycoprotein; MHC II; Transmembrane.
FT NON_TER 1 1
FT NON_TER 79 79
SQ SEQUENCE 79 AA; 9592 MW; 2FF6F64F235B68918 CRC64;

Query Match 71.2%; Score 42; DB 7; Length 79;
Best Local Similarity 87.5%; Pred. No. 2.1;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFD 9
Db 72 RHNYGVFD 79

RESULT 12
Q9MWY9 PRELIMINARY; PRT; 79 AA.
AC Q9MWY9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II DR antigen beta subunit (Fragment).
GN LEPA-DRB.
OS Leopardus pardalis (Ocelot).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Leopardus.
OX NCBI_TaxID=32538;
RN [1]
RP SEQUENCE FROM N.A.
RA Yuhki N., Elzirik E., Johnson W.E., O'Brien S.J.;
RT "Sequence Diversity of Major Histocompatibility Complex Class II DRB
RT Exon 2 Region of Two Sister Species of the Felidae, Ocelot (Leopardus
RT pardalis) and Margay (Leopardus wiedii).";
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF057840; AAF70893.1; -.
DR InterPro: IPR000353; MHC_II_beta.
DR Pfam: PF00969; MHC_II_beta; 1.
DR ProDom: PD000328; MHC_II_beta; 1.
KW Glycoprotein; MHC II; Transmembrane.
FT NON_TER 1 1
FT NON_TER 79 79
SQ SEQUENCE 79 AA; 9776 MW; 39FBA0F34A45D79 CRC64;

Query Match 71.2%; Score 42; DB 7; Length 79;
Best Local Similarity 87.5%; Pred. No. 2.1;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFD 9
Db 72 RHNYGVFD 79

RESULT 13
Q9MWY8 PRELIMINARY; PRT; 79 AA.
AC Q9MWY8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II DR antigen beta subunit (Fragment).
GN LEPA-DRB.
OS Leopardus pardalis (Ocelot).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Leopardus.
OX NCBI_TaxID=32538;
RN [1]
RP SEQUENCE FROM N.A.

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RA Yuhki N., Elzirik E., Johnson W.E., O'Brien S.J.;
RT "Sequence Diversity of Major Histocompatibility Complex Class II DRB
RT Exon 2 Region of Two Sister Species of the Felidae, Ocelot (Leopardus
RT pardalis) and Margay (Leopardus wiedii).";
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF057841; AAF70894.1; -.
DR InterPro; IPR000353; MHC_II_beta.
DR Pfam; PF00969; MHC_II_beta; 1.
DR ProDom; PD000328; MHC_II_beta; 1.
KW Glycoprotein; MHC II; Transmembrane.
FT NON_TER 1
FT NON_TER 79
SQ SEQUENCE 79 AA; 9673 MW; E698AB6C06764E32 CRC64;

Query Match 71.2%; Score 42; DB 7; Length 79;
Best Local Similarity 87.5%; Pred. No. 2.1;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFD 9
Db |||||
72 RHNYGVFD 79

RESULT 14
Q9MWY6 PRELIMINARY; PRT; 79 AA.
AC Q9MWY6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II DR antigen beta subunit (Fragment).
GN LEPA-DRB.
OS Leopardus pardalis (Ocelot).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Leopardus.
OX NCBI_TaxID=32538;
RN [1]
RP SEQUENCE FROM N.A.
RA Yuhki N., Elzirik E., Johnson W.E., O'Brien S.J.;
RT "Sequence Diversity of Major Histocompatibility Complex Class II DRB
RT Exon 2 Region of Two Sister Species of the Felidae, Ocelot (Leopardus
RT pardalis) and Margay (Leopardus wiedii).";
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF057843; AAF70896.1; -.
DR InterPro; IPR000353; MHC_II_beta.
DR Pfam; PF00969; MHC_II_beta; 1.
DR ProDom; PD000328; MHC_II_beta; 1.
KW Glycoprotein; MHC II; Transmembrane.
FT NON_TER 1
FT NON_TER 79
SQ SEQUENCE 79 AA; 9598 MW; E3916A304302D83B CRC64;

Query Match 71.2%; Score 42; DB 7; Length 79;
Best Local Similarity 87.5%; Pred. No. 2.1;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFD 9
Db |||||
72 RHNYGVFD 79

RESULT 15
Q9MWY5 PRELIMINARY; PRT; 79 AA.
AC Q9MWY5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II DR antigen beta subunit (Fragment).
GN LEPA-DRB.
OS Leopardus pardalis (Ocelot).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Leopardus.
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OX NCBI_TaxID=32538;
RN [1]
RP SEQUENCE FROM N.A.
RA Yuhki N., Elzirik E., Johnson W.E., O'Brien S.J.;
RT "Sequence Diversity of Major Histocompatibility Complex Class II DRB
RT Exon 2 Region of Two Sister Species of the Felidae, Ocelot (Leopardus
RT pardalis) and Margay (Leopardus wiedii).";
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF057844; AAF70897.1; -.
DR InterPro; IPR000353; MHC_II_beta.
DR Pfam; PF00969; MHC_II_beta; 1.
DR ProDom; PD000328; MHC_II_beta; 1.
KW Glycoprotein; MHC II; Transmembrane.
FT NON_TER 1
FT NON_TER 79
SQ SEQUENCE 79 AA; 9528 MW; 93E16A304FF0430B CRC64;

Query Match 71.2%; Score 42; DB 7; Length 79;
Best Local Similarity 87.5%; Pred. No. 2.1;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFD 9
Db |||||
72 RHNYGVFD 79
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Search completed: November 18, 2002, 17:40:44
Job time : 10.4912 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:21:57 ; Search time 13 8235 Seconds
(without alignments)
96.394 Million cell updates/sec

Title: US-09-016-061-64

Perfect score: 59

Sequence: 1 ARHNYGSFDY 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	59	100.0	10	22	AAW76022
3	51	86.4	10	19	AAW76010
4	51	86.4	10	22	AAW76010
5	51	86.4	117	19	AAW76001
6	51	86.4	117	19	AAW76001
7	51	86.4	117	20	AAW76001
8	51	86.4	117	20	AAW76001
9	51	86.4	117	22	AAW76001
10	51	86.4	117	22	AAW76001

11	51	86.4	117	22	AAW76022	Vitaxin heavy chain
12	51	86.4	117	22	AAW76022	Antibody LM609 hea
13	51	86.4	118	20	AAW76022	Humanised LM609 an
14	51	86.4	118	20	AAW76022	Humanised LM609 an
15	51	86.4	118	20	AAW76022	Humanised LM609 an
16	51	86.4	118	20	AAW76022	Humanised LM609 an
17	51	86.4	130	20	AAW76022	Murine monoclonal
18	50	84.7	10	19	AAW76022	LM609 grafted anti
19	50	84.7	10	22	AAW76022	Mutant VH CDR3 pep
20	49	83.1	117	16	AAW76022	Human IgE receptor
21	49	83.1	117	16	AAW76022	Human IgE receptor
22	49	83.1	117	18	AAW76022	Heavy chain variab
23	49	83.1	117	18	AAW76022	Heavy chain variab
24	49	83.1	117	18	AAW76022	Heavy chain variab
25	49	83.1	239	20	AAW76022	Human antiFc epsil
26	49	83.1	242	20	AAW76022	Human antiFc epsil
27	48	81.4	10	19	AAW76022	LM609 grafted anti
28	48	81.4	10	22	AAW76022	Mutant VH CDR3 pep
29	46	78.0	10	19	AAW76022	LM609 grafted anti
30	46	78.0	10	19	AAW76022	LM609 grafted anti
31	46	78.0	10	19	AAW76022	LM609 grafted anti
32	46	78.0	10	19	AAW76022	LM609 grafted anti
33	46	78.0	10	19	AAW76022	LM609 grafted anti
34	46	78.0	10	19	AAW76022	LM609 grafted anti
35	46	78.0	10	19	AAW76022	LM609 grafted anti
36	46	78.0	10	19	AAW76022	LM609 grafted anti
37	46	78.0	10	19	AAW76022	LM609 grafted anti
38	46	78.0	10	19	AAW76022	LM609 grafted anti
39	46	78.0	10	22	AAW76022	Mutant VH CDR3 pep
40	46	78.0	10	22	AAW76022	Mutant VH CDR3 pep
41	46	78.0	10	22	AAW76022	Mutant VH CDR3 pep
42	46	78.0	10	22	AAW76022	Mutant VH CDR3 pep
43	46	78.0	10	22	AAW76022	Mutant VH CDR3 pep
44	46	78.0	10	22	AAW76022	Mutant VH CDR3 pep
45	46	78.0	10	22	AAW76022	Mutant VH CDR3 pep

ALIGNMENTS

RESULT 1
AAW76022
ID AAW76022 standard; Protein; 10 AA.
XX
AC AAW76022;
XX
DT 02-NOV-1998 (first entry)
XX
DE LM609 grafted antibody V-H region CDR3 protein fragment #4.
XX
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
XX
OS Mus sp.
XX
PN WO9833919-A2.
XX
PD 06-AUG-1998.
XX
PF 30-JAN-1998; 98WO-US01826.
XX
PR 30-JAN-1997; 97US-0791391.
XX
PA (IXSY-) IXSYS INC.
XX
PI Glaser SM, Huse WD;
XX
DR WPI; 1998-437472/37.
DR N-PSDB; AAW49859.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 XX Claim 62; Page 41; 129pp; English.
 XX
 CC AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
 CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
 CC antibodies contain non-murine framework regions so are suitable for use
 CC in humans. Enhanced types of LM609 have affinity more than 90 times
 CC greater than that of parent the parent antibody.
 XX
 SQ Sequence 10 AA;

Query Match 100.0%; Score 59; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0013;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFDY 10
 |||||

Db 1 ARHNYGSFDY 10

RESULT 2

AA61380
 ID AAB61380 standard; peptide; 10 AA.

XX AAB61380;

DT 03-APR-2001 (first entry)

DE Mutant VH CDR3 peptide #3.

XX LM609; grafted antibody; alphavbeta3 integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis.
 XX

OS Unidentified.

XX WO200078815-A1.

XX 28-DEC-2000.

XX 23-JUN-2000; 2000WO-US17454.

XX 24-JUN-1999; 99US-0339922.

XX (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX Huse WD, Wu H;

XX WPI; 2001-050110/06.

XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -
 XX

XX Disclosure; Page 41; 132pp; English.

XX The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphavbeta3 integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphavbeta3-mediated diseases such as angiogenesis, inflammatory

CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.

XX Sequence 10 AA;

Query Match 100.0%; Score 59; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0013;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFDY 10
 |||||

Db 1 ARHNYGSFDY 10

RESULT 3

AAW76010

ID AAW76010 standard; protein; 10 AA.

XX AAW76010;

DT 02-NOV-1998 (first entry)

DE LM609 grafted antibody V-H region CDR3 protein fragment #1.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.

XX Mus sp.

XX WO9833919-A2.

XX 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

XX Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

XX N-PSDB; AAV49847.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX

PS Disclosure; Page 40; 129pp; English.

XX AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
 CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
 CC antibodies contain non-murine framework regions so are suitable for use
 CC in humans. Enhanced types of LM609 have affinity more than 90 times
 CC greater than that of parent the parent antibody.

XX Sequence 10 AA;

Query Match 86.4%; Score 51; DB 19; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.029; 1; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFDY 10
 DB 1 ARHNYGSFAY 10
 |||||

RESULT 4
 AAB61368
 ID AAB61368 standard; peptide; 10 AA.
 AC AAB61368;
 XX
 DT 03-APR-2001 (first entry)
 XX
 DE LM609 VH CDR3 peptide.
 XX
 KW LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis.
 XX

OS Unidentified.
 PN WO200078815-A1.
 XX
 PD 28-DEC-2000.
 XX

PF 23-JUN-2000; 2000WO-US17454.
 XX
 PR 24-JUN-1999; 99US-0339922.
 XX

PA (MOLE-) APPLIED MOLECULAR EVOLUTION.

PI Huse WD, Wu H;
 PI WPI; 2001-050110/06.
 DR

XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis.

PS Disclosure; Page 39; 132pp; English.

XX The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphavbeta_3 integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.

XX Sequence 10 AA;

Query Match 86.4%; Score 51; DB 22; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.029;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFDY 10
 DB 1 ARHNYGSFAY 10
 |||||

RESULT 5
 AAW76001
 ID AAW76001 standard; Protein; 117 AA.
 XX

AC AAW76001;
 XX
 DT 02-NOV-1998 (first entry)
 XX
 DE Vitaxin antibody heavy chain variable region protein fragment.
 XX
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.
 XX
 OS Mus sp.
 XX
 PN WO9833919-A2.
 XX
 PD 06-AUG-1998.
 XX
 PF 30-JAN-1998; 98WO-US01826.
 XX
 PR 30-JAN-1997; 97US-0791391.
 XX
 PA (IXSY-) IXSYS INC.
 XX
 PI Glaser SM, Huse WD;
 XX
 DR WPI; 1998-437472/37.
 DR N-PSDB; AAV49820.
 XX
 PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 PS Claim 1; Fig 1a; 129pp; English.
 XX
 CC This sequence represents a fragment of the vitaxin antibody variable
 CC heavy chain region. Vitaxin and the antibody LM609 bind selectively to
 CC integrin alphavbeta3 and can be used to inhibit binding of alphavbeta3
 CC to a ligand and thus block integrin-mediated signal transduction. This is
 CC useful in the treatment, prevention and diagnosis of alphavbeta3-mediated
 CC disease, specifically angiogenesis and restenosis (but also e.g.
 CC (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,
 CC cancer, psoriasis, rheumatoid arthritis, macular degeneration,
 CC osteoporosis etc.). The antibodies contain non-murine framework regions
 CC so are suitable for use in humans. Enhanced types of LM609 have affinity
 CC more than 90 times greater than that of parent the parent antibody.
 XX
 SQ Sequence 117 AA;
 Query Match 86.4%; Score 51; DB 19; Length 117;
 Best Local Similarity 90.0%; Pred. No. 0.37;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ARHNYGSFDY 10
 DB 97 ARHNYGSFAY 106
 |||||

RESULT 6
 AAW76003
 ID AAW76003 standard; Protein; 117 AA.
 XX
 AC AAW76003;
 XX
 DT 02-NOV-1998 (first entry)
 XX
 DE LM609 antibody heavy chain variable region protein fragment.
 XX
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;

KW macular degeneration; osteoporosis.

XX Mus sp.

XX WO9833919-A2.

XX 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

XX Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

XX N-PSDB; AAV49822.

XX Humanised antibody. Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis

XX Claim 43; Fig 2a; 129pp; English.

XX This sequence represents the LM609 antibody variable heavy chain region.
XX LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3
XX and can be used to inhibit binding of alphavbeta3 to a ligand and thus
XX block integrin-mediated signal transduction. This is useful in the
XX treatment, prevention and diagnosis of alphavbeta3-mediated disease,
XX specifically angiogenesis and restenosis (but also e.g. (non-)immune
XX inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
XX psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
XX etc.). The antibodies contain non-murine framework regions so are
XX suitable for use in humans. Enhanced types of LM609 have affinity more
XX than 90 times greater than that of parent the parent antibody.

XX Sequence 117 AA;

Query Match 86.4%; Score 51; DB 19; Length 117;

Best Local Similarity 90.0%; Pred. No. 0.37;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFDY 10

Db 97 ARHNYGSFAY 106

RESULT 7

AAV06381

ID AAY06381 standard; Protein; 117 AA.

XX AAY06381;

XX 06-SEP-1999 (first entry)

XX Murine monoclonal antibody LM609 VH region.

XX Humanised antibody; antibody humanisation; antibody engineering;
KW LM609; monoclonal antibody; complementarity determining region;
KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
KW cancer; therapy; diagnosis.

XX Mus musculus.

XX WO9929888-A1.

XX 17-JUN-1999.

XX 04-DEC-1998; 98WO-US25828.

XX 05-DEC-1997; 97US-0986016.

XX (SCRI) SCRIPPS RES INST.

XX Barbas CF, Rader C;

XX WPI; 1999-394979/33.

XX Production of humanized mouse monoclonal antibodies

XX Disclosure; Page 52-53; 55pp; English.

XX This sequence represents the heavy chain variable region of murine
CC monoclonal antibody LM609. LM609 is directed to integrin
CC alpha-v beta-3. It selectively promotes apoptosis of vascular
CC cells that have been stimulated to undergo angiogenesis, making it
CC a tool for cancer diagnosis and therapy. The invention provides
CC humanised antibodies, especially humanised LM609. In such humanized
CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
CC grafted onto a human light chain, and a heavy chain CDR from a mouse
CC antibody is grafted onto a human antibody heavy chain to produce
CC libraries from which a humanised murine antibody having the desired
CC specificity is selected. By preserving the original CDR sequences
CC such as the HCDR3 and LCDR3 sequences of LM609 (see AAY06371-72), the
CC humanisation strategy ensures epitope conservation.

XX Sequence 117 AA;

Query Match 86.4%; Score 51; DB 20; Length 117;

Best Local Similarity 90.0%; Pred. No. 0.37;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFDY 10

Db 97 ARHNYGSFAY 106

RESULT 8

AAV06387

ID AAY06387 standard; Protein; 117 AA.

XX AAY06387;

XX 06-SEP-1999 (first entry)

XX Humanised LM609 antibody VH domain.

XX Humanised antibody; antibody humanisation; antibody engineering;
KW LM609; monoclonal antibody; complementarity determining region;
KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
KW cancer; therapy; diagnosis.

XX Homo sapiens.

XX Synthetic.

XX Key Location/Qualifiers

FT Peptide 1..2 /note= "vector-encoded residues"

FT Region 31..35 /note= "CDR1"

FT Region 50..66 /note= "CDR2"

FT Region 107..117 /note= "CDR3"

XX WO9929888-A1.

XX 17-JUN-1999.

XX 04-DEC-1998; 98WO-US25828.

XX 05-DEC-1997; 97US-0986016.

XX (SCRI) SCRIPPS RES INST.

XX
PI Barbas CF, Rader C;
XX WPI; 1999-394979/33.
XX
XX Production of humanized mouse monoclonal antibodies
XX
XX Disclosure; Page 52; 55pp; English.
XX
XX This sequence represents the heavy chain variable region of a
XX humanized LM609 antibody. LM609 is directed to human integrin
XX alpha-v beta-3. It selectively promotes apoptosis of vascular
XX cells that have been stimulated to undergo angiogenesis, making it
XX a tool for cancer diagnosis and therapy. The invention provides
XX humanised antibodies, especially humanised LM609. In such humanized
XX antibodies, a light chain CDR from a mouse antibody such as LM609 is
XX grafted onto a human light chain, and a heavy chain CDR from a mouse
XX antibody is grafted onto a human antibody heavy chain to produce
XX libraries from which a humanised murine antibody having the desired
XX specificity is selected. By preserving the original CDR sequences
XX such as the HCDR3 and LCDR3 sequences of LM609 (see AAY06371-72), the
XX humanisation strategy ensures epitope conservation.
XX
SQ Sequence 117 AA;

Query Match 86.4%; Score 51; DB 20; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.37;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ARHNYGSFDY 10
Db 97 ARHNYGSFAY 106
|||||||

RESULT 9
AAG63587
ID AAG63587 standard; Protein; 117 AA.
XX
AC AAG63587;
XX
DT 15-OCT-2001 (first entry)
XX
DE A heavy chain variable region of LM609 grafted antibody.
XX
KW Grafted antibody; LM609; integrin; alphavbeta3; inflammatory disorder;
KW chronic articular rheumatism; psoriasis; diabetic retinopathy;
KW neovascular glaucoma; capillary proliferation; atherosclerotic plaque;
KW cancer.
XX
OS Mus sp.
XX
PN US2001011125-A1.
XX
PD 02-AUG-2001.
XX
PF 30-JAN-1997; 97US-0790540.
XX
PR 30-JAN-1997; 97US-0790540.
XX
PA (HUSE/) HUSE W D.
XX
PI Huse WD;
XX
XX WPI; 2001-496171/54.
DR N-PSDB; AAH74623.
XX
XX New LM609 grafted antibody exhibiting selective binding affinity to
XX PT alphavbeta3, comprising at least one LM609 grafted heavy and light
XX PT chain polypeptide, useful for diagnosing and treating e.g. inflammatory
XX PT disorders or cancer -
XX
XX Claim 1; Fig 1A; 25pp; English.

XX
CC The present sequence represents the heavy chain variable region of the
CC grafted monoclonal antibody LM609. LM609 is a murine antibody which
CC specifically recognises the integrin alphavbeta3, and inhibits its
CC functional activity. The LM609 grafted antibody has the
CC complementary determining regions (CDRs) substituted into a non-murine
CC framework. Nucleic acids encoding LM609 grafted heavy and light chain
CC polypeptides and fragments are useful in diagnostic and therapeutic
CC purposes, such as in the production of LM609 grafted antibodies and
CC fragments having binding specificity and inhibitory activity against
CC the integrin alphavbeta3. The antibody can be used for the diagnosis
CC or treatment of alphavbeta3-mediated diseases (e.g. inflammatory
CC disorders, chronic articular rheumatism, psoriasis, disorders
CC associated with inappropriate or inopportune invasion of vessels such
CC as diabetic retinopathy, neovascular glaucoma and capillary
CC proliferation in atherosclerotic plaques, or cancers), and to inhibit
CC binding activity of alphavbeta3 that are necessary for progression of
XX an alphavbeta3-mediated disease.
XX
SQ Sequence 117 AA;

Query Match 86.4%; Score 51; DB 22; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.37;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ARHNYGSFDY 10
Db 97 ARHNYGSFAY 106
|||||||

RESULT 10
AAG63589
ID AAG63589 standard; Protein; 117 AA.
XX
AC AAG63589;
XX
DT 15-OCT-2001 (first entry)
XX
DE A heavy chain variable region of LM609 antibody.
XX
KW Grafted antibody; LM609; integrin; alphavbeta3; inflammatory disorder;
KW chronic articular rheumatism; psoriasis; diabetic retinopathy;
KW neovascular glaucoma; capillary proliferation; atherosclerotic plaque;
KW cancer.
XX
OS Mus sp.
XX
PN US2001011125-A1.
XX
PD 02-AUG-2001.
XX
PF 30-JAN-1997; 97US-0790540.
XX
PR 30-JAN-1997; 97US-0790540.
XX
PA (HUSE/) HUSE W D.
XX
PI Huse WD;
XX
XX WPI; 2001-496171/54.
DR N-PSDB; AAH74625.
XX
XX New LM609 grafted antibody exhibiting selective binding affinity to
XX PT alphavbeta3, comprising at least one LM609 grafted heavy and light
XX PT chain polypeptide, useful for diagnosing and treating e.g. inflammatory
XX PT disorders or cancer -
XX
XX Disclosure; Fig 2A; 25pp; English.
XX
XX The present sequence represents the heavy chain variable region of the
XX monoclonal antibody LM609. LM609 is a murine antibody which specifically
XX recognises the integrin alphavbeta3, and inhibits its functional activity.
XX The specification describes a LM609 grafted antibody which has the

CC complementarity determining regions (CDRs) substituted into a non-murine
 CC framework. Nucleic acids encoding LM609 grafted heavy and light chain
 CC polypeptides and fragments are useful in diagnostic and therapeutic
 CC purposes, such as in the production of LM609 grafted antibodies and
 CC fragments having binding specificity and inhibitory activity against
 CC the integrin alphavbeta3. The antibody can be used for the diagnosis
 CC or treatment of alphavbeta3-mediated diseases (e.g. inflammatory
 CC disorders, chronic articular rheumatism, psoriasis, disorders
 CC associated with inappropriate or inopportune invasion of vessels such
 CC as diabetic retinopathy, neovascular glaucoma and capillary
 CC proliferation in atherosclerotic plaques, or cancers), and to inhibit
 CC binding activity of alphavbeta3 that are necessary for progression of
 CC an alphavbeta3-mediated disease.

XX SQ Sequence 117 AA;

Query Match 86.4%; Score 51; DB 22; Length 117;
 Best Local Similarity 90.0%; Pred. No. 0.37;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ARHNYGSFDY 10
 |||||
 Db 97 ARHNYGSFAY 106

RESULT 11

AAB61359
 ID AAB61359 standard; protein; 117 AA.

AC AAB61359;

DT 03-APR-2001 (first entry)

DE Vitaxin heavy chain variable region protein.

XX LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis.

XX Unidentified.

XX WO200078815-A1.

XX 28-DEC-2000.

XX 23-JUN-2000; 2000WO-US17454.

XX 24-JUN-1999; 99US-0339922.

XX (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX Huse WD, Wu H;

XX WPI; 2001-050110/06.

XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -

XX Disclosure; Fig 1; 132pp; English.

XX The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphavbeta_3 integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.

SQ Sequence 117 AA;

Query Match 86.4%; Score 51; DB 22; Length 117;
 Best Local Similarity 90.0%; Pred. No. 0.37;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ARHNYGSFDY 10
 |||||
 Db 97 ARHNYGSFAY 106

RESULT 12

AAB61361
 ID AAB61361 standard; protein; 117 AA.

XX AAB61361;

DT 03-APR-2001 (first entry)

DE Antibody LM609 heavy chain variable region protein.

XX LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis.

XX Unidentified.

XX WO200078815-A1.

XX 28-DEC-2000.

XX 23-JUN-2000; 2000WO-US17454.

XX 24-JUN-1999; 99US-0339922.

XX (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX Huse WD, Wu H;

XX WPI; 2001-050110/06.

XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -

XX Disclosure; Fig 2; 132pp; English.

XX The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphavbeta_3 integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.

SQ Sequence 117 AA;

Query Match 86.4%; Score 51; DB 22; Length 117;
 Best Local Similarity 90.0%; Pred. No. 0.37;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ARHNYGSFDY 10
 |||||
 Db 97 ARHNYGSFAY 106

RESULT 13

AAY06384
 ID AAY06384 standard; protein; 118 AA.

```

XX AC AAY06384;
XX DT
XX DE
XX DE 06-SEP-1999 (first entry)
XX DE Humanised LM609 antibody VH domain.
XX DE
XX KW Humanised antibody; antibody humanisation; antibody engineering;
XX KW LM609; monoclonal antibody; complementarity determining region;
XX KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
XX KW cancer; therapy; diagnosis.
XX OS Homo sapiens.
XX OS Synthetic.
XX FH
XX FT Key Location/Qualifiers
XX FT Peptide 1..2
XX FT /note= "vector-encoded residues"
XX FT Region 31..37
XX FT /note= "CDR1"
XX FT Region 52..67
XX FT /note= "CDR2"
XX FT Region 100..107
XX FT /note= "CDR3"
XX PN WO9929888-A1.
XX PD 17-JUN-1999.
XX PF 04-DEC-1998; 98WO-US25828.
XX PR 05-DEC-1997; 97US-0986016.
XX PA (SCRI ) SCRIPPS RES INST.
XX PI Barbas CF, Rader C;
XX PI WPI; 1999-394979/33.
XX DR Production of humanized mouse monoclonal antibodies
XX PT Disclosure; Page 51; 55pp; English.
XX PS
XX CC This sequence represents the heavy chain variable region of a
XX CC humanised LM609 antibody. LM609 is directed to human integrin
XX CC alpha-v beta-3. It selectively promotes apoptosis of vascular
XX CC cells that have been stimulated to undergo angiogenesis, making it
XX CC a tool for cancer diagnosis and therapy. The invention provides
XX CC humanised antibodies, especially humanised LM609. In such humanized
XX CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
XX CC grafted onto a human light chain, and a heavy chain CDR from a mouse
XX CC antibody is grafted onto a human antibody heavy chain to produce
XX CC libraries from which a humanised murine antibody having the desired
XX CC specificity is selected. By preserving the original CDR sequences
XX CC such as the HCDR3 and LCDR3 sequences of LM609 (see AAY06371-72), the
XX CC humanisation strategy ensures epitope conservation.
XX SQ
XX Sequence 118 AA;
XX Query Match 86.4%; Score 51; DB 20; Length 118;
XX Best Local Similarity 90.0%; Pred. No. 0.37;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX QY 1 ARHNYGSFDY 10
XX | | | | | | | |
XX Db 98 ARHNYGSFAY 107
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XX RESULT 14
XX AAY06385
XX ID AAY06385 standard; Protein; 118 AA.
XX AC AAY06385;

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XX DT
XX DE
XX DE 06-SEP-1999 (first entry)
XX DE Humanised LM609 antibody VH domain.
XX DE
XX KW Humanised antibody; antibody humanisation; antibody engineering;
XX KW LM609; monoclonal antibody; complementarity determining region;
XX KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
XX KW cancer; therapy; diagnosis.
XX OS Homo sapiens.
XX OS Synthetic.
XX FH
XX FT Key Location/Qualifiers
XX FT Peptide 1..2
XX FT /note= "vector-encoded residues"
XX FT Region 31..37
XX FT /note= "CDR1"
XX FT Region 52..67
XX FT /note= "CDR2"
XX FT Region 100..107
XX FT /note= "CDR3"
XX PN WO9929888-A1.
XX PD 17-JUN-1999.
XX PF 04-DEC-1998; 98WO-US25828.
XX PR 05-DEC-1997; 97US-0986016.
XX PA (SCRI ) SCRIPPS RES INST.
XX PI Barbas CF, Rader C;
XX PI WPI; 1999-394979/33.
XX DR Production of humanized mouse monoclonal antibodies
XX PT Disclosure; Page 51; 55pp; English.
XX PS
XX CC This sequence represents the heavy chain variable region of a
XX CC humanised LM609 antibody. LM609 is directed to human integrin
XX CC alpha-v beta-3. It selectively promotes apoptosis of vascular
XX CC cells that have been stimulated to undergo angiogenesis, making it
XX CC a tool for cancer diagnosis and therapy. The invention provides
XX CC humanised antibodies, especially humanised LM609. In such humanized
XX CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
XX CC grafted onto a human light chain, and a heavy chain CDR from a mouse
XX CC antibody is grafted onto a human antibody heavy chain to produce
XX CC libraries from which a humanised murine antibody having the desired
XX CC specificity is selected. By preserving the original CDR sequences
XX CC such as the HCDR3 and LCDR3 sequences of LM609 (see AAY06371-72), the
XX CC humanisation strategy ensures epitope conservation.
XX SQ
XX Sequence 118 AA;
XX Query Match 86.4%; Score 51; DB 20; Length 118;
XX Best Local Similarity 90.0%; Pred. No. 0.37;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX QY 1 ARHNYGSFDY 10
XX | | | | | | | |
XX Db 98 ARHNYGSFAY 107
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XX RESULT 15
XX AAY06386
XX ID AAY06386 standard; Protein; 118 AA.
XX AC AAY06386;
XX DT 06-SEP-1999 (first entry)

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XX
DE Humanised LM609 antibody VH domain.
XX
KW Humanised antibody; antibody humanisation; antibody engineering;
KW LM609; monoclonal antibody; complementarity determining region;
KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
KW cancer; therapy; diagnosis.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..2
FT /note= "vector-encoded residues"
FT Region 31..37
FT /note= "CDR1"
FT Region 52..67
FT /note= "CDR2"
FT Region 100..107
FT /note= "CDR3"
XX
PN WO929888-A1.
XX
PD 17-JUN-1999.
XX
XX 04-DEC-1998; 98WO-US25828.
XX
XX 05-DEC-1997; 97US-0986016.
XX
PA (SCRI ) SCRIPPS RES INST.
XX
XX Barbas CF, Rader C;
XX
XX WPI; 1999-394979/33.
XX
PT Production of humanized mouse monoclonal antibodies
XX
XX Disclosure; Page 51-52; 55pp; English.
XX
XX This sequence represents the heavy chain variable region of a
CC humanised LM609 antibody. LM609 is directed to human integrin
CC alpha-v beta-3. It selectively promotes apoptosis of vascular
CC cells that have been stimulated to undergo angiogenesis, making it
CC a tool for cancer diagnosis and therapy. The invention provides
CC humanised antibodies, especially humanised LM609. In such humanized
CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
CC grafted onto a human light chain, and a heavy chain CDR from a mouse
CC antibody is grafted onto a human antibody heavy chain to produce
CC libraries from which a humanised murine antibody having the desired
CC specificity is selected. By preserving the original CDR sequences
CC such as the HCDR3 and LCDR3 sequences of LM609 (see AAY06371-72), the
CC humanisation strategy ensures epitope conservation.
XX
SQ Sequence 118 AA;
Query Match 86.4%; Score 51; DB 20; Length 118;
Best Local Similarity 90.0%; Pred. No. 0.37;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ARHNYGSFDY 10
Db 98 ARHNYGSFAY 107
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Search completed: November 18, 2002, 17:31:37
Job time : 13.8235 secs
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 18, 2002, 17:54:45 ; Search time 1.96078 Seconds
(without alignments)
76.811 Million cell updates/sec

Title: US-09-016-061-64
Perfect score: 59
Sequence: 1 ARHNYGSFDY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 97044 seqs, 15060890 residues

Total number of hits satisfying chosen parameters: 97044

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications, AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
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- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	51	86.4	117	8	US-08-790-540A-2
2	51	86.4	117	8	US-08-790-540A-6
3	51	86.4	117	8	US-08-791-391A-2
4	51	86.4	117	8	US-08-791-391A-6
5	37	62.7	111	10	US-09-855-271-6
6	37	62.7	135	10	US-09-855-271-28
7	36	61.0	14	1	US-08-677-599B-22
8	36	61.0	101	10	US-09-764-853-432
9	36	61.0	602	10	US-09-841-132-495
10	36	61.0	602	10	US-09-841-132-565
11	34	57.6	30	10	US-09-839-884-40
12	34	57.6	240	9	US-09-968-561A-2
13	34	57.6	240	10	US-09-192-854-2
14	34	57.6	287	10	US-09-415-540-5
15	33	55.9	14	1	US-08-677-599B-21
16	33	55.9	196	10	US-09-741-669-368
17	33	55.9	196	10	US-09-912-020-376
18	33	55.9	244	10	US-09-940-391-1
19	33	55.9	258	10	US-09-452-239-4

20	33	55.9	258	10	US-09-452-239-38	Sequence 38, Appl
21	33	55.9	258	10	US-09-452-239-19	Sequence 49, Appl
22	33	55.9	260	10	US-09-452-239-12	Sequence 12, Appl
23	33	55.9	349	10	US-09-766-366-4	Sequence 4, Appl
24	33	55.9	428	12	US-10-062-254-372	Sequence 372, Appl
25	33	55.9	517	10	US-09-747-835A-48	Sequence 48, Appl
26	33	55.9	1511	10	US-09-801-368-250	Sequence 250, Appl
27	33	55.9	2789	10	US-09-801-574-57	Sequence 57, Appl
28	32	54.2	14	1	US-08-677-599B-11	Sequence 11, Appl
29	32	54.2	14	1	US-08-677-599B-12	Sequence 12, Appl
30	32	54.2	14	1	US-08-677-599B-13	Sequence 13, Appl
31	32	54.2	14	1	US-08-677-599B-14	Sequence 14, Appl
32	32	54.2	14	1	US-08-677-599B-15	Sequence 15, Appl
33	32	54.2	14	1	US-08-677-599B-16	Sequence 16, Appl
34	32	54.2	14	1	US-08-677-599B-17	Sequence 17, Appl
35	32	54.2	14	1	US-08-677-599B-18	Sequence 18, Appl
36	32	54.2	14	1	US-08-677-599B-19	Sequence 19, Appl
37	32	54.2	14	1	US-08-677-599B-20	Sequence 20, Appl
38	32	54.2	14	1	US-08-677-599B-23	Sequence 23, Appl
39	32	54.2	15	10	US-09-756-983-11	Sequence 11, Appl
40	32	54.2	25	1	US-08-677-599B-8	Sequence 8, Appl
41	32	54.2	93	12	US-10-081-281-121	Sequence 121, Appl
42	32	54.2	94	10	US-09-766-378A-37	Sequence 37, Appl
43	32	54.2	181	10	US-09-815-837-103	Sequence 103, Appl
44	32	54.2	183	10	US-09-815-837-16	Sequence 16, Appl
45	32	54.2	184	10	US-09-815-837-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1
US-08-790-540A-2
; Sequence 2, Application US/08790540A
; Patent No. US20010011125A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,540A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-790-540A-2
Query Match 86.4%; Score 51; DB 8; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.013;

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Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ARHNYGSFDY 10
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Db 97 ARHNYGSFAY 106

RESULT 2
US-08-790-540A-6
; Sequence 6, Application US/08790540A
; Patent No. US20010011125A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TELECOMMUNICATION INFORMATION:
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,540A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-790-540A-6

Query Match 86.4%; Score 51; DB 8; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.013;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ARHNYGSFDY 10
   |||||
Db 97 ARHNYGSFAY 106

RESULT 3
US-08-791-391A-2
; Sequence 2, Application US/08791391A
; Patent No. US20010016645A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TELECOMMUNICATION INFORMATION:
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,391A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-391A-2

Query Match 86.4%; Score 51; DB 8; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.013;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ARHNYGSFDY 10
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Db 97 ARHNYGSFAY 106

RESULT 4
US-08-791-391A-6
; Sequence 6, Application US/08791391A
; Patent No. US20010016645A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TELECOMMUNICATION INFORMATION:
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,391A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-391A-6
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Query Match 86.4%; Score 51; DB 8; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.013;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFDY 10
||| |||||
Db 97 ARHNYGSFAY 106

RESULT 5
US-09-855-271-6
; Sequence 6, Application US/09855271
; Patent No. US20020042089A1
; GENERAL INFORMATION:
; APPLICANT: Bodmer, Mark W
; APPLICANT: Athwal, Diljeet Singh
; APPLICANT: Entage, John Spencer
; TITLE OF INVENTION: Interleukin-5 Specific Recombinant Antibodies
; FILE REFERENCE: CARP-0088
; CURRENT APPLICATION NUMBER: US/09/855,271
; CURRENT FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 09/347,061
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Rattus rattus
US-09-855-271-6

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Best Local Similarity 70.0%; Pred. No. 3.9;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARHNYGSFDY 10
||| |||||
Db 91 AREYGYFDY 100

RESULT 6
US-09-855-271-28
; Sequence 28, Application US/09855271
; Patent No. US20020042089A1
; GENERAL INFORMATION:
; APPLICANT: Bodmer, Mark W
; APPLICANT: Athwal, Diljeet Singh
; APPLICANT: Entage, John Spencer
; TITLE OF INVENTION: Interleukin-5 Specific Recombinant Antibodies
; FILE REFERENCE: CARP-0088
; CURRENT APPLICATION NUMBER: US/09/855,271
; CURRENT FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 09/347,061
; PRIOR FILING DATE: 1999-07-02
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. US20020042089A1e1 Sequence
US-09-855-271-28

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Best Local Similarity 70.0%; Pred. No. 4.7;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 115 AREYGYFDY 124

RESULT 7
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; Sequence 22, Application US/08677599B
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; GENERAL INFORMATION:
; APPLICANT: Sucia-Foca, Nicole
; TITLE OF INVENTION: METHODS FOR DETECTING ORGAN ALLOGRAFT
; TITLE OF INVENTION: REJECTION AND USES THEREOF
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/677,599B
; FILING DATE: 08-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq., John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 50161-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212/278/0400
; TELEFAX: 212/391/0525
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-677-599B-22

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Best Local Similarity 100.0%; Pred. No. 0.71;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYG 6
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Db 9 ARHNYG 14

RESULT 8
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; Patent No. US20020090672A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJ206
; CURRENT APPLICATION NUMBER: US/09/764,853
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 939
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 432
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-853-432

Query Match 61.0%; Score 36; DB 10; Length 101;
Best Local Similarity 85.7%; Pred. No. 5.3;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
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Db 64 RHNYSSF 70

RESULT 9

US-09-841-132-495
; Sequence 495, Application US/09841132
; Patent No. US20020061848A1
; GENERAL INFORMATION:
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Probst, Peter
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C8
; CURRENT APPLICATION NUMBER: US/09/841,132
; CURRENT FILING DATE: 2001-04-23
; NUMBER OF SEQ ID NOS: 599
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 495
; LENGTH: 602
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-841-132-495

Query Match 61.0%; Score 36; DB 10; Length 602;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 472 YGSFDY 477

RESULT 10

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; Sequence 565, Application US/09841132
; Patent No. US20020061848A1
; GENERAL INFORMATION:
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Probst, Peter
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C8
; CURRENT APPLICATION NUMBER: US/09/841,132
; CURRENT FILING DATE: 2001-04-23
; NUMBER OF SEQ ID NOS: 599
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 565
; LENGTH: 602
; TYPE: PRT
; ORGANISM: C. Trachomatis D serovar
US-09-841-132-565

Query Match 61.0%; Score 36; DB 10; Length 602;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 YGSFDY 10
|||||
Db 472 YGSFDY 477

RESULT 11

US-09-839-884-40
; Sequence 40, Application US/09839884
; Patent No. US20020076739A1
; GENERAL INFORMATION:
; APPLICANT: Aebersold, Rudolf H.
; APPLICANT: Gelb, Michael H.

; APPLICANT: Gygi, Steven
; APPLICANT: Scott, C R
; APPLICANT: Turecek, Frantisek
; APPLICANT: Gerber, Scott A
; APPLICANT: Rist, Beate
; TITLE OF INVENTION: Rapid Quantitative Analysis of Proteins or Protein
; TITLE OF INVENTION: Function in Complex Mixture
; FILE REFERENCE: 64-98A
; CURRENT APPLICATION NUMBER: US/09/839,884
; CURRENT FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: 09/383,062
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 60/097,788
; PRIOR FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40
; LENGTH: 30
; TYPE: PRT
; ORGANISM: yeast
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (2)
; OTHER INFORMATION: C at position 2 is ICAT-labeled cysteinyl residue.
US-09-839-884-40

Query Match 57.6%; Score 34; DB 10; Length 30;
Best Local Similarity 83.3%; Pred. No. 3.5;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
|||||
Db 10 HNYGAF 15

RESULT 12

US-09-968-561A-2
; Sequence 2, Application US/09968561A
; Patent No. US20020164642A1
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, Ian M
; APPLICANT: Winter, Gregory
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligand
; FILE REFERENCE: 8039/1073B
; CURRENT APPLICATION NUMBER: US/09/968,561A
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: GB 9722131.1
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/065,248
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/066,729
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: PCT/GB98/03135
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: US 09/511,939
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-968-561A-2

Query Match 57.6%; Score 34; DB 9; Length 240;
Best Local Similarity 71.4%; Pred. No. 29;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 NYGSFDY 10
:|:|:|
Db 99 SYGAFDY 105

RESULT 13
US-09-192-854-2
; Sequence 2, Application US/09192854
; Patent No. US20020068276A1
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, Ian
; TITLE OF INVENTION: Methods for Selecting Functional Peptides
; FILE REFERENCE: 3789/72916
; CURRENT APPLICATION NUMBER: US/09/192,854
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/066,729
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-192-854-2

Query Match 57.6%; Score 34; DB 10; Length 240;
Best Local Similarity 71.4%; Pred. No. 29;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 NYGSFDY 10
DB 99 SYGAFDY 105

RESULT 14
US-09-415-540-5
; Sequence 5, Application US/09415540
; Patent No. US20010010911A1
; GENERAL INFORMATION:
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: A NOVEL HUMAN PYROPHOSPHATASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/415,540
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/741,437
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0148 US
; TELEPHONE: (415) 855-0555
; TELEFAX: (415) 845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 287 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank

CLONE: 4199
US-09-415-540-5

Query Match 57.6%; Score 34; DB 10; Length 287;
Best Local Similarity 83.3%; Pred. No. 35;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
DB 92 HNYGAF 97

RESULT 15
US-08-677-599B-21
; Sequence 21, Application US/08677599B
; Patent No. US20020155117A1
; GENERAL INFORMATION:
; APPLICANT: Sucia-Foca, Nicole
; TITLE OF INVENTION: METHODS FOR DETECTING ORGAN ALLOGRAFT
; REJECTION AND USES THEREOF
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/677,599B
; FILING DATE: 08-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq., John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 50161-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212/278/0400
; TELEFAX: 212/391/0525
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-677-599B-21

Query Match 55.9%; Score 33; DB 1; Length 14;
Best Local Similarity 83.3%; Pred. No. 2.5;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYG 6
DB 9 SRHNYG 14

Search completed: November 18, 2002, 18:45:15
Job time : 1.96078 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:01 : Search time 4.2402 Seconds
(without alignments)
69.390 Million cell updates/sec

Title: US-09-016-061-64

Perfect score: 59

Sequence: 1 ARHNGSFDY 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/1/iaa/5A-COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B-COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A-COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B-COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS-COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	64.4	94	3	US-09-147-550-14
2	38	64.4	94	3	US-09-147-550-45
3	38	64.4	94	3	US-09-147-550-48
4	38	64.4	94	3	US-09-147-550-77
5	38	64.4	94	3	US-09-147-550-84
6	38	64.4	94	3	US-09-147-550-90
7	38	64.4	94	3	US-09-147-550-101
8	38	64.4	94	4	US-09-557-917-14
9	38	64.4	94	4	US-09-557-917-45
10	38	64.4	94	4	US-09-557-917-48
11	38	64.4	94	4	US-09-557-917-77
12	38	64.4	94	4	US-09-557-917-84
13	38	64.4	94	4	US-09-557-917-90
14	38	64.4	94	4	US-09-557-917-101
15	37	62.7	36	1	US-08-053-131-84
16	37	62.7	36	1	US-08-645-641-84
17	37	62.7	36	1	US-07-853-408B-84
18	37	62.7	36	2	US-08-096-762-84
19	37	62.7	36	2	US-08-308-865-84
20	37	62.7	36	4	US-08-042-353-281
21	37	62.7	36	4	US-08-758-417A-129
22	37	62.7	36	5	PCT-US92-10983-84
23	37	62.7	111	2	US-08-470-139-6
24	37	62.7	111	4	US-09-347-061-6
25	37	62.7	111	4	US-09-537-911A-67
26	37	62.7	135	2	US-08-470-139-28
27	37	62.7	135	3	US-08-284-516C-36

ALIGNMENTS

RESULT 1

US-09-147-550-14

; Sequence 14, Application US/09147550

; Patent No. 6090540

; GENERAL INFORMATION:

; APPLICANT: Aida, Yoko

; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF

; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550

; CURRENT FILING DATE: 1999-04-23

; EARLIER APPLICATION NUMBER: PCT/JP97/02485

; EARLIER FILING DATE: 1997-07-17

; EARLIER APPLICATION NUMBER: JP 8-190933

; EARLIER FILING DATE: 1996-07-19

; EARLIER APPLICATION NUMBER: JP 9-77979

; EARLIER FILING DATE: 1997-03-28

; NUMBER OF SEQ ID NOS: 115

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 14

; LENGTH: 94

; TYPE: PRT

; ORGANISM: BOVINE

US-09-147-550-14

Query Match 64.4%; Score 38; DB 3; Length 94;
Best Local Similarity 75.0%; Pred. No. 9.8;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNGSFD 9
Db 80 RHNGVFE 87
|||||

RESULT 2

US-09-147-550-45

; Sequence 45, Application US/09147550

; Patent No. 6090540

; GENERAL INFORMATION:

; APPLICANT: Aida, Yoko

; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF

; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550

; CURRENT FILING DATE: 1999-04-23

; EARLIER APPLICATION NUMBER: PCT/JP97/02485

; EARLIER FILING DATE: 1997-07-17

; EARLIER APPLICATION NUMBER: JP 8-190933

; EARLIER FILING DATE: 1996-07-19

; EARLIER APPLICATION NUMBER: JP 9-77979

; EARLIER FILING DATE: 1996-07-19

; EARLIER APPLICATION NUMBER: JP 9-77979

; EARLIER FILING DATE: 1996-07-19

; EARLIER APPLICATION NUMBER: JP 9-77979

; EARLIER FILING DATE: 1996-07-19

; EARLIER APPLICATION NUMBER: JP 9-77979

; EARLIER FILING DATE: 1996-07-19

; EARLIER APPLICATION NUMBER: JP 9-77979

; EARLIER FILING DATE: 1996-07-19

; EARLIER APPLICATION NUMBER: JP 9-77979

; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-45

Query Match 64.4%; Score 38; DB 3; Length 94;
Best Local Similarity 75.0%; Pred. No. 9.8;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFD 9
||||| I;
Db 80 RHNYGVFE 87

RESULT 3

US-09-147-550-48
; Sequence 48, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-48

Query Match 64.4%; Score 38; DB 3; Length 94;
Best Local Similarity 75.0%; Pred. No. 9.8;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFD 9
||||| I;
Db 80 RHNYGVFE 87

RESULT 4

US-09-147-550-77
; Sequence 77, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 77
; LENGTH: 94

; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-77

Query Match 64.4%; Score 38; DB 3; Length 94;
Best Local Similarity 75.0%; Pred. No. 9.8;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFD 9
||||| I;
Db 80 RHNYGVFE 87

RESULT 5

US-09-147-550-84
; Sequence 84, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-84

Query Match 64.4%; Score 38; DB 3; Length 94;
Best Local Similarity 75.0%; Pred. No. 9.8;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFD 9
||||| I;
Db 80 RHNYGVFE 87

RESULT 6

US-09-147-550-90
; Sequence 90, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 90
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-90

Query Match 64.4%; Score 38; DB 3; Length 94;

Best Local Similarity 75.0%; Pred. No. 9.8;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFD 9
Db 80 RHNYGVFE 87

RESULT 7
US-09-147-550-101
; Sequence 101, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 101
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-101

Query Match 64.4%; Score 38; DB 3; Length 94;
Best Local Similarity 75.0%; Pred. No. 9.8;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFD 9
Db 80 RHNYGVFE 87

RESULT 8
US-09-557-917-14
; Sequence 14, Application US/09557917
; Patent No. 6284457
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 14
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-14

Query Match 64.4%; Score 38; DB 4; Length 94;
Best Local Similarity 75.0%; Pred. No. 9.8;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFD 9

Best Local Similarity 75.0%; Pred. No. 9.8;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFD 9
Db 80 RHNYGVFE 87

RESULT 9
US-09-557-917-45
; Sequence 45, Application US/09557917
; Patent No. 6284457
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 45
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-45

Query Match 64.4%; Score 38; DB 4; Length 94;
Best Local Similarity 75.0%; Pred. No. 9.8;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFD 9
Db 80 RHNYGVFE 87

RESULT 10
US-09-557-917-48
; Sequence 48, Application US/09557917
; Patent No. 6284457
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 48
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-48

Query Match 64.4%; Score 38; DB 4; Length 94;
Best Local Similarity 75.0%; Pred. No. 9.8;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFD 9


```

Db      80 RHNYGVFE 87
||||| I:
US-09-557-917-77
; Sequence 77, Application US/09557917
; Patent No. 6284457
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 77
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-77

Query Match          64.4%; Score 38; DB 4; Length 94;
Best Local Similarity 75.0%; Pred. No. 9.8;
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY      2 RHNYGSFD 9
||||| I:
Db      80 RHNYGVFE 87

US-09-557-917-84
; Sequence 84, Application US/09557917
; Patent No. 6284457
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-84

Query Match          64.4%; Score 38; DB 4; Length 94;
Best Local Similarity 75.0%; Pred. No. 9.8;
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY      2 RHNYGSFD 9
||||| I:
Db      80 RHNYGVFE 87

US-09-557-917-101
; Sequence 101, Application US/09557917
; Patent No. 6284457
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-101

Query Match          64.4%; Score 38; DB 4; Length 94;
Best Local Similarity 75.0%; Pred. No. 9.8;
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY      2 RHNYGSFD 9
||||| I:
Db      80 RHNYGVFE 87

```

RESULT 15
US-08-053-131-84
; Sequence 84 Application US/08053131
; Patent No. 5661016
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 197
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Hourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 200
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/053,131
; FILING DATE: 26-APR-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,860
; FILING DATE: 16-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/810,279
; FILING DATE: 17-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/853,408
; FILING DATE: 18-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14643-9-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-053-131-84

Query Match 62.7% Score 37; DB 1; Length 36;
Best Local Similarity 66.7%; Pred. No. 5.5;
Matches 8; Conservative 1; Mismatches 1; Indels 2; Gaps 1;

Qy 1 ARHNY--GSFDY 10
||| | |||
Db 3 ARHYGSGSYDY 14

Search completed: November 18, 2002, 17:43:36
Job time : 4.2402 secs

GenCore version 5.1.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:01 ; Search time 4.90196 Seconds
(without alignments)
196.114 Million cell updates/sec

Title: US-09-016-061-66

Perfect score: 60

Sequence: 1 ARHNYGSFY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR_73: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	70.0	195	2 G86742	Conserved hypothet
2	39	65.0	113	2 S26468	Ig heavy chain v r
3	39	65.0	2288	2 T29999	hypothetical prote
4	38	63.3	25	2 PH1686	Ig heavy chain v r
5	38	63.3	25	2 PH1700	Ig heavy chain v r
6	38	63.3	56	2 E49038	Ig lambda chain v
7	38	63.3	130	2 S06817	Ig heavy chain v r
8	38	63.3	144	2 T38634	40s ribosomal prot
9	38	63.3	233	2 S76857	hypothetical prote
10	38	63.3	377	2 I50147	3beta-hydroxy-delt
11	38	63.3	502	2 B90103	T-complex protein
12	38	63.3	1144	2 A36968	p1-like adhesin pr
13	37	61.7	102	2 S14581	Ig heavy chain v r
14	37	61.7	192	2 T38535	probable transloca
15	37	61.7	386	2 S51436	probable membrane
16	37	61.7	641	2 J65017	zinc-finger transc
17	37	61.7	1289	2 D87789	protein C34G6.4 (i
18	36	60.0	82	2 I51106	Major Histocompat
19	36	60.0	89	2 S38688	MHC class II histo
20	36	60.0	89	2 S38683	MHC class II histo
21	36	60.0	89	2 S38684	MHC class II histo
22	36	60.0	177	2 C84952	aminoacyl-tRNA hyd
23	36	60.0	225	2 I47095	MHC class II OVAR-
24	36	60.0	233	2 H82163	arginyl-tRNA-prote
25	36	60.0	302	2 AD3106	hypothetical prote
26	36	60.0	305	2 H98180	hypothetical prote
27	36	60.0	306	2 B28170	reaction center pr
28	36	60.0	446	2 T19625	hypothetical prote
29	36	60.0	470	2 H71667	glutamate-tRNA lig

30 36 60.0 718 2 G84902
31 36 60.0 786 2 S37031
32 36 60.0 786 2 P95977
33 36 60.0 2161 1 A45389
34 35.5 59.2 45 2 PL0094
35 35 58.3 9 2 S36850
36 35 58.3 27 2 PH1719
37 35 58.3 98 2 B24754
38 35 58.3 108 2 S26316
39 35 58.3 110 2 S26317
40 35 58.3 124 2 H30539
41 35 58.3 124 2 G30539
42 35 58.3 124 2 F30539
43 35 58.3 167 2 T16454
44 35 58.3 219 2 T32443
45 35 58.3 316 2 T15395

ALIGNMENTS

RESULT 1

G86742
conserved hypothetical protein yjgF [imported] - Lactococcus lactis subsp. lactis (st
C:Species: Lactococcus lactis subsp. lactis
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 17-May-2002
C:Accession: G86742
R:Boletín, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Eh
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis
A:Reference number: A86825; MUID:21235186; PMID:11337471
A:Accession: G86742
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-195 <STO>
A:Cross-references: GB:AE005176; PID:gl2723879; PIDN:AAK05041.1; GSPDB:GN00146
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: yjgF
C:Superfamily: hypothetical protein bl011

Query Match 70.0%; Score 42; DB 2; Length 195;
Best Local Similarity 66.7%; Pred. No. 3.8;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFY 9
|:|:|:|:|
Db 103 AKHNWGFY 111

RESULT 2

S26468
Ig heavy chain v region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S26468
R:Kavaler, J.
Submitted to the EMBL Data Library, April 1991
A:Reference number: S26459
A:Accession: S26468
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-113 <KAV>
A:Cross-references: EMBL:X59107; NID:g51944; PIDN:CAA41833.1; PID:g51945
C:Superfamily: immunoglobulin v region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:11-94/Domain: immunoglobulin homology <IMM>

Query Match 65.0%; Score 39; DB 2; Length 113;
Best Local Similarity 66.7%; Pred. No. 7.6;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFY 9

Db 93 ARHPYGNYY 101
||| |||::|

RESULT 3

T29999
hypothetical protein ZC8.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T29999
R:Latreille, P.; Bradshaw, H.
submitted to the EMBL Data Library, July 1996
A:Description: The sequence of C. elegans cosmid ZC8.
A:Reference number: Z20719
A:Accession: T29999
A:Status: preliminary; translated from GB/EMBL/DDBY
A:Molecule type: DNA
A:Residues: 1-2288 <LAT>
A:Cross-references: EMBL:U64862; PIDN:AAB52624.1; GSPDB:GN00028; CBSP:ZC8.4
A:Experimental source: strain Bristol N2; clone ZC8
C:Genetics:
A:Gene: CBSP:ZC8.4
A:Map position: X
A:Introns: 43/2; 80/3; 110/3; 153/2; 274/3; 738/2; 1249/1; 1392/3; 1454/1; 1602/1; 1686/

Query Match

Best Local Similarity 65.0%; Score 39; DB 2; Length 2288;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ARHNYGSFY 10
:: || |||| ||:
Db 34 SRSNGEYF 43

RESULT 4

PH1686
Ig heavy chain V region (clone NP-6-17) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 17-Mar-1999
C:Accession: PH1686
R:McHeyzer-Williams, M.G.; McLean, M.J.; Lalor, P.A.; Nossal, G.J.V.
J. Exp. Med. 178, 295-307, 1993
A:Title: Antigen-driven B cell differentiation in vivo.
A:Reference number: PH1675; MUID:93301607; PMID:8315385
A:Accession: PH1686
A:Molecule type: mRNA
A:Residues: 1-25 <MCH>
A:Experimental source: B cell
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin

Query Match

Best Local Similarity 63.3%; Score 38; DB 2; Length 25;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ARHNYGSFY 10
||: ||| ||
Db 13 ARVYGSTY 22

RESULT 5

PH1700
Ig heavy chain V region (clone NP-7-13) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 17-Mar-1999
C:Accession: PH1700
R:McHeyzer-Williams, M.G.; McLean, M.J.; Lalor, P.A.; Nossal, G.J.V.
J. Exp. Med. 178, 295-307, 1993
A:Title: Antigen-driven B cell differentiation in vivo.
A:Reference number: PH1675; MUID:93301607; PMID:8315385
A:Accession: PH1700
A:Molecule type: mRNA
A:Residues: 1-25 <MCH>

A:Experimental source: B cell
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin

Query Match 63.3%; Score 38; DB 2; Length 25;
Best Local Similarity 70.0%; Pred. No. 2.6;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ARHNYGSFY 10
||: ||| ||
Db 13 ARVYGSYY 22

RESULT 6

E49038
Ig lambda chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C:Accession: E49038
R:Weiss, U.; Zobebelein, R.; Rajewsky, K.
Eur. J. Immunol. 22, 511-517, 1992
A:Title: Accumulation of somatic mutants in the B cell compartment after primary immunization
A:Reference number: A49038; MUID:92164733; PMID:1537385
A:Accession: E49038
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-56 <WET>
A:Cross-references: GB:S85736; NID:g246322; PIDN:AAB21563.1; PID:g246323
A:Experimental source: spleen
A:Note: sequence extracted from NCBI backbone (NCBIN:85736, NCBI:P:85804)
C:Keywords: heterotrimer; immunoglobulin

Query Match

Best Local Similarity 70.0%; Score 38; DB 2; Length 56;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ARHNYGSFY 10
||: ||| ||
Db 42 ARVYGSYY 51

RESULT 7

S06817
Ig heavy chain V region (clone 11C7) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1991 #sequence_revision 11-Nov-1994 #text_change 23-Jul-1999
C:Accession: S06817
R:Miller III, A.; Glasel, J.A.
J. Mol. Biol. 209, 763-778, 1989
A:Title: Comparative sequence and immunochemical analyses of murine monoclonal anti-mouse Ig heavy chain V region (clone 11C7) - mouse
A:Reference number: S06815; MUID:90064531; PMID:2555519
A:Accession: S06817
A:Molecule type: mRNA
A:Residues: 1-130 <MIL>
A:Cross-references: EMBL:X17165; NID:g51917; PIDN:CAA35043.1; PID:g930155
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>
F:22-96/Disulfide bonds: #status predicted

Query Match 63.3%; Score 38; DB 2; Length 130;
Best Local Similarity 75.0%; Pred. No. 1.3;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 HNYGSFY 10
: ||| ||
Db 103 YNYGSHY 110

RESULT 8

T38634
40s ribosomal protein S10 - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Jun-2000
 C:Accession: T38634
 R:McLean, J.; Harlits, D.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
 submitted to the EMBL Data Library, September 1997
 A:Reference number: Z21722
 A:Accession: T38634
 A:Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: DNA
 A:Residues: 1-144 <MC1>
 A:Cross-references: EMBL:Z98979; PIDN:CAB11701.1; GSPDB:GN00066; SPDB:SPAC31G5.17c
 A:Experimental source: strain 972h-; cosmid c31G5
 C:Genetics:
 A:Gene: SPDB:SPAC31G5.17c
 A:Map position: 1
 A:Introns: 26/1
 C:Superfamily: rat ribosomal protein S10; ribosomal protein S10 homology

Query Match 63.3%; Score 38; DB 2; Length 144;
 Best Local Similarity 66.7%; Pred. No. 14;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFY 10
 I:I:I I:I
 Db 58 RYNWGFY 66

RESULT 9
 S76857
 hypothetical protein - Synecocystis sp. (strain PCC 6803)
 C:Species: Synecocystis sp.
 A:Variety: PCC 6803
 C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
 C:Accession: S76857
 R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
 O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
 DNA Res. 3, 109-136, 1996
 A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecocystis
 S.
 A:Reference number: S74322; MUID:97061201; PMID:8905231
 A:Accession: S76857
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-233 <KAN>
 A:Cross-references: EMBL:D90917; GB:AB001339; NID:g1653836; PIDN:BAAL9769.1; PID:g1653836
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 63.3%; Score 38; DB 2; Length 233;
 Best Local Similarity 55.6%; Pred. No. 23;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFY 10
 I:I:I I:I
 Db 98 RHYGTLY 106

RESULT 10
 I50147
 3beta-hydroxy-Delta5-steroid dehydrogenase multifunctional protein - chicken
 N:Contains: 3beta-hydroxy-Delta5-steroid dehydrogenase (EC 1.1.1.145); steroid Delta-5
 C:Species: Gallus gallus (chicken)
 C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 11-Jun-1999
 C:Accession: I50147; I50220
 R:Nakabayashi, O.; Nomura, O.; Nishimori, K.; Mizuno, S.
 Gene 162, 261-265, 1995
 A:Title: The cDNA cloning and transient expression of a chicken gene encoding a 3 beta-h
 A:Reference number: I50147; MUID:96032354; PMID:7557440
 A:Accession: I50147
 A:Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: mRNA
 A:Residues: 1-377 <NAK>
 A:Cross-references: GB:D43762; NID:g1019355; PIDN:BAAL97819.1; PID:g1019356
 A:Accession: I50220
 A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA
 A:Residues: 1-377 <NA2>
 A:Cross-references: GB:D43763; NID:g1019357; PIDN:BAAL97820.1; PID:g1019358
 C:Superfamily: 3beta-hydroxy-Delta5-steroid dehydrogenase
 C:Keywords: Intramolecular oxidoreductase; isomerase; NAD; oxidoreductase; steroid bi

Query Match 63.3%; Score 38; DB 2; Length 377;
 Best Local Similarity 70.0%; Pred. No. 37;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARHNYGSFY 10
 I:I:I I:I
 Db 250 ARHNGQFY 259

RESULT 11
 B90103
 T-complex protein gamma SU [imported] - Guillardia theta nucleomorph
 C:Species: nucleomorph Guillardia theta
 A:Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
 C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
 C:Accession: B90103
 R:Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.;
 Nature 410, 1091-1096, 2001
 A:Title: The highly reduced genome of an enslaved algal nucleus.
 A:Reference number: A99082; MUID:11323671; PMID:11323671
 A:Accession: B90103
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-502 <DOU>
 A:Cross-references: GB:AJ010592; NID:g4583663; PIDN:CAB40401.1; GSPDB:GN00151
 C:Genetics:
 A:Map position: 2
 A:Genome: nucleomorph
 C:Keywords: nucleomorph

Query Match 63.3%; Score 38; DB 2; Length 502;
 Best Local Similarity 62.5%; Pred. No. 49;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 HNYGSFY 10
 I:I:I I:I
 Db 444 HNYGKYY 451

RESULT 12
 A36968
 P1-like adhesin precursor - Mycoplasma pirum
 C:Species: Mycoplasma pirum
 C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 07-Dec-1999
 C:Accession: A36968
 R:Tham, T.N.; Ferris, S.; Bahraoui, E.; Canarelli, S.; Montagnier, L.; Blanchard, A.
 J. Bacteriol. 176, 781-788, 1994
 A:Title: Molecular characterization of the P1-like adhesin gene from Mycoplasma pirum
 A:Reference number: A36968; MUID:94131957; PMID:8300531
 A:Accession: A36968
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1144 <THA>
 A:Cross-references: GB:L19685; NID:g404770; PIDN:AAC36866.1; PID:g404771
 C:Genetics:
 A:Genetic code: SGC3

Query Match 63.3%; Score 38; DB 2; Length 1144;
 Best Local Similarity 55.6%; Pred. No. 114e+02;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFY 10
 I:I:I I:I
 Db 885 RNYGSFY 893

RESULT 13

S14581

Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C:Accession: S14581
R:Chen, Q.; Stenzel-Poore, M.; Rittenberg, M.B.
submitted to the EMBL Data Library, March 1991
A:Description: Natural polyclonal antibodies differ from Ag-induced antibodies in VH C
A:Reference number: S14484
A:Accession: S14581
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-102 <CH>
A:Cross-references: EMBL:X58553; NID:g51295; PIDN:CAA41510.1; PID:g51296
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:7-90/Domain: immunoglobulin homology <IMM>

Query Match 61.7%; Score 37; DB 2; Length 102;
Best Local Similarity 70.0%; Pred. No. 15;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ARHNYGSFY 10
|| :||| ||
Db 89 ARWHYGSSYY 98

RESULT 14

T38535
probable translation protein - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T38535
R:Oliver, K.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, September 1997
A:Reference number: 221748
A:Accession: T38535
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-192 <OLI>
A:Cross-references: EMBL:Z99165; PIDN:CAB16260.1; GSPDB:GN00066; SPDB:SPAC2F3.02
A:Experimental source: strain 972h; cosmid c2F3
C:Genetics:
A:Gene: SPDB:SPAC2F3.02
A:Map position: 1

Query Match 61.7%; Score 37; DB 2; Length 192;
Best Local Similarity 66.7%; Pred. No. 29;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RHNYGSFY 10
|:|:| |
Db 139 RNYGKCY 147

RESULT 15

S51436
probable membrane protein YLR191w - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein I9470.1
C:Species: Saccharomyces cerevisiae
C:Date: 23-Feb-1995 #sequence_revision 12-May-1995 #text_change 06-Feb-1998
C:Accession: S51436
R:Wohldmann, P.
submitted to the EMBL Data Library, November 1994
A:Description: The sequence of S. cerevisiae cosmid 9470.
A:Reference number: S51414
A:Accession: S51436
A:Molecule type: DNA
A:Residues: 1-386 <WOH>
A:Cross-references: EMBL:U17246; NID:g577192; PID:g577193; MIPS:YLR191w
C:Genetics:
A:Gene: SGD:pEX13
A:Cross-references: SGD:S0004181; MIPS:YLR191w

A:Map position: 12R
C:Superfamily: SH3 homology
C:Keywords: transmembrane protein
F:264-280/Domain: transmembrane #status predicted <TMM>
F:313-367/Domain: SH3 homology <SH3>

Query Match 61.7%; Score 37; DB 2; Length 386;
Best Local Similarity 85.7%; Pred. No. 57;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 HNYGSFY 9
:|||||
Db 117 NNYGSFY 123

Search completed: November 18, 2002, 17:47:04
Job time : 4.90196 secs


```
DR InterPro: IPR005326; S10_plectin.
DR Pfam: PF03501; S10_plectin; 1.
KW Ribosomal protein; Multigene family.
SQ SEQUENCE 144 AA; 16275 MW; C0F58FEBED8B8905 CRC64;

Query Match 63.3%; Score 38; DB 1; Length 144;
Best Local Similarity 66.7%; Pred. No. 4.9;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFY 10
   I:L:| | | |
DB 58 RYNGWFEY 66

RESULT 2
RS1B_SCHPO
ID RS1B_SCHPO STANDARD; PRT; 147 AA.
AC O13614;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 40S ribosomal protein S10-B
GN RPS10B OR SPBP22H7.08 OR P1023.
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
[1]
SEQUENCE FROM N.A.
RP STRAIN=972;
RC MEDLINE=20089027; PubMed=10620777;
RX Machida M., Yamazaki S., Kunihiro S., Tanaka T., Kushida M., Jinno K.,
RA Haikawa Y., Yamazaki J., Yamamoto S., Sekine M., Oguchi A., Nagai Y.,
RA Sakai M., Aoki K., Ogura K., Kudo Y., Kikuchi H., Zhang M.Q.,
RA Yangida M.;
RT "A 38 kb segment containing the cdc2 gene from the left arm of fission
RT yeast chromosome II: sequence analysis and characterization of the
RT genomic DNA and cDNAs encoded on the segment.";
RL Yeast 16:71-80(2000).
RN [2]
SEQUENCE FROM N.A.
RP STRAIN=972;
RC MEDLINE=21848401; PubMed=11859360;
RX Wood V., Williams R., Rajandream M.A., Lyne M., Stewart A.,
RA Sgouros J., Peat N., Hayes J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown J., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volkart G., Aert R., Robben J., Grymonprez B.,
RA Welljens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).
CC -!- MISCELLANEOUS: THERE ARE TWO GENES FOR S10 IN S.POMBE.
CC -!- SIMILARITY: BELONGS TO THE S10E FAMILY OF RIBOSOMAL PROTEINS.
-----
CC
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-----
DR EMBL: AB004535; BAA21402.1; -.
DR EMBL: AL590883; CAC37376.1; -.
DR InterPro: IPR005326; S10_plectin.
DR Pfam: PF03501; S10_plectin; 1.
KW Ribosomal protein; Multigene family.
SQ SEQUENCE 147 AA; 16443 MW; 0B2516EF35EFF4FA CRC64;

Query Match 63.3%; Score 38; DB 1; Length 147;
Best Local Similarity 66.7%; Pred. No. 5;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFY 10
   I:L:| | | |
DB 58 RYNGWFEY 66

RESULT 3
CCSA_LOTJA
ID CCSA_LOTJA STANDARD; PRT; 323 AA.
AC Q9BBP4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cytochrome c biogenesis protein ccsa.
GN CCSA.
OS Lotus japonicus.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Lotaeae; Lotus.
OX NCBI_TaxID=34305;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=Accession MG-20;
RC MEDLINE=21082929; PubMed=11214967;
RX Kato T., Kaneko T., Sato S., Nakamura Y., Tabata S.;
RT "Complete structure of the chloroplast genome of a legume, Lotus
RT japonicus.";
RL DNA Res. 7:323-330(2000).
CC -!- FUNCTION: REQUIRED DURING CYTOCHROME BIOGENESIS AT THE STEP OF
CC HEME ATTACHMENT (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CCME/CYCK/CCL1/NRFE/CCSA FAMILY.
-----
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-----
DR EMBL: AF002983; BAB33244.1; -.
DR InterPro: IPR002541; CytC_asm.
DR Pfam: PF01578; CytC_asm; 1.
KW Cytochrome c-type biogenesis; Chloroplast.
SQ SEQUENCE 323 AA; 37185 MW; 5A034E3E2829FE35 CRC64;

Query Match 61.7%; Score 37; DB 1; Length 323;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
   I:| | | | |
DB 315 HNYGSF 320
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RESULT 4
PEXD_YEAST
ID PEXD_YEAST STANDARD; PRT; 386 AA.
AC P80667;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Peroxisomal membrane protein PAS20 (Peroxin-13).
GN PEX13 OR PAS20 OR YUK191W OR L9470.1.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=97011156; PubMed=8858166;
RX Elgermsa Y., Kwast L., Klein A., Voorn-Brouwer T., van den Berg M.,
RA Tabak H.F., Distel B.;
RT "The SH3 domain of the Saccharomyces cerevisiae peroxisomal membrane
protein Pex13p functions as a docking site for Pex5p, a mobile
receptor for the import PPS1-containing proteins.";
RT J. Cell Biol. 135:97-109(1996).
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=S288C / AB972;
RX Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,
RA Favellio A., Fulton L., Gattung S., Greco T., Kirsten J., Kucaba T.,
RA Hallsworth K., Hawkins J., Hillier L., Jier M., Johnson D.,
RA Johnston L., Langston J., Latreille P., Le T., Mardis E., Menezes S.,
RA Miller N., Nhan M., Pauley A., Peluso D., Rifken L., Riles L.,
RA Talch A., Trevasakis E., Vignati D., Wilcox L., Wohlman P., Vaudin M.,
RA Wilson R., Waterston R.;
RL Submitted (Nov-1994) to the EMBL/GenBank/DBJ databases.
[3]
RN PARTIAL SEQUENCE, AND CHARACTERIZATION.
RP STRAIN=S288C;
RX MEDLINE=97011157; PubMed=8858167;
RA Erdmann R., Blobel G.;
RT "Identification of Pex13p a peroxisomal membrane receptor for the
PPS1 recognition factor.";
RL J. Cell Biol. 135:111-121(1996).
CC -1- FUNCTION: COMPONENT OF THE PEROXISOMAL TRANSLLOCATION MACHINERY
CC WITH PEX14 AND PEX17. INTERACTS WITH THE PPS1 RECEPTOR
CC (PAS10/PEX5).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Peroxisomal.
CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
CC
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-----
DR EMBL; S82971; AAB46885.1; -
DR EMBL; U37420; AAA79308.1; -
DR EMBL; U17246; AAB67453.1; -
DR EMBL; U14913; AAB67448.1; -
DR HSSP; Q06187; IAWX.
DR SGD; S0004181; PEX13.
DR InterPro; IPR001452; SH3.
DR Pfam; PF00018; SH3; 1.
DR PRINTS; PR00452; SH3DOMAIN.
DR ProDom; PD000066; SH3; 1.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PS00002; SH3; 1.
KW Peroxisome; Transport; Protein transport; Transmembrane; SH3 domain.
FT DOMAIN 1 263 LUMENAL (POTENTIAL).
FT TRANSMEM 264 280
FT DOMAIN 281 386 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 306 372 SH3.

SQ SEQUENCE 386 AA; 42706 MW; DBEA9A2372185860 CRC64;
Query Match 61.7%; Score 37; DB 1; Length 386;
Best Local Similarity 85.7%; Pred. No. 20;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSFY 9
Db 117 HNYGSFY 123

RESULT 5
PTH_BUCAI
ID PTH_BUCAI STANDARD; PRT; 177 AA.
AC P57287;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Peptidyl-tRNA hydrolase (EC 3.1.1.29) (PTH).
GN PTH OR BU190.
OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
symbiotic bacterium).
OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.
OX NCBI_TaxID=118099;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=Tokyo 1998;
RX MEDLINE=20445173; PubMed=10993077;
RA Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
RT "Genome sequence of the endocellular bacterial symbiont of aphids
Buchnera sp. APS.";
RL Nature 407:81-86(2000).
CC -1- FUNCTION: THE NATURAL SUBSTRATE FOR THIS ENZYME MAY BE PEPTIDYL-
CC TRNAS WHICH DROP OFF THE RIBOSOME DURING PROTEIN SYNTHESIS
CC (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: N-substituted aminoacyl-tRNA + H(2)O = N-
CC substituted amino acid + tRNA.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE PTH FAMILY.
CC
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-----
DR EMBL; AP001118; BAB12907.1; -
DR HSSP; P23932; 2PTH.
DR InterPro; IPR001328; Pept_tRNA_hydro.
DR Pfam; PF01195; Pept_tRNA_hydro; 1.
DR ProDom; PD005324; Pept_tRNA_hydro; 1.
DR TIGRFAMs; TIGR00447; pth; 1.
DR PROSITE; PS01195; PEPT_TRNA_HYDROL_1; FALSE_NEG.
DR PROSITE; PS01196; PEPT_TRNA_HYDROL_2; 1.
KW Hydrolase; Complete proteome.
SQ SEQUENCE 177 AA; 20576 MW; BD18DA8FEF0DFAAF CRC64;
Query Match 60.0%; Score 36; DB 1; Length 177;
Best Local Similarity 75.0%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNVSFY 9
Db 16 RHNVSFY 23

RESULT 6
RCXM_RHORU
ID RCXM_RHORU STANDARD; PRT; 305 AA.
AC P10718;
Query Match 60.0%; Score 36; DB 1; Length 177;
Best Local Similarity 75.0%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Reaction center protein M chain (Photosynthetic reaction center M subunit).
DE PUFM.
GN Rhodospirillum rubrum.
OS Bacteria; Proteobacteria; alpha subdivision; Rhodospirillaceae;
OC Rhodospirillum.
OX NCBI_TaxID=1085;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88227960; PubMed=2836391;
RA Bellanger G., Berard J., Corribeau P., Gingras G.;
RT "The structural genes coding for the L and M subunits of
Rhodospirillum rubrum photoreaction center.";
RL J. Biol. Chem. 263:7632-7638(1988).
RN [2]
RP SEQUENCE OF 1-50.
RX MEDLINE=84133817; PubMed=6199280;
RA Theiler R., Suter F., Zuber H.;
RT "N-terminal sequences of subunits L and M of the photosynthetic
reaction centre from Rhodospirillum rubrum G-9". Separation of the
subunits by gel filtration on hydroxypropylated Sephadex G 100 in
organic solvents.";
RT Hoppe-Seyler's Z. Physiol. Chem. 364:1765-1776(1983).
RL
CC -!- FUNCTION: THE REACTION CENTER IS A MEMBRANE-BOUND COMPLEX THAT
MEDIATES THE INITIAL PHOTOCHEMICAL EVENT IN THE ELECTRON TRANSFER
PROCESS OF PHOTOSYNTHESIS.
CC
CC -!- SUBUNIT: REACTION CENTER IS COMPOSED OF FOUR BACTERIOCHLOROPHYLLS,
TWO BACTERIOPEOPHYTINS, TWO UBIQUINONES, ONE IRON, AND THREE
HIGHLY HYDROPHOBIC POLYPEPTIDE CHAINS (DESIGNATED L, M, AND H).
CC
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC
CC -!- SIMILARITY: BELONGS TO THE REACTION CENTER L/M CHAINS / PSBA /
PSBD FAMILY.
CC
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CC
CC EMBL; J03731; AAA26465.1; -
DR PIR; B28170; B28170.
DR HSP; P02953; 2RCR.
DR InterPro; IPR000484; Photo_RC.
DR Pfam; PF00124; photORC; 1.
DR PRINTS; PR00256; REACTNCENTRE.
DR ProDom; PD000551; Photo_RC; 1.
DR TIGRFAMs; TIGR01115; pufM; 1.
DR PROSITE; PS00244; REACTION_CENTER; 1.
KW Transmembrane; Electron transport; Photosynthesis; Reaction center;
KW Iron; Magnesium.
FT INIT.MET 0
FT TRANSMEM 52 78
FT TRANSMEM 110 139
FT TRANSMEM 142 167
FT TRANSMEM 197 225
FT TRANSMEM 259 285
FT METAL 200 200 MAGNESIUM (BACTERIOCHLOROPHYLL B).
FT METAL 217 217 IRON (NON HEME).
FT METAL 232 232 IRON (NON HEME).
FT METAL 264 264 IRON (NON HEME).
FT BINDING 250 250 QUINONE A.
SQ SEQUENCE 305 AA; 34017 MW; 75B2A5236F0EDB79 CRC64;
Query Match 60.0%; Score 36; DB 1; Length 305;
Best Local Similarity 71.4%; Pred. No. 24;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 4 NVGSFY 10

DB 190 NYGNFFY 196
|||:|:|
RESULT 7
TSA2_HUMAN
ID TSA2_HUMAN STANDARD; PRT; 309 AA.
AC Q8WYR4;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Testis-specific gene A2 (Male meiotic metaphase chromosome-associated
acidic protein) (Meichroacidin).
GN TSA2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98246622; PubMed=9578619;
RA Tsuchida J., Nishina Y., Wakabayashi N., Nozaki M., Sakai Y.,
RA Nishimune Y.;
RT "Molecular cloning and characterization of meichroacidin (male meiotic
metaphase chromosome-associated acidic protein).";
RL Dev. Biol. 197:67-76(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98246622; PubMed=9578619;
RA Shimizu N., Kudoh J., Shibuya K.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: May play an important role in male meiosis (By
similarity).
CC
CC -!- SUBCELLULAR LOCATION: Cytoplasmic in late spermatocytes, secondary
spermatocytes and round spermatids. Gathered around metaphase
chromosomes during meiotic divisions (By similarity).
CC
CC -!- TISSUE SPECIFICITY: Testis specific.
CC
CC -!- SIMILARITY: CONTAINS 6 MORN REPEATS.
CC
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CC
CC EMBL; AB06536; BAB83694.1; -
DR EMBL; AB041016; BAB92995.1; -
DR Genew; HGNC:12371; TSGA2.
DR InterPro; IPR003409; MORN.
DR Pfam; PF02493; MORN; 6.
KW Meiosis; Repeat.
FT DOMAIN 195 201 POLY-GLU.
FT DOMAIN 298 301 POLY-GLU.
FT REPEAT 20 43 MORN REPEAT 1.
FT REPEAT 44 66 MORN REPEAT 2.
FT REPEAT 67 89 MORN REPEAT 3.
FT REPEAT 90 112 MORN REPEAT 4.
FT REPEAT 113 135 MORN REPEAT 5.
FT REPEAT 159 181 MORN REPEAT 6.
SQ SEQUENCE 309 AA; 35124 MW; 09A20A766D5A6AB8 CRC64;
Query Match 60.0%; Score 36; DB 1; Length 309;
Best Local Similarity 55.6%; Pred. No. 24;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 2 RHNYGSFY 10
|||:|:|
DB 99 RHGIVY 107

RESULT 8

SYE2_RICPR ID SYE2_RICPR STANDARD; PRT; 470 AA.
 AC O9ZCT8;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Glutamyl-tRNA synthetase 2 (EC 6.1.1.17) (Glutamate--tRNA ligase 2) (Glurs 2).
 DE (Glurs 2).
 GN GLUTX2 OR RP623.
 OS Rickettsia prowazekii.
 OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
 OC Rickettsiaceae; Rickettsiae; Rickettsia.
 OX NCBI_TaxID=782;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Madrid E;
 RX MEDLINE=99039499; PubMed=9823893;
 RA Andersson S.G.E., Zomorodipour A., Andersson J.O., Podowski R.M., Naeslund A.K.,
 RA Sichert-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
 RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
 RT "The genome sequence of Rickettsia prowazekii and the origin of
 RT mitochondria.";
 RL Nature 396:133-140(1998).
 CC -1- CATALYTIC ACTIVITY: ATP + L-glutamate + tRNA(Glu) = AMP +
 CC diphosphate + L-glutamyl-tRNA(Glu).
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-tRNA SYNTHETASE FAMILY.
 CC -----
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 CC -----
 DR EMBL: AJ235272; CAAL5066.1; -;
 DR HSP; P27000; IGLN.
 DR InterPro: IPR004527; GltX_bact.
 DR InterPro: IPR000924; Glu_tRNA-synt_lc.
 DR InterPro: IPR001412; tRNA-synt_I.
 DR Pfam: PF00749; tRNA-synt_lc; 1.
 DR PRINTS: PR00987; TRNASYNTHGLU.
 DR TIGRFAMS: TIGR00464; gltX_bact; 1.
 DR PROSITE: PS00178; AA_TRNA_LIGASE_I; FALSE_NEG.
 KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
 KW Complete proteome.
 FT SITE 10 20 "HIGH" REGION.
 FT SITE 239 243 "KMSKS" REGION.
 FT BINDING 242 242 ATP (BY SIMILARITY).
 SQ SEQUENCE 470 AA; 53696 MW; DF1CE50A20B9A9DF CRC64;

Query Match 60.08; Score 36; DB 1; Length 470;
 Best Local Similarity 66.78; Pred. No. 37;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSFY 9

|||||

Db 31 ARHNNKFF 39

RESULT 9

EXOP_RHIME ID EXOP_RHIME STANDARD; PRT; 786 AA.
 AC P33698;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Succinoglycan biosynthesis transport protein exop.
 GN EXOP OR RB1086 OR SMB20961.
 OS Rhizobium meliloti (Sinorhizobium meliloti).

OG Plasmid pSymb (megaplasmid 2).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Sinorhizobium.
 OX NCBI_TaxID=382;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1021;
 RX MEDLINE=94042869; PubMed=8226645;
 RA Glucksmann M.A., Reuber T.L., Walker G.C.;
 RT "Family of glycosyl transferases needed for the synthesis of
 RT succinoglycan by Rhizobium meliloti";
 RL J. Bacteriol. 175:7033-7044(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1021;
 RX MEDLINE=94042870; PubMed=8226646;
 RA Glucksmann M.A., Reuber T.L., Walker G.C.;
 RT "Genes needed for the modification, polymerization, export, and
 RT processing of succinoglycan by Rhizobium meliloti: a model for
 RT succinoglycan biosynthesis";
 RL J. Bacteriol. 175:7045-7055(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RCR2011 / SU47;
 RX MEDLINE=94067019; PubMed=8246891;
 RA Becker A., Kleickmann A., Keller M., Arnold W., Puehler A.;
 RT "Identification and analysis of the Rhizobium meliloti exoAMONP genes
 RT involved in exopolysaccharide biosynthesis and mapping of promoters
 RT located on the exoHKLAMONP fragment";
 RL Mol. Gen. Genet. 241:367-379(1993).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1021;
 RX MEDLINE=21396508; PubMed=11481431;
 RA Finau T.M., Weidner S., Wong K., Buhrmester J., Chain P.,
 RA Vorhoefer F.J., Hernandez-Lucas I., Becker A., Gouzy J.,
 RA Golding B., Puehler A.;
 RT "The complete sequence of the 1,683-kb pSymb megaplasmid from the N2-
 RT fixing endosymbiont Sinorhizobium meliloti";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).
 CC -1- PATHWAY: Exopolysaccharide biosynthesis.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
 CC -1- SIMILARITY: SOME, TO B.SOLANACEARUM EPSB.
 CC -----
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 CC -----
 DR EMBL: L20758; AAA16042.1; -;
 DR EMBL: 222636; CAAR80349.1; -;
 DR EMBL: AL603645; CAC49486.1; -;
 DR PIR: B49349; B49349.
 DR PIR: S37031; S37031.
 DR PIR: S39960; S39960.
 DR InterPro: IPR003856; Wzz.
 DR Pfam: PF02706; Wzz; 1.
 DR TIGRFAMS: TIGR01005; eps_transp_fam; 1.
 KW Exopolysaccharide synthesis; Transport; Transmembrane; ATP-binding;
 KW Plasmid; Complete proteome.
 FT DOMAIN 1 42 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 43 66 POTENTIAL.
 FT DOMAIN 67 689 PERIPLASMIC (POTENTIAL).
 FT TRANSMEM 690 711 POTENTIAL.
 FT DOMAIN 712 786 CYTOPLASMIC (POTENTIAL).
 FT NP_BIND 583 590 ATP (POTENTIAL).
 SQ SEQUENCE 786 AA; 86123 MW; E19E771E31F2030C CRC64;

Query Match 60.08; Score 36; DB 1; Length 786;
 Best Local Similarity 62.5%; Pred. No. 62;

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Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFY 9
   |||:|
Db 768 RHRYGKY 775

RESULT 10
YX12 CAEEL
ID YX12 CAEEL STANDARD; PRT; 316 AA.
AC Q1123;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 35.1 kDa protein C03F11.2 in chromosome X.
GN C03F11.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Bentley D.;
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: WEAK, IN THE N-TERMINUS, TO C.ELEGANS F53B1.5.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X78423; CAA55188.1; -.
DR InterPro; IPR001362; GH_32.
DR Pfam; PF00251; Glyco_hydro_32; 1.
DR PROSITE; PS00609; GLYCOSYL_HYDROL_F32; 1.
KW Hydrolase; Glycosidase; Glycoprotein; Cell wall; Zymogen; Signal.
FT SIGNAL 1 ?
FT PROPEP ? ?
FT CHAIN ? ? 583
FT BETA-FRUCTOFURANOSIDASE, INSOLUBLE
FT ISOENZYME 3.
FT CARBOHYD 164
FT CARBOHYD 280
FT CARBOHYD 303
FT CARBOHYD 340
FT CARBOHYD 361
FT CARBOHYD 561
SQ SEQUENCE 583 AA; 66381 MW; 1DBF591CD94749AF CRC64;

Query Match 58.3%; Score 35; DB 1; Length 583;
Best Local Similarity 62.5%; Pred No. 69;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHNYGSFY 9
   |||:|
Db 313 RYDYGNY 320

RESULT 12
INV1 DAUCA
ID INV1 DAUCA STANDARD; PRT; 592 AA.
AC P26792;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Beta-fructofuranosidase, insoluble isoenzyme 1 precursor (EC 3.2.1.26)
DE (Sucrose-6-phosphate hydrolase 1) (Invertase 1) (Cell wall beta-
DE fructosidase 1).
GN INV1.
OS Daucus carota (Carrot).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids II; Apiales; Apiaceae; Daucus.
OX NCBI_TaxID=4039;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=cv. Queen Anne's Lace;
RX MEDLINE=93005650; PubMed=2152110;
RA Sturm A.; Chrispeels M.J.;
RT "cDNA cloning of carrot extracellular beta-fructosidase and its
RT expression in response to wounding and bacterial infection.";
RL Plant Cell 2:1107-1119(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94035200; PubMed=8220495;
RA Ramloch-Lorenz K.; Knudsen S.; Sturm A.;
RT "Molecular characterization of the gene for carrot cell wall beta-
RT fructosidase.";
RL Plant J. 4:545-554(1993).
CC -!- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN PHLOEM UNLOADING AND IN

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Plant Mol. Biol. 28:189-194(1995).
-!- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN PHLOEM UNLOADING AND IN
CC STRESS RESPONSE.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of terminal non-reducing beta-D-
CC fructofuranoside residues in beta-D-fructofuranosides
CC -!- SUBCELLULAR LOCATION: IONICALLY BOUND TO THE CELL WALL.
CC -!- SIMILARITY: BELONGS TO FAMILY 32 OF GLYCOSYL HYDROLASES.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X78423; CAA55188.1; -.
DR InterPro; IPR001362; GH_32.
DR Pfam; PF00251; Glyco_hydro_32; 1.
DR PROSITE; PS00609; GLYCOSYL_HYDROL_F32; 1.
KW Hydrolase; Glycosidase; Glycoprotein; Cell wall; Zymogen; Signal.
FT SIGNAL 1 ?
FT PROPEP ? ?
FT CHAIN ? ? 583
FT BETA-FRUCTOFURANOSIDASE, INSOLUBLE
FT ISOENZYME 3.
FT CARBOHYD 164
FT CARBOHYD 280
FT CARBOHYD 303
FT CARBOHYD 340
FT CARBOHYD 361
FT CARBOHYD 561
SQ SEQUENCE 583 AA; 66381 MW; 1DBF591CD94749AF CRC64;

Query Match 58.3%; Score 35; DB 1; Length 583;
Best Local Similarity 62.5%; Pred No. 69;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHNYGSFY 9
   |||:|
Db 313 RYDYGNY 320

RESULT 12
INV1 DAUCA
ID INV1 DAUCA STANDARD; PRT; 592 AA.
AC P26792;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Beta-fructofuranosidase, insoluble isoenzyme 1 precursor (EC 3.2.1.26)
DE (Sucrose-6-phosphate hydrolase 1) (Invertase 1) (Cell wall beta-
DE fructosidase 1).
GN INV1.
OS Daucus carota (Carrot).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids II; Apiales; Apiaceae; Daucus.
OX NCBI_TaxID=4039;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=cv. Queen Anne's Lace;
RX MEDLINE=93005650; PubMed=2152110;
RA Sturm A.; Chrispeels M.J.;
RT "cDNA cloning of carrot extracellular beta-fructosidase and its
RT expression in response to wounding and bacterial infection.";
RL Plant Cell 2:1107-1119(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94035200; PubMed=8220495;
RA Ramloch-Lorenz K.; Knudsen S.; Sturm A.;
RT "Molecular characterization of the gene for carrot cell wall beta-
RT fructosidase.";
RL Plant J. 4:545-554(1993).
CC -!- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN PHLOEM UNLOADING AND IN

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CC STRESS RESPONSE.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of terminal non-reducing beta-D-
CC fructofuranoside residues in beta-D-fructofuranosides.
CC -!- SUBCELLULAR LOCATION: IONICALLY BOUND TO THE CELL WALL.
CC -!- TISSUE SPECIFICITY: IN LEAVES AND ROOTS OF YOUNG PLANTS.
CC -!- INDUCTION: By wounding and bacterial infection.
CC -!- SIMILARITY: BELONGS TO FAMILY 32 OF GLYCOSYL HYDROLASES.
CC -----
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CC -----
DR EMBL; M58362; AAA03516.1; -.
DR EMBL; X69321; CAA49162.1; -.
DR PIR; JQ0991; JQ0991.
DR GlycoSuiteDB; P26792; -.
DR InterPro; IPR001362; GH_32.
DR Pfam; PF00251; Glyco_hydro_32; 1.
DR PROSITE; PS00609; GLYCOSYL_HYDROL_F32; 1.
KW Hydrolase; Glycosidase; Glycoprotein; Cell wall; Zymogen; Signal.
FT SIGNAL 1 31
FT PROPEP 32 48
FT CHAIN 49 592
FT ACT_SITE 74 74
FT CARBOHYD 170 170
FT CARBOHYD 195 195
FT CARBOHYD 311 311
FT CARBOHYD 348 348
FT CARBOHYD 570 570
FT CONFLICT 133 133
FT CONFLICT 487 487
SQ SEQUENCE 592 AA; 66813 MW; E3DF05355D277D0C CRC64;

Query Match 58.3%; Score 35; DB 1; Length 592;
Best Local Similarity 62.5%; Pred. No. 70;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHNYGSFY 9
DB 321 RYDYGNYF 328

RESULT 13
INV2_DAUCA STANDARD; PRT; 592 AA.
AC Q39692;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Beta-fructofuranosidase, Insoluble Isoenzyme 2 precursor (EC 3.2.1.26)
DE (Sucrose-6-phosphate hydrolase 2) (Invertase 2) (Cell wall beta-
DE fructosidase 2).
GN INV2.
OS Daucus carota (Carrot).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids II; Apiales; Apiaceae; Daucus.
OX NCBI_TaxID=4039;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Queen Anne's Lace;
RX MEDLINE=95306787; PubMed=7787183;
RA Lorenz K., Lienhard S., Sturm A.;
RT "Structural organization and differential expression of carrot beta-
RT fructofuranosidase genes: identification of a gene coding for a

```

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RT flower bud-specific isozyme.";
RT Plant Mol. Biol. 28:189-194(1995).
CC -!- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN PHLOEM UNLOADING AND IN
CC STRESS RESPONSE.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of terminal non-reducing beta-D-
CC fructofuranoside residues in beta-D-fructofuranosides.
CC -!- SUBCELLULAR LOCATION: IONICALLY BOUND TO THE CELL WALL.
CC -!- SIMILARITY: BELONGS TO FAMILY 32 OF GLYCOSYL HYDROLASES.
CC -----
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CC -----
DR EMBL; X78424; CAA55189.1; -.
DR InterPro; IPR001362; GH_32.
DR Pfam; PF00251; Glyco_hydro_32; 1.
DR PROSITE; PS00609; GLYCOSYL_HYDROL_F32; 1.
KW Hydrolase; Glycosidase; Glycoprotein; Cell wall; Zymogen; Signal.
FT SIGNAL 1 7
FT PROPEP ? 592
FT CHAIN ? 592
FT ACT_SITE 75 75
FT CARBOHYD 171 171
FT CARBOHYD 195 195
FT CARBOHYD 310 310
FT CARBOHYD 347 347
FT CARBOHYD 568 568
FT SEQUENCE 592 AA; 67397 MW; 2734603836709133 CRC64;

Query Match 58.3%; Score 35; DB 1; Length 592;
Best Local Similarity 62.5%; Pred. No. 70;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHNYGSFY 9
DB 320 RYDYGNYF 327

RESULT 14
TNFC_PIG STANDARD; PRT; 150 AA.
AC Q9TSV8;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Lymphotoxin-beta (LTX-beta) (Tumor necrosis factor C) (TNF-C) (Tumor
DE necrosis factor ligand superfamily member 3) (Fragment).
GN LTB OR TNFSF3 OR TNFC.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Large white; TISSUE=Fibroblast;
RX MEDLINE=21108615; PubMed=11169259;
RA Chardon P., Rogel-Gallard C., Cattolico L., Duprat S., Vaiman M.,
RA Renard C.;
RT "Sequence of the swine major histocompatibility complex region
RT containing all non-classical class I genes.";
RL Tissue Antigens 57:55-65(2001).
CC -!- FUNCTION: Cytokine that binds to LTBR/TNFRSF3. May play a specific
CC role in immune response regulation. Provides the membrane anchor
CC for the attachment of the heterotrimeric complex to the cell
CC surface.
CC -!- SUBUNIT: Heterotrimer of either two LTB and one LTA subunits or
CC (less prevalent) two LTA and one LTB subunits.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein (By similarity).

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CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
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CC -----
DR EMBL: AJ251914; CAB63851.1; -
DR InterPro: IPR003636; TNF_abc.
DR InterPro: IPR000478; TNF_family.
DR Pfam: PF00229; TNF; 1.
DR PRINTS: PR01234; TNECROSISFCT.
DR ProDom: PD002012; TNF_abc; 1.
DR SMART: SM00207; TNF; 1.
DR PROSITE: PS00251; TNF_1; 1.
DR PROSITE: PS00049; TNF_2; 1.
KW Cytokine; Cytotoxin; Glycoprotein.
FT CARBOHYD 128 128 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 150 AA; 16423 MW; FE5C4CC657658B48 CRC64;

Query Match 56.7%; Score 34; DB 1; Length 150;
Best Local Similarity 55.6%; Pred. No. 26;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 RHNYGSFY 10
DB 100 RHEYGPLY 108

RESULT 15
IF2A_PYRAB STANDARD; PRT; 275 AA.
AC Q9V0E4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable translation initiation factor 2 alpha subunit (eIF-2-alpha).
GN EIF2A OR PAB0568.
OS Pyrococcus abyssi.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OX NCBI_TaxID=29292;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GE5 / Orsay;
RA Heilig R.;
RT "Pyrococcus abyssi genome sequence: insights into archaeal chromosome
RL structure and evolution.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: EIF-2 FUNCTIONS IN THE EARLY STEPS OF PROTEIN SYNTHESIS
CC BY FORMING A TERNARY COMPLEX WITH GTP AND INITIATOR TRNA
CC (BY SIMILARITY).
CC -!- SUBUNIT: HETEROTRIMER COMPOSED OF AN ALPHA, A BETA, AND A GAMMA
CC CHAIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE EIF-2-ALPHA FAMILY.
CC -!- SIMILARITY: CONTAINS 1 S1 MOTIF DOMAIN.
CC -----
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CC -----
DR EMBL: AJ249285; CAB49760.1; -
DR HSSP: P05055; ISRO.
DR InterPro: IPR003029; S1.
DR Pfam: PF00575; S1; 1.
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DR SMART: SM00316; S1; 1.
DR PROSITE: PS0126; S1; 1.
KW Initiation factor; Protein biosynthesis; RNA-binding;
FT Complete proteome.
FT DOMAIN 12 83 S1 MOTIF.
SQ SEQUENCE 275 AA; 31912 MW; B2659F3A49879B4F CRC64;

Query Match 56.7%; Score 34; DB 1; Length 275;
Best Local Similarity 83.3%; Pred. No. 48;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
DB 23 HNYGAF 28

Search completed: November 18, 2002, 17:33:26
Job time : 3.45098 secs
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GenCore version 5.1.3
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OM protein - protein search, using sw model
Run on: November 18, 2002, 17:22:01 ; Search time 10.4412 Seconds
(without alignments)
197.341 Million cell updates/sec

Title: US-09-016-061-66
Perfect score: 60
Sequence: 1 ARHNYGSFY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : SPTREMBL_21.*
- 1: sp_archaea.*
 - 2: sp_bacteria.*
 - 3: sp_fungi.*
 - 4: sp_human.*
 - 5: sp_invertebrate.*
 - 6: sp_mammal.*
 - 7: sp_mhc.*
 - 8: sp_organelle.*
 - 9: sp_phage.*
 - 10: sp_plant.*
 - 11: sp_rodent.*
 - 12: sp_virus.*
 - 13: sp_vertebrate.*
 - 14: sp_unclassified.*
 - 15: sp_virus.*
 - 16: sp_bacteriap.*
 - 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				Query	Match	Length	DB	ID	Description
Result No.	Score	Match	Length	DB	ID				
1	43	71.7	839	10	Q9LIE5				
2	42	70.0	195	16	Q9CG29				
3	40	66.7	219	5	Q9VY18				
4	39	65.0	143	16	Q8XYU2				
5	39	65.0	536	17	Q8U2P1				
6	39	65.0	581	10	Q93X59				
7	39	65.0	660	10	Q8RX28				
8	39	65.0	1108	10	Q9FNQ7				
9	39	65.0	2288	5	Q23081				
10	39	65.0	2315	5	Q95ZK3				
11	38	63.3	89	7	O19495				
12	38	63.3	233	16	P74653				
13	38	63.3	377	13	Q91997				
14	38	63.3	502	10	Q9XG35				
15	38	63.3	1144	2	Q50371				
16	37	61.7	170	11	Q925S2				

17	37	61.7	192	3	O14085	O14085 schizosacch
18	37	61.7	287	4	Q96SV1	Q96SV1 homo sapien
19	37	61.7	333	2	Q47734	Q47734 enterococcu
20	37	61.7	356	11	Q9JJC2	Q9JJC2 mus musculu
21	37	61.7	368	2	Q9AL13	Q9AL13 enterococcu
22	37	61.7	383	11	Q9Z2E9	Q9Z2E9 mus musculu
23	37	61.7	383	11	Q9JMF1	Q9JMF1 mus musculu
24	37	61.7	398	4	Q9BSQ0	Q9BSQ0 homo sapien
25	37	61.7	484	4	Q96G97	Q96G97 homo sapien
26	37	61.7	468	6	Q9BE23	Q9BE23 macaca fasc
27	37	61.7	643	3	Q01864	Q01864 penicillium
28	37	61.7	661	12	O8QVL2	O8QVL2 hamster par
29	37	61.7	806	5	Q97288	Q97288 plasmodium
30	37	61.7	897	2	O85661	O85661 proteus mir
31	37	61.7	1285	5	O01495	O01495 caenorhabdi
32	37	61.7	5317	5	O8TA74	O8TA74 hemiceintrot
33	36	60.0	39	7	P79474	P79474 cervus elap
34	36	60.0	39	7	P79477	P79477 cervus elap
35	36	60.0	39	7	P79478	P79478 cervus elap
36	36	60.0	39	7	P79479	P79479 cervus elap
37	36	60.0	67	7	Q8SP02	Q8SP02 hapalemur g
38	36	60.0	74	6	Q9TTM4	Q9TTM4 bos taurus
39	36	60.0	75	7	Q9GIJ5	Q9GIJ5 bos taurus
40	36	60.0	76	7	Q9TBC2	Q9TBC2 macaca mula
41	36	60.0	77	7	Q9GJ91	Q9GJ91 ovis aries
42	36	60.0	77	7	Q9GJ90	Q9GJ90 ovis aries
43	36	60.0	77	7	Q9GJ82	Q9GJ82 ovis aries
44	36	60.0	78	6	Q97968	Q97968 ovis aries
45	36	60.0	78	6	O97835	O97835 ovis aries

ALIGNMENTS

RESULT 1

Q9LIE5 ID Q9LIE5 PRELIMINARY: PRT; 839 AA.
AC Q9LIE5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Far-red impaired response protein, mutator-like transposase-like
DE protein, phytochrome A signaling protein-like.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=20363099; PubMed=10907853;
RA Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.
RT Sequence features of the regions of 4,251,695 bp covered by ninety Pl,
RT TAC and BAC clones.";
RL DNA Res. 7:217-221(2000).
DR EMBL: AP001306; BAB03065.1; -
DR InterPro: IPR004330; FArL;
DR InterPro: IPR001000; Glyco_hydro_10.
DR Pfam: PF03101; FArL; 1.
DR PROSITE: PS00591; GLYCOSYL-HYDROL_F10; UNKNOWN_1.
SQ SEQUENCE 839 AA; 95996 MW; CBBF60DF8B679F8 CRC64;

Query Match 71.7%; Score 43; DB 10; Length 839;
Best Local Similarity 87.5%; Pred. No. 25;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ARHNYGSF 8
Db 274 SRHNYGSF 281

RESULT 2
ID Q9CGZ9 PRELIMINARY; PRT; 195 AA.
AC Q9CGZ9;
RC STRAIN=21235186; PubMed=11337471;
RX MEDLINE=21235186; PubMed=11337471;
RA Bolotin A., Wincker P., Mauger S., Jaillon O., Mialme K.,
RA Weissenbach J., Ehrlich S.D., Sorokin A.;
RT "The complete genome sequence of the lactic acid bacterium Lactococcus
lactis ssp. lactis IL1403."
RL Genome Res. 11:731-753(2001).
DR EMBL; A006328; AAK05041.1; -.
DR InterPro; IPR000868; Isochorismatase.
DR Pfam; PF00857; Isochorismatase; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 195 AA; 21535 MW; A408E9F70EC7B43F CRC64;

Query Match 70.0%; Score 42; DB 16; Length 195;
Best Local Similarity 66.7%; Pred. No. 7.7;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSF 9
Db 103 AKHNGAFY 111

RESULT 3
Q9VVY8
ID Q9VVY8 PRELIMINARY; PRT; 219 AA.
AC Q9VVY8;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yeaman M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burfi K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

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RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirska R., Rector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2193(2000).
DR EMBL; AE003517; AAF49167.1; -.
DR FlyBase; FBgn0036866; CG14092.
SQ SEQUENCE 219 AA; 23269 MW; 9BE657EA89FEB43D CRC64;

Query Match 66.7%; Score 40; DB 5; Length 219;
Best Local Similarity 85.7%; Pred. No. 20;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 NYGSEFY 10
Db 43 NYGSEFY 49

RESULT 4
Q8XYU2 PRELIMINARY; PRT; 143 AA.
ID Q8XYU2;
AC Q8XYU2;
RX MEDLINE=21681879; PubMed=11823852;
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
DE Hypothetical protein RSC1664.
GN RSC1664 OR RS04045.
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
OC Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GM1000;
RX MEDLINE=21681879; PubMed=11823852;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
RA Chandler M., Choise N., Claudel-Renard C., Cunnac S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin V., Schiex T.,
RA Sigulier P., Thebault P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum."
RL Nature 415:497-502(2002).
DR EMBL; AL646065; CAD15366.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 143 AA; 15556 MW; 4E710B20861E097C CRC64;

Query Match 65.0%; Score 39; DB 16; Length 143;
Best Local Similarity 62.5%; Pred. No. 19;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSFY 10
Db 111111111

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Db 117 HNYGTFHF 124
RESULT 5
Q8U2P1 PRELIMINARY; PRT; 536 AA.
AC Q8U2P1;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical protein PF0792.
GN PF0792.
OS Pyrococcus furiosus.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=2261;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VC1 / DSM 3638 / ATCC 43587 / JCM 8422;
RA Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
RT "The complete sequence of the Pyrococcus furiosus genome.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE010196; AAL80916.1;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 536 AA; 63059 MW; B96D6766B7163E54 CRC64;

Query Match 65.0%; Score 39; DB 17; Length 536;
Best Local Similarity 66.7%; Pred. No. 79;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFY 10
|||||
DB 8 RHNYGLWI 16

RESULT 6
Q93X59 PRELIMINARY; PRT; 581 AA.
AC Q93X59;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Fructan 1-exohydrolase IIB precursor (EC 3.2.1.80).
GN 1-FEH IIB.
OS Cichorium intybus (Chicory).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae; Cichorium.
OX NCBI_TaxID=13427;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV, FLASH; TISSUE=ROOT;
RX MEDLINE=21351405; PubMed=11457968;
RA Van den Ende W., Michiels A., Van Wouterghem D., Clerens S.P.,
RA De Roover J., Van Laere A.;
RT "Defoliation induces fructan 1-exohydrolase II in withloof chicory
RT roots. Cloning and purification of two isoforms, fructan 1-
RT exohydrolase IIA and fructan 1-exohydrolase IIB. Mass fingerprint of
RT the fructan 1-exohydrolase II enzymes.";
RL Plant Physiol. 126:1186-1195(2001).
CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF TERMINAL NON-REDUCING BETA-D-
CC FRUCTOFURANOSIDE RESIDUES IN BETA-D-FRUCTOFURANOSIDES.
CC -1- SIMILARITY: BELONGS TO FAMILY 32 OF GLYCOSYL HYDROLASES.
DR EMBL; AJ295034; CAC37923.1;
DR InterPro; IPR001362; GH_32.
DR Pfam; PF00251; Glyco_hydro_32; 1.
DR PROSITE; PS00609; GLYCOSYL_HYDROL_F32; UNKNOWN_1.
KW Glycoprotein; Glycosidase; Hydrolase; Signal.
FT SIGNAL 1 38 POTENTIAL.
FT CHAIN 39 FRUCTAN 1-EXOXYDROLASE IIB.
SQ SEQUENCE 581 AA; 65269 MW; 978EAL39FDC9C5D CRC64;

Query Match 65.0%; Score 39; DB 10; Length 581;

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Best Local Similarity 75.0%; Pred. No. 87;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFY 9
|||||
DB 305 RYNYGGFY 312

RESULT 7
Q8RX28 PRELIMINARY; PRT; 660 AA.
AC Q8RX28;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative histone deacetylase.
GN AT5G61060.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
RA Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,
RA Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,
RA Carlinici P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
RA Sakurai T., Satou M., Seki M., Shim P., Southwick A., Shinozaki K.,
RA Davis R.W., Ecker J.R., Theologis A.;
RT "Arabidopsis Full Length cDNA Clones.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY090936; AAM13986.1;
SQ SEQUENCE 660 AA; 72722 MW; A40906BF82B397DE CRC64;

Query Match 65.0%; Score 39; DB 10; Length 660;
Best Local Similarity 75.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFY 9
|||||
DB 222 RHEYGGFY 229

RESULT 8
Q9FNQ7 PRELIMINARY; PRT; 1108 AA.
AC Q9FNQ7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Similarity to histone deacetylase.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=98069011; PubMed=9405937;
RA Kotani H., Nakamura Y., Sato S., Kaneko T., Asamizu E., Miyajima N.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. II.
RT Sequence features of the regions of 1,044,062 bp covered by thirteen
RT physically assigned pl clones.";
RL DNA Res. 4:291-300(1997).
DR EMBL; AB006696; BAB10370.1;
DR InterPro; IPR000286; His_deacetylse.
DR Pfam; PF00850; Hist_deacetyl; 2.
DR PRINTS; PR01270; HDASUPER.

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SQ  SEQUENCE  1108 AA;  123609 MW;  9BCF5A2BCD90A1E2 CRC64;

Query Match      65.0%;  Score 39;  DB 10;  Length 1108;
Best Local Similarity 75.0%;  Pred. No. 1.8e+02;
Matches 6;  Conservative 0;  Mismatches 2;  Indels 0;  Gaps 0;

Qy  2 RHNYGSFY 9
    |||||
Db  898 RHEYGGEY 905

RESULT 9
Q23081 PRELIMINARY;  PRT;  2288 AA.
AC Q23081;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical 262.2 kDa protein.
GN ZC8.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=BRISTOL N2;
RC MEDLINE=99069613; PubMed=9851916;
RX None;
RA "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium. ";
RL Science 282:2012-2018(1998).
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=BRISTOL N2;
RC Latreille P., Bradshaw H.;
RA "The sequence of C. elegans
RT submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
[3]
RN SEQUENCE FROM N.A.
RP STRAIN=BRISTOL N2;
RC Waterston R.;
RA "Direct Submission. ";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RW EMBL; U64862; AAB52624.1; -.
DR Hypothetical protein.
SQ SEQUENCE 2288 AA; 262171 MW; 06D1700A0F4ACD2F CRC64;

Query Match      65.0%;  Score 39;  DB 5;  Length 2288;
Best Local Similarity 60.0%;  Pred. No. 3.9e+02;
Matches 6;  Conservative 2;  Mismatches 2;  Indels 0;  Gaps 0;

Qy  1 ARNYGSFY 10
    :||| |
Db  34 SRSNYGEFY 43

RESULT 10
Q95ZK3 PRELIMINARY;  PRT;  2315 AA.
AC Q95ZK3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical protein ZC8.4b.
GN ZC8.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=BRISTOL N2;

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DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein slr1652.
GN SLR1652.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asanizu E., Nakamura Y.,
RA Miyajima N., Hiroseawa M., Sugitara M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
RA Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
DR EMBL: D90917; BAA18769.1; -.
DR InterPro: IPR002741; DUF56.
DR Pfam: PF01879; DUF56; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 233 AA; 24737 MW; 19C8BFF4272F08B2 CRC64;

Query Match 63.3%; Score 38; DB 16; Length 233;
Best Local Similarity 55.6%; Pred. No. 48;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFY 10
| | | | |
Db 98 RHSTGLFY 106

RESULT 13
Q91997 PRELIMINARY; PRT; 377 AA.
AC Q91997;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE 3BETA-hydroxysteroid dehydrogenase/DELTA5-DELTA4 isomerase.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=ADRENAL GLAND;
RX MEDLINE=96032354; PubMed=7557440;
RA Nakabayashi O., Nomura O., Nishimori K., Mizuno S.;
RT "The cDNA cloning and transient expression of a chicken gene encoding
RT a 3 beta-hydroxysteroid dehydrogenase/delta 5-->4 isomerase unique to
RT major steroidogenic tissues.";
RL Gene 162:261-265(1995).
DR EMBL: D43763; BAA07820.1; -.
DR EMBL: D43762; BAA07819.1; -.
DR InterPro: IPR002225; 3Beta_HSD.
DR Pfam: PF01073; 3Beta_HSD; 1.
KW Isomerase.
SQ SEQUENCE 377 AA; 42881 MW; 22D9C5B8C7AD605C CRC64;

Query Match 63.3%; Score 38; DB 13; Length 377;
Best Local Similarity 70.08; Pred. No. 82;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARHNYGSFY 10
| | | | |
Db 250 ARHRTQFY 259

RESULT 14
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Q9XG35
ID Q9XG35 PRELIMINARY; PRT; 502 AA.
AC Q9XG35;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE T-complex protein gamma SU.
GN TCGP.
OS Guillardia theta (Cryptomonas phi).
OC Eukaryota; Cryptophyta; Cryptomonadaceae; Guillardia.
OX NCBI_TaxID=55529;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20087226; PubMed=10618395;
RA Zauner S., Fraunholz M., Wastl J., Penny S.L., Beaton M.,
RA Cavalier-Smith T., Maier U., Douglas S.;
RT "Chloroplast protein and centrosomal genes, a tRNA intron, and odd
RT telomeres in an unusually compact eukaryotic genome, the cryptomonad
RT nucleomorph.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:200-205(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21223349; PubMed=11323671;
RA Douglas S., Zauner S., Fraunholz M., Beaton M., Penny S., Deng L.,
RA Wu X., Reith M., Cavalier-Smith T., Maier U.;
RT "The highly reduced genome of an enslaved algal nucleus."?
RL Nature 410:1091-1096(2001).
DR EMBL: AJ010592; CAB40401.1; -.
DR InterPro: IPR002194; Chaperonin_TCP-1.
DR InterPro: IPR002423; Cpn60/TCP-1.
DR Pfam: PF00118; cpn60_TCF1; 1.
DR PRINTS: PR00304; TCOMPLEXTCP1.
DR PROSITE: PS00750; TCP1_1; 1.
KW ATP-binding; Chaperone.
SQ SEQUENCE 502 AA; 57514 MW; ALB4789A2DA9F787 CRC64;

Query Match 63.3%; Score 38; DB 10; Length 502;
Best Local Similarity 62.5%; Pred. No. 11e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 HNYGSFY 10
| | | | |
Db 444 HNYGKYY 451

RESULT 15
Q50371 PRELIMINARY; PRT; 1144 AA.
ID Q50371
AC Q50371;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Pl-like adhesin.
OS Mycoplasma pirum.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
OC Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2122;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BER;
RC MEDLINE=94113957; PubMed=8300531;
RA Tham T.N., Ferris S., Bahraoui E., Canarelli S., Montagnier L.,
RA Blanchard A.;
RT "Molecular characterization of the Pl-like adhesin gene from
RT Mycoplasma pirum.";
RL J. Bacteriol. 176:781-788(1994).
DR EMBL: L19685; AAC36866.1; -.
SQ SEQUENCE 1144 AA; 126732 MW; E7801C55C102D930 CRC64;

Query Match 63.3%; Score 38; DB 2; Length 1144;
Best Local Similarity 55.6%; Pred. No. 2.7e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
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QY 2 RHNYSFY 10
: : : : :
Db 885 KQNYGSFY 893

Search completed: November 18, 2002, 17:40:45
Job time : 11.4912 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 18, 2002, 17:21:57 ; Search time 13.8235 Seconds
(without alignments)
96.394 Million cell updates/sec

Title: US-09-016-061-66

Perfect score: 60

Sequence: 1 ARHNYGSFY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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21: /SID22/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SID22/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	60	100.0	10	AAW76023	LM609 grafted anti
2	60	100.0	10	AAW76023	Mutant VH CDR3 pep
3	53	88.3	10	AAW76039	LM609 grafted anti
4	53	88.3	10	AAW76040	LM609 grafted anti
5	53	88.3	10	AAW76040	Multiple mutant VH
6	53	88.3	10	AAW76040	Multiple mutant VH
7	51	85.0	10	AAW76010	LM609 grafted anti
8	51	85.0	10	AAW76010	LM609 VH CDR3 pep
9	51	85.0	117	AAW76001	Vitaxin antibody h
10	51	85.0	117	AAW76003	LM609 antibody hea

11	51	85.0	117	20	AAW06381	Murine monoclonal
12	51	85.0	117	20	AAW06387	Humanised LM609 an
13	51	85.0	117	22	AAW06387	A heavy chain vari
14	51	85.0	117	22	AAW06389	A heavy chain vari
15	51	85.0	117	22	AAW06389	Vitaxin heavy cha
16	51	85.0	117	22	AAW06389	Humanised LM609 hea
17	51	85.0	118	20	AAW06384	Humanised LM609 an
18	51	85.0	118	20	AAW06385	Humanised LM609 an
19	51	85.0	118	20	AAW06386	Humanised LM609 an
20	51	85.0	118	20	AAW06383	Humanised LM609 an
21	51	85.0	130	20	AAW06379	Murine monoclonal
22	50	83.3	10	19	AAW76022	LM609 grafted anti
23	50	83.3	10	22	AAW61380	Mutant VH CDR3 pep
24	48	80.0	10	19	AAW76038	LM609 grafted anti
25	48	80.0	10	19	AAW76021	LM609 grafted anti
26	48	80.0	10	22	AAW61379	Mutant VH CDR3 pep
27	48	80.0	10	22	AAW61396	Multiple mutant VH
28	46	76.7	10	19	AAW76020	LM609 grafted anti
29	46	76.7	10	19	AAW76024	LM609 grafted anti
30	46	76.7	10	19	AAW76025	LM609 grafted anti
31	46	76.7	10	19	AAW76026	LM609 grafted anti
32	46	76.7	10	19	AAW76027	LM609 grafted anti
33	46	76.7	10	19	AAW76028	LM609 grafted anti
34	46	76.7	10	19	AAW76029	LM609 grafted anti
35	46	76.7	10	19	AAW76030	LM609 grafted anti
36	46	76.7	10	22	AAW61378	Mutant VH CDR3 pep
37	46	76.7	10	22	AAW61382	Mutant VH CDR3 pep
38	46	76.7	10	22	AAW61383	Mutant VH CDR3 pep
39	46	76.7	10	22	AAW61384	Mutant VH CDR3 pep
40	46	76.7	10	22	AAW61385	Mutant VH CDR3 pep
41	46	76.7	10	22	AAW61386	Mutant VH CDR3 pep
42	46	76.7	10	22	AAW61387	Mutant VH CDR3 pep
43	46	76.7	10	22	AAW61388	Mutant VH CDR3 pep
44	43	71.7	110	20	AAW84099	Vitronectin alpha-
45	43	71.7	117	20	AAW84093	Murine vitronectin

ALIGNMENTS

RESULT 1

AAW76023
ID AAW76023 standard; Protein; 10 AA.

AC AAW76023;

DT 02-NOV-1998 (first entry)

DE LM609 grafted antibody V-H region CDR3 protein fragment #5.

XX Vitaxin; antibody; variable region; heavy chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.

OS Mus sp.

PN WO9833919-A2.

XX 06-AUG-1998.

PF 30-JAN-1998; 98WO-US01826.

PR 30-JAN-1997; 97US-0791391.

PA (IXSY-) IXSYS INC.

PI Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

DR N-PSDB; AAW49860.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
XX Claim 62; Page 41; 129pp; English.
XX
CC AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
CC antibodies contain non-murine framework regions so are suitable for use
CC in humans. Enhanced types of LM609 have affinity more than 90 times
CC greater than that of parent the parent antibody.
XX
XX Sequence 10 AA;
SQ
Query Match 100.0%; Score 60; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ARHNYGSFY 10
DB 1 ARHNYGSFY 10
|||||
RESULT 2
AAB61381
ID AAB61381 standard; peptide; 10 AA.
XX
XX AAB61381;
XX
XX 03-APR-2001 (first entry)
XX
XX Mutant VH CDR3 peptide #4.
XX
XX LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
KW inflammatory; cancer; retina; restenosis; osteoporosis.
XX
XX Unidentified.
XX
XX WO200078815-A1.
XX
XX 28-DEC-2000.
XX
XX 23-JUN-2000; 2000WO-US17454.
XX
XX 24-JUN-1999; 99US-0339922.
XX
XX (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX
XX Huse WD, Wu H;
XX
XX WPI; 2001-050110/06.
XX
XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
PT osteoporosis -
XX
XX Disclosure; Page 41; 132pp; English.
XX
XX The present invention relates to enhanced LM609 grafted antibodies
CC exhibiting selective binding affinity to alphavbeta_3 integrin or
CC their functional fragments. The antibodies or their functional
CC fragments can be used in the diagnosis and treatment of
CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory

CC diseases (such as psoriasis and chronic articular rheumatism),
CC disorders associated with inappropriate or inopportune invasion of
CC vessels (such as diabetic retinopathy, neovascular glaucoma and
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
CC diseases (such as macular degeneration), restenosis and
CC osteoporosis.
XX
XX Sequence 10 AA;
SQ
Query Match 100.0%; Score 60; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ARHNYGSFY 10
DB 1 ARHNYGSFY 10
|||||
RESULT 3
AAW76039
ID AAW76039 standard; Protein; 10 AA.
XX
XX AAW76039;
XX
XX 02-NOV-1998 (first entry)
XX
XX LM609 grafted antibody V-H region CDR3 protein fragment #15.
XX
XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
XX
XX Mus sp.
XX
XX WO9833919-A2.
XX
XX 06-AUG-1998.
XX
XX 30-JAN-1998; 98WO-US01826.
XX
XX 30-JAN-1997; 97US-0791391.
XX
XX (IXSY-) IXSYS INC.
XX
XX Glaser SM, Huse WD;
XX
XX WPI; 1998-437472/37.
XX
XX N-PSDB; AAV49876.
XX
XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
XX Claim 62; Page 43; 129pp; English.
XX
XX AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
CC antibodies contain non-murine framework regions so are suitable for use
CC in humans. Enhanced types of LM609 have affinity more than 90 times
CC greater than that of parent the parent antibody.
XX
XX Sequence 10 AA;
SQ

Query Match 88.3%; Score 53; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.027;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFY 9
 |||||
 Db 1 ARHNYGSFY 9

RESULT 4
 AAW76040
 ID AAW76040 standard; Protein; 10 AA.

XX
 AC AAW76040;

XX 02-NOV-1998 (first entry)

XX LM609 grafted antibody V-H region CDR3 protein fragment #16.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.

XX Mus sp.

OS
 PN WO9833919-A2.

PD 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

PR 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

PI Glaser SM, Huse WD;

DR WPI: 1998-437472/37.

DR N-PSDB; AAV49877.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

XX Claim 62; Page 43; 129pp; English.

XX AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
 CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
 CC antibodies contain non-murine framework regions so are suitable for use
 CC in humans. Enhanced types of LM609 have affinity more than 90 times
 CC greater than that of parent the parent antibody.

XX Sequence 10 AA;

Query Match 88.3%; Score 53; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.027;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFY 9
 |||||
 Db 1 ARHNYGSFY 9

RESULT 5

AAB61397
 ID AAB61397 standard; peptide; 10 AA.

XX
 AC AAB61397;

XX 03-APR-2001 (first entry)

XX Multiple mutant VH CDR3 #3.

XX LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis.

XX Unidentified.

OS
 PN WO200078815-A1.

PD 28-DEC-2000.

XX 23-JUN-2000; 2000WO-US17454.

PR 24-JUN-1999; 99US-0339922.

XX (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX Huse WD, Wu H;

XX WPI: 2001-050110/06.

XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -

XX Disclosure; Page 43; 132pp; English.

XX The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphavbeta_3 integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.

XX Sequence 10 AA;

Query Match 88.3%; Score 53; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.027;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFY 9

Db 1 ARHNYGSFY 9

RESULT 6

AAB61398
 ID AAB61398 standard; peptide; 10 AA.

XX
 AC AAB61398;

XX 03-APR-2001 (first entry)

XX Multiple mutant VH CDR3 #4.

XX LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis.

```

XX OS Unidentified.
XX PN WO200078815-A1.
XX PD 28-DEC-2000.
XX PF 23-JUN-2000; 2000WO-US17454.
XX PR 24-JUN-1999; 99US-0339922.
XX PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX PI Huse WD, Wu H;
XX DR WPI; 2001-050110/06.
XX PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity
XX PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
XX PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
XX PT osteoporosis -
XX PS Disclosure; Page 43; 132pp; English.
XX CC The present invention relates to enhanced LM609 grafted antibodies
XX CC exhibiting selective binding affinity to alphavbeta_3 integrin or
XX CC their functional fragments. The antibodies or their functional
XX CC fragments can be used in the diagnosis and treatment of
XX CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
XX CC diseases (such as psoriasis and chronic articular rheumatism),
XX CC disorders associated with inappropriate or inopportune invasion of
XX CC vessels (such as diabetic retinopathy, neovascular glaucoma and
XX CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
XX CC diseases (such as macular degeneration), restenosis and
XX CC osteoporosis.
XX SQ Sequence 10 AA;
XX Query Match 88.3%; Score 53; DB 22; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 0.027;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ARHNYGSFY 9
DB 1 ARHNYGSFY 9
|||||||
RESULT 7
AAW76010
ID AAW76010 standard; Protein; 10 AA.
XX AC AAW76010;
XX DT 02-NOV-1998 (first entry)
XX DE LM609 grafted antibody V-H region CDR3 protein fragment #1.
XX KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
XX KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
XX KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
XX KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
XX KW macular degeneration; osteoporosis; primer; V-H region; CDR;
XX KW complementarity determining region.
XX OS Mus 'sp.
XX PN WO9833919-A2.
XX PD 06-AUG-1998.
XX PF 30-JAN-1998; 98WO-US01826.
XX PR 30-JAN-1997; 97US-0791391.

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XX PA (IXSY-) IXSYS INC.
XX PI Glaser SM, Huse WD;
XX DR WPI; 1998-437472/37.
XX DR N-PSDB; AAV49847.
XX PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
XX PT integrin - and related grafted antibodies based on murine monoclonal
XX PT LM609, also related nucleic acid, used to treat, prevent or diagnose
XX PT angiogenesis or restenosis
XX PS Disclosure; Page 40; 129pp; English.
XX CC AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
XX CC LM609 heavy and light chain variable region. LM609 and the antibody
XX CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
XX CC inhibit binding of alphavbeta3 to a ligand and thus block
XX CC integrin-mediated signal transduction. This is useful in the treatment,
XX CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
XX CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
XX CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
XX CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
XX CC antibodies contain non-murine framework regions so are suitable for use
XX CC in humans. Enhanced types of LM609 have affinity more than 90 times
XX CC greater than that of parent the parent antibody.
XX SQ Sequence 10 AA;
XX Query Match 85.0%; Score 51; DB 19; Length 10;
XX Best Local Similarity 90.0%; Pred. No. 0.056;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ARHNYGSFY 10
DB 1 ARHNYGSFY 10
|||||||
RESULT 8
AAB61368
ID AAB61368 standard; peptide; 10 AA.
XX AC AAB61368;
XX DT 03-APR-2001 (first entry)
XX DE LM609 VH CDR3 peptide.
XX KW LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
XX KW inflammatory; cancer; retina; restenosis; osteoporosis.
XX OS Unidentified.
XX PN WO200078815-A1.
XX PD 28-DEC-2000.
XX PF 23-JUN-2000; 2000WO-US17454.
XX PR 24-JUN-1999; 99US-0339922.
XX PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX PI Huse WD, Wu H;
XX DR WPI; 2001-050110/06.
XX PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity
XX PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
XX PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
XX PT osteoporosis -
XX PR

```


PS Disclosure; Page 39; 132pp; English.

XX The present invention relates to enhanced LM609 grafted antibodies

CC exhibiting selective binding affinity to alphavbeta3 integrin or

CC their functional fragments. The antibodies or their functional

CC fragments can be used in the diagnosis and treatment of

CC alphavbeta3-mediated diseases such as angiogenesis, inflammatory

CC diseases (such as psoriasis and chronic articular rheumatism),

CC disorders associated with inappropriate or inopportune invasion of

CC vessels (such as diabetic retinopathy, neovascular glaucoma and

CC cancer disorders such as tumours and Kaposi's sarcoma), retinal

CC diseases (such as macular degeneration), restenosis and

XX osteoporosis.

XX

SQ Sequence 10 AA;

Query Match 85.0%; Score 51; DB 22; Length 10;

Best Local Similarity 90.0%; Pred. No. 0.056;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ARHNYGSFY 10

DB 1 ARHNYGSFY 10

RESULT 9

AAW76001

ID AAW76001 standard; Protein; 117 AA.

XX AAW76001;

AC

XX

XX

DT 02-NOV-1998 (first entry)

XX

DE Vitaxin antibody heavy chain variable region protein fragment.

XX

KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;

KW LM609; inhibitor; integrin-mediated signal transduction; treatment;

KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;

KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;

KW macular degeneration; osteoporosis.

XX

OS Mus sp.

XX

XX WO9833919-A2.

PN

XX

PD 06-AUG-1998.

XX

PF 30-JAN-1998; 98WO-US01826.

XX

XX 30-JAN-1997; 97US-0791391.

XX

XX (IXSY-) IXSYS INC.

XX

XX Glaser SM, Huse WD;

PI

XX

DR WPI; 1998-437472/37.

DR N-PSDB; AAV49820.

XX

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3

PT integrin - and related grafted antibodies based on murine monoclonal

PT LM609, also related nucleic acid, used to treat, prevent or diagnose

PT angiogenesis or restenosis.

XX

XX Claim 1; Fig 1a; 129pp; English.

PS

XX This sequence represents a fragment of the vitaxin antibody variable

CC heavy chain region. Vitaxin and the antibody LM609 bind selectively to

CC integrin alphavbeta3 and can be used to inhibit binding of alphavbeta3

CC to a ligand and thus block integrin-mediated signal transduction. This is

CC useful in the treatment, prevention and diagnosis of alphavbeta3-mediated

CC disease, specifically angiogenesis and restenosis (but also e.g.

CC (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,

CC cancer, psoriasis, rheumatoid arthritis, macular degeneration,

CC

CC osteoporosis etc.). The antibodies contain non-murine framework regions

CC so are suitable for use in humans. Enhanced types of LM609 have affinity

CC more than 90 times greater than that of parent the parent antibody.

XX

SQ Sequence 117 AA;

Query Match 85.0%; Score 51; DB 19; Length 117;

Best Local Similarity 90.0%; Pred. No. 0.68;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ARHNYGSFY 10

DB 97 ARHNYGSFY 106

RESULT 10

AAW76003

ID AAW76003 standard; Protein; 117 AA.

XX

AC AAW76003;

XX

DT 02-NOV-1998 (first entry)

XX

DE LM609 antibody heavy chain variable region protein fragment.

XX

KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;

KW LM609; inhibitor; integrin-mediated signal transduction; treatment;

KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;

KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;

KW macular degeneration; osteoporosis.

XX

OS Mus sp.

XX

XX WO9833919-A2.

PN

XX

PD 06-AUG-1998.

XX

PF 30-JAN-1998; 98WO-US01826.

XX

XX 30-JAN-1997; 97US-0791391.

XX

XX (IXSY-) IXSYS INC.

XX

XX Glaser SM, Huse WD;

PI

XX

DR WPI; 1998-437472/37.

DR N-PSDB; AAV49820.

XX

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3

PT integrin - and related grafted antibodies based on murine monoclonal

PT LM609, also related nucleic acid, used to treat, prevent or diagnose

PT angiogenesis or restenosis.

XX

XX Claim 43; Fig 2a; 129pp; English.

PS

XX This sequence represents the LM609 antibody variable heavy chain region.

CC LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3

CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus

CC block integrin-mediated signal transduction. This is useful in the

CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,

CC specifically angiogenesis and restenosis (but also e.g. (non-)immune

CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,

CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis

CC etc.). The antibodies contain non-murine framework regions so are

CC suitable for use in humans. Enhanced types of LM609 have affinity more

CC than 90 times greater than that of parent the parent antibody.

XX

SQ Sequence 117 AA;

Query Match 85.0%; Score 51; DB 19; Length 117;

Best Local Similarity 90.0%; Pred. No. 0.68;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFY 10
 Db 97 ARHNYGSFAY 106

RESULT 11
 AAY06381
 ID AAY06381 standard; Protein; 117 AA.
 AC AAY06381;
 XX 06-SEP-1999 (first entry)
 DT Murine monoclonal antibody LM609 VH region.
 XX Humanised antibody; antibody humanisation; antibody engineering;
 DE LM609; monoclonal antibody; complementarity determining region;
 KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
 KW cancer; therapy; diagnosis.
 XX Mus musculus.
 OS WO9929888-A1.
 PN 17-JUN-1999.
 XX 04-DEC-1998; 98WO-US25828.
 XX 05-DEC-1997; 97US-0986016.
 XX (SCRI) SCRIPPS RES INST.
 PA Barbas CF, Rader C;
 PI WPI; 1999-394979/33.
 XX Production of humanized mouse monoclonal antibodies
 PT Disclosure; Page 52-53; 55pp; English.
 XX This sequence represents the heavy chain variable region of murine
 CC monoclonal antibody LM609. LM609 is directed to integrin
 CC alpha-v beta-3. It selectively promotes apoptosis of vascular
 CC cells that have been stimulated to undergo angiogenesis, making it
 CC a tool for cancer diagnosis and therapy. The invention provides
 CC humanised antibodies, especially humanised LM609. In such humanized
 CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
 CC grafted onto a human light chain, and a heavy chain CDR from a mouse
 CC antibody is grafted onto a human antibody heavy chain to produce
 CC libraries from which a humanised murine antibody having the desired
 CC specificity is selected. By preserving the original CDR sequences
 CC such as the HCDR3 and LCDR3 sequences of LM609 (see AAY06371-72), the
 CC humanisation strategy ensures epitope conservation.
 XX

QY 1 ARHNYGSFY 10
 Db 97 ARHNYGSFAY 106

RESULT 12
 AAY06387
 ID AAY06387 standard; Protein; 117 AA.
 XX AAY06387;
 AC 06-SEP-1999 (first entry)
 DT
 XX

QY 1 ARHNYGSFY 10
 Db 97 ARHNYGSFAY 106

Query Match 85.0%; Score 51; DB 20; Length 117;
 Best Local Similarity 90.0%; Pred. No. 0.68;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFY 10
 Db 97 ARHNYGSFAY 106

RESULT 13
 AAG63587
 ID AAG63587 standard; Protein; 117 AA.
 XX AAG63587;
 AC 15-OCT-2001 (first entry)
 DT
 XX A heavy chain variable region of LM609 grafted antibody.
 DE

DE Humanised LM609 antibody VH domain.
 XX Humanised antibody; antibody humanisation; antibody engineering;
 KW LM609; monoclonal antibody; complementarity determining region;
 KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
 KW cancer; therapy; diagnosis.
 XX Homo sapiens.
 OS Synthetic.
 XX Key Location/Qualifiers
 FH 1..2
 FT Peptide /note= "vector-encoded residues"
 FT Region 31..35
 FT /note= "CDR1"
 FT Region 50..66
 FT /note= "CDR2"
 FT Region 107..117
 FT /note= "CDR3"
 XX WO9929888-A1.
 PN 17-JUN-1999.
 XX 04-DEC-1998; 98WO-US25828.
 XX 05-DEC-1997; 97US-0986016.
 XX (SCRI) SCRIPPS RES INST.
 PA Barbas CF, Rader C;
 PI WPI; 1999-394979/33.
 XX Production of humanized mouse monoclonal antibodies
 PT Disclosure; Page 52; 55pp; English.
 XX This sequence represents the heavy chain variable region of a
 CC humanised LM609 antibody. LM609 is directed to human integrin
 CC alpha-v beta-3. It selectively promotes apoptosis of vascular
 CC cells that have been stimulated to undergo angiogenesis, making it
 CC a tool for cancer diagnosis and therapy. The invention provides
 CC humanised antibodies, especially humanised LM609. In such humanized
 CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
 CC grafted onto a human light chain, and a heavy chain CDR from a mouse
 CC antibody is grafted onto a human antibody heavy chain to produce
 CC libraries from which a humanised murine antibody having the desired
 CC specificity is selected. By preserving the original CDR sequences
 CC such as the HCDR3 and LCDR3 sequences of LM609 (see AAY06371-72), the
 CC humanisation strategy ensures epitope conservation.
 XX

QY 1 ARHNYGSFY 10
 Db 97 ARHNYGSFAY 106

Query Match 85.0%; Score 51; DB 20; Length 117;
 Best Local Similarity 90.0%; Pred. No. 0.68;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFY 10
 Db 97 ARHNYGSFAY 106

RESULT 13
 AAG63587
 ID AAG63587 standard; Protein; 117 AA.
 XX AAG63587;
 AC 15-OCT-2001 (first entry)
 DT
 XX A heavy chain variable region of LM609 grafted antibody.
 DE

KW Grafted antibody; LM609; integrin; alphavbeta3; inflammatory disorder;
 KW chronic articular rheumatism; psoriasis; diabetic retinopathy;
 KW neovascular glaucoma; capillary proliferation; atherosclerotic plaque;
 KW cancer.

XX Synthetic.

OS Mus sp.

XX PN US2001011125-A1.

XX PD 02-AUG-2001.

XX PF 30-JAN-1997; 97US-0790540.

XX PR 30-JAN-1997; 97US-0790540.

XX PA (HUSE/) HUSE W D.

XX PI Huse WD;

XX DR WPI: 2001-496171/54.

XX DR N-PSDB; AAH74625.

XX PT New LM609 grafted antibody exhibiting selective binding affinity to
 PT alphavbeta3, comprising at least one LM609 grafted heavy and light
 PT chain polypeptide, useful for diagnosing and treating e.g. inflammatory
 PT disorders or cancer.

XX PS Claim 1; Fig 1A; 25pp; English.

XX CC The present sequence represents the heavy chain variable region of the
 CC grafted monoclonal antibody LM609. LM609 is a murine antibody which
 CC specifically recognises the integrin alphavbeta3, and inhibits its
 CC functional activity. The LM609 grafted antibody has the
 CC complementary determining regions (CDRs) substituted into a non-murine
 CC framework. Nucleic acids encoding LM609 grafted heavy and light chain
 CC polypeptides and fragments are useful in diagnostic and therapeutic
 CC purposes, such as in the production of LM609 grafted antibodies and
 CC fragments having binding specificity and inhibitory activity against
 CC the integrin alphavbeta3. The antibody can be used for the diagnosis
 CC or treatment of alphavbeta3-mediated diseases (e.g. inflammatory
 CC disorders, chronic articular rheumatism, psoriasis, disorders
 CC associated with inappropriate or inopportune invasion of vessels such
 CC as diabetic retinopathy, neovascular glaucoma and capillary
 CC proliferation in atherosclerotic plaques, or cancers), and to inhibit
 CC binding activity of alphavbeta3 that are necessary for progression of
 CC an alphavbeta3-mediated disease.

XX SQ Sequence 117 AA;

Query Match 85.0%; Score 51; DB 22; Length 117;

Best Local Similarity 90.0%; Pred. No. 0.68;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFY 10

DB 97 ARHNYGSFAY 106

RESULT 14

AAG63589

ID AAG63589 standard; Protein; 117 AA.

XX AC AAG63589;

XX DT 15-OCT-2001 (first entry)

XX DE A heavy chain variable region of LM609 antibody.

XX Grafted antibody; LM609; integrin; alphavbeta3; inflammatory disorder;
 KW chronic articular rheumatism; psoriasis; diabetic retinopathy;
 KW neovascular glaucoma; capillary proliferation; atherosclerotic plaque;
 KW cancer.

XX OS Mus sp.

XX PN US2001011125-A1.

XX PD 02-AUG-2001.

XX PF 30-JAN-1997; 97US-0790540.

XX PR 30-JAN-1997; 97US-0790540.

XX PA (HUSE/) HUSE W D.

XX PI Huse WD;

XX DR WPI: 2001-496171/54.

XX DR N-PSDB; AAH74625.

XX PT New LM609 grafted antibody exhibiting selective binding affinity to
 PT alphavbeta3, comprising at least one LM609 grafted heavy and light
 PT chain polypeptide, useful for diagnosing and treating e.g. inflammatory
 PT disorders or cancer.

XX PS Disclosure; Fig 2A; 25pp; English.

XX CC The present sequence represents the heavy chain variable region of the
 CC monoclonal antibody LM609. LM609 is a murine antibody which specifically
 CC recognises the integrin alphavbeta3, and inhibits its functional activity.
 CC The specification describes a LM609 grafted antibody which has the
 CC complementarity determining regions (CDRs) substituted into a non-murine
 CC framework. Nucleic acids encoding LM609 grafted heavy and light chain
 CC polypeptides and fragments are useful in diagnostic and therapeutic
 CC purposes, such as in the production of LM609 grafted antibodies and
 CC fragments having binding specificity and inhibitory activity against
 CC the integrin alphavbeta3. The antibody can be used for the diagnosis
 CC or treatment of alphavbeta3-mediated diseases (e.g. inflammatory
 CC disorders, chronic articular rheumatism, psoriasis, disorders
 CC associated with inappropriate or inopportune invasion of vessels such
 CC as diabetic retinopathy, neovascular glaucoma and capillary
 CC proliferation in atherosclerotic plaques, or cancers), and to inhibit
 CC binding activity of alphavbeta3 that are necessary for progression of
 CC an alphavbeta3-mediated disease.

XX SQ Sequence 117 AA;

Query Match 85.0%; Score 51; DB 22; Length 117;

Best Local Similarity 90.0%; Pred. No. 0.68;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFY 10

DB 97 ARHNYGSFAY 106

RESULT 15

AAB61359

ID AAB61359 standard; protein; 117 AA.

XX AC AAB61359;

XX DT 03-APR-2001 (first entry)

XX DE Vitaxin heavy chain variable region protein.

XX LM609; grafted antibody; alphavbeta3 integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis.

XX OS Unidentified.

XX PN WO200078815-A1.

XX XX 28-DEC-2000.

PF 23-JUN-2000; 2000WO-US17454.
XX
PR 24-JUN-1999; 99US-0339922.
XX
PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX
PI Huse WD, Wu H;
XX
XX WPI; 2001-050110/06.
DR
XX
XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
PT osteoporosis -
XX
XX Disclosure; Fig 1; 132pp; English.
PS
XX
CC The present invention relates to enhanced LM609 grafted antibodies
CC exhibiting selective binding affinity to alphaVbeta_3 integrin or
CC their functional fragments. The antibodies or their functional
CC fragments can be used in the diagnosis and treatment of
CC alphaVbeta_3-mediated diseases such as angiogenesis, inflammatory
CC diseases (such as psoriasis and chronic articular rheumatism),
CC disorders associated with inappropriate or inopportune invasion of
CC vessels (such as diabetic retinopathy, neovascular glaucoma and
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
CC diseases (such as macular degeneration), restenosis and
CC osteoporosis.
XX
XX SQ Sequence 117 AA;

Query Match 85.0%; Score 51; DB 22; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.68;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFY 10
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Db 97 ARHNYGSFAY 106

Search completed: November 18, 2002, 17:31:37
Job time : 13.8235 secs

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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:54:45 ; Search time 1.96078 Seconds
(without alignments)
76.811 Million cell updates/sec

Title: US-09-016-061-66

Perfect score: 60

Sequence: 1 ARHNYGSFVY 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 97044 seqs, 15060890 residues

Total number of hits satisfying chosen parameters: 97044

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
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2	51	85.0	117	8	US-08-790-540A-6
3	51	85.0	117	8	US-08-791-391A-2
4	51	85.0	117	8	US-08-791-391A-6
5	38	63.3	101	10	US-09-764-853-432
6	37	61.7	334	10	US-09-935-330A-34
7	37	61.7	398	10	US-09-731-872-288
8	37	61.7	403	10	US-09-731-872-249
9	37	61.7	462	10	US-09-745-763-189
10	37	61.7	643	10	US-09-801-368-236
11	36	60.0	14	1	US-08-677-599B-22
12	36	60.0	235	10	US-09-925-301-1293
13	35	58.3	144	10	US-09-881-823-12
14	34	56.7	30	10	US-09-839-884-40
15	34	56.7	87	10	US-09-965-602-48
16	34	56.7	259	10	US-09-905-176-20
17	34	56.7	287	10	US-09-415-540-5
18	33	55.0	14	1	US-08-677-599B-21
19	33	55.0	44	10	US-09-764-853-779

20	33	55.0	137	10	US-09-939-980-431	Sequence 431, Appl
21	33	55.0	171	10	US-09-347-331-4	Sequence 4, Appl
22	33	55.0	349	10	US-09-766-366-4	Sequence 4, Appl
23	33	55.0	512	10	US-09-815-242-11232	Sequence 11232, A
24	32	53.3	14	1	US-08-677-599B-11	Sequence 11, Appl
25	32	53.3	14	1	US-08-677-599B-12	Sequence 12, Appl
26	32	53.3	14	1	US-08-677-599B-13	Sequence 13, Appl
27	32	53.3	14	1	US-08-677-599B-14	Sequence 14, Appl
28	32	53.3	14	1	US-08-677-599B-15	Sequence 15, Appl
29	32	53.3	14	1	US-08-677-599B-16	Sequence 16, Appl
30	32	53.3	14	1	US-08-677-599B-17	Sequence 17, Appl
31	32	53.3	14	1	US-08-677-599B-18	Sequence 18, Appl
32	32	53.3	14	1	US-08-677-599B-19	Sequence 19, Appl
33	32	53.3	14	1	US-08-677-599B-20	Sequence 20, Appl
34	32	53.3	14	1	US-08-677-599B-23	Sequence 23, Appl
35	32	53.3	15	10	US-09-756-983-11	Sequence 11, Appl
36	32	53.3	25	1	US-08-677-599B-8	Sequence 8, Appl
37	32	53.3	93	12	US-10-081-281-121	Sequence 121, Appl
38	32	53.3	94	10	US-09-766-378A-37	Sequence 37, Appl
39	32	53.3	100	10	US-09-764-898-222	Sequence 222, Appl
40	32	53.3	181	10	US-09-815-837-103	Sequence 103, Appl
41	32	53.3	183	10	US-09-815-837-16	Sequence 16, Appl
42	32	53.3	184	10	US-09-815-837-15	Sequence 15, Appl
43	32	53.3	185	10	US-09-815-837-13	Sequence 13, Appl
44	32	53.3	185	10	US-09-815-837-14	Sequence 14, Appl
45	32	53.3	186	10	US-09-815-837-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1

US-08-790-540A-2

; Sequence 2, Application US/08790540A

; Patent No. US20010011125A1

; GENERAL INFORMATION:

; APPLICANT: Huse, William D.

; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human

; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use

; NUMBER OF SEQUENCES: 24

; CORRESPONDENCE ADDRESSES:

; ADDRESSEE: Campbell & Flores LLP

; STREET: 4370 La Jolla Village Drive, Suite 700

; CITY: San Diego

; STATE: California

; COUNTRY: United States

; ZIP: 92122

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/790,540A

; FILING DATE: 30-JAN-1997

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: Campbell, Cathryn A.

; REGISTRATION NUMBER: 31,815

; REFERENCE/DOCKET NUMBER: P-IX 2405

; TELEPHONE: (619) 535-9001

; TELEFAX: (619) 535-8949

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 117 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-790-540A-2

Query Match

Best Local Similarity

85.0%; Score 51; DB 8; Length 117;
90.0%; Pred. No. 0.024;

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Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFY 10
   |||||
Db 97 ARHNYGSFAY 106

RESULT 2
US-08-790-540A-6
; Sequence 6, Application US/08790540A
; Patent No. US20010011125A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,540A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-790-540A-6

Query Match 85.0%; Score 51; DB 8; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.024;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFY 10
   |||||
Db 97 ARHNYGSFAY 106

RESULT 3
US-08-791-391A-2
; Sequence 2, Application US/08791391A
; Patent No. US20010016645A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,391A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-391A-2

Query Match 85.0%; Score 51; DB 8; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.024;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFY 10
   |||||
Db 97 ARHNYGSFAY 106

RESULT 4
US-08-791-391A-6
; Sequence 6, Application US/08791391A
; Patent No. US20010016645A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,391A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-391A-6
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,391A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-391A-2

Query Match 85.0%; Score 51; DB 8; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.024;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFY 10
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Db 97 ARHNYGSFAY 106

RESULT 4
US-08-791-391A-6
; Sequence 6, Application US/08791391A
; Patent No. US20010016645A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,391A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-391A-6
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Query Match      85.0%; Score 51; DB 8; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.024;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFY 10
Db 97 ARHNYGSFAY 106

RESULT 5
US-09-764-853-432
; Sequence 432, Application US/09764853
; Patent No. US20020090672A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJ206
; CURRENT APPLICATION NUMBER: US/09/764,853
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 939
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 432
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-853-432

Query Match      63.3%; Score 38; DB 10; Length 101;
Best Local Similarity 75.0%; Pred. No. 3.6;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFY 9
Db 64 RHNYSEFH 71

RESULT 6
US-09-935-390A-34
; Sequence 34, Application US/09935390A
; Patent No. US20020076761A1
; GENERAL INFORMATION:
; APPLICANT: Escobedo, Jaime
; Qulanjin, Hu
; Garcia, Pablo
; Williams, Lewis T.
; Kochakota, Srinivas
; TITLE OF INVENTION: Secreted Human Proteins
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/935,390A
; FILING DATE: 22-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/988,671
; FILING DATE: 1997-12-11
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane E. R. Potter
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 1369,002

;
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 923-2718
; TELEFAX: (510) 655-3542
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 334 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. US20020076761A1
; SEQUENCE DESCRIPTION: SEQ ID NO: 34:
US-09-935-390A-34

Query Match      61.7%; Score 37; DB 10; Length 334;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 YGSFY 10
Db 49 YGSFY 54

RESULT 7
US-09-731-872-288
; Sequence 288, Application US/09731872
; Patent No. US20020102604A1
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean Baptiste
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Jobert, Severin
; TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS
; FILE REFERENCE: 78.US3.REG
; CURRENT APPLICATION NUMBER: US/09/731,872
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/169,629
; PRIOR FILING DATE: 1999-12-08
; PRIOR APPLICATION NUMBER: US 60/187,470
; PRIOR FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 482
; SOFTWARE: Patent.pm
; SEQ ID NO 288
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -21...-1
US-09-731-872-288

Query Match      61.7%; Score 37; DB 10; Length 398;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 YGSFY 10
Db 49 YGSFY 54

RESULT 8
US-09-731-872-249
; Sequence 249, Application US/09731872
; Patent No. US20020102604A1
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean Baptiste
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Jobert, Severin
; TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS
; FILE REFERENCE: 78.US3.REG
; CURRENT APPLICATION NUMBER: US/09/731,872
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/169,629
; PRIOR FILING DATE: 1999-12-08
```

; PRIOR APPLICATION NUMBER: US 60/187,470
; NUMBER OF SEQ ID NOS: 482
; SOFTWARE: Patent.pm
; SEQ ID NO 249
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -21...-1
US-09-731-872-249

Query Match 61.7%; Score 37; DB 10; Length 403;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 YGSFY 10
| | | | |
DB 49 YGSFY 54

RESULT 9

US-09-745-763-189
; Sequence 189, Application US/09745763
; Patent No. US20020065394A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth

; McCoy, John M.
; LaVallie, Edward R.
; Collins-Racie, Lisa A.
; Evans, Cheryl
; Merberg, David
; Treacy, Maurice
; Seaulding, Vikki

TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
ENCODING THEM

NUMBER OF SEQUENCES: 219
CORRESPONDENCE ADDRESS:
ADDRESS: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: MA
COUNTRY: U.S.A.

ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/745,763
FILING DATE: 18-Jun-2000

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Sprunger, Suzanne A.
REGISTRATION NUMBER: 41,323
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8284
TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 189:
SEQUENCE CHARACTERISTICS:
LENGTH: 462 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 189:
US-09-745-763-189

Query Match 61.7%; Score 37; DB 10; Length 462;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 YGSFY 10
| | | | |
DB 113 YGSFY 118

RESULT 10

US-09-801-368-236
; Sequence 236, Application US/09801368
; Patent No. US20020128250A1
; GENERAL INFORMATION:
; APPLICANT: Busby, Robert
; APPLICANT: Cali, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Milne, Todd
; APPLICANT: No. US20020128250A1man, Thea
; APPLICANT: Royer, John
; APPLICANT: Salama, Sofie
; APPLICANT: Sherman, Amir
; APPLICANT: Silva, Jeff
; APPLICANT: Summers, Eric

; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
; FILE REFERENCE: 109272.147
; CURRENT APPLICATION NUMBER: US/09/801.368
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 09/487,558
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/160,587
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 236
; LENGTH: 643
; TYPE: PRT

; ORGANISM: Penicillium chrysogenum
US-09-801-368-236

Query Match 61.7%; Score 37; DB 10; Length 643;
Best Local Similarity 62.5%; Pred. No. 34;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFY 10
| : | | : | |
DB 212 HSYGNLYY 219

RESULT 11

US-08-677-599B-22
; Sequence 22, Application US/08677599B
; Patent No. US20020155117A1
; GENERAL INFORMATION:

; APPLICANT: Sucia-Foca, Nicole
; TITLE OF INVENTION: METHODS FOR DETECTING ORGAN ALLOGRAFT
; TITLE OF INVENTION: REJECTION AND USES THEREOF
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/677,599B
FILING DATE: 08-JUL-1996


```
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq., John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 50161-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212/278/0400
; TELEFAX: 212/391/0525
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-677-599B-22

Query Match          60.0%; Score 36; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYG 6
Db 9 ARHNYG 14

RESULT 12
US-09-925-301-1293
; Sequence 1293, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1293
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: SITE
; LOCATION: (229)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-301-1293

Query Match          60.0%; Score 36; DB 10; Length 235;
Best Local Similarity 50.0%; Pred. No. 19;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSFYY 10
Db 139 SKHNLGIFYF 148

RESULT 13
US-09-881-823-12
; Sequence 12, Application US/09881823
; Patent No. US20020068066A1
; GENERAL INFORMATION:
; APPLICANT: SHI, WENYUAN
; APPLICANT: ANDERSON, MAXWELL
; APPLICANT: MORRISON, SHERIE
; APPLICANT: TRINH, RYAN
; APPLICANT: WINS, LETITIA
; APPLICANT: CHEN, LI
; TITLE OF INVENTION: Method for the Treatment and Prevention of Dental Caries

; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq., John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 50161-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212/278/0400
; TELEFAX: 212/391/0525
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-677-599B-22

Query Match          60.0%; Score 36; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYG 6
Db 9 ARHNYG 14

RESULT 12
US-09-925-301-1293
; Sequence 1293, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1293
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: SITE
; LOCATION: (229)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-301-1293

Query Match          60.0%; Score 36; DB 10; Length 235;
Best Local Similarity 50.0%; Pred. No. 19;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSFYY 10
Db 139 SKHNLGIFYF 148

RESULT 13
US-09-881-823-12
; Sequence 12, Application US/09881823
; Patent No. US20020068066A1
; GENERAL INFORMATION:
; APPLICANT: SHI, WENYUAN
; APPLICANT: ANDERSON, MAXWELL
; APPLICANT: MORRISON, SHERIE
; APPLICANT: TRINH, RYAN
; APPLICANT: WINS, LETITIA
; APPLICANT: CHEN, LI
; TITLE OF INVENTION: Method for the Treatment and Prevention of Dental Caries

; FILE REFERENCE: 22851-032
; CURRENT APPLICATION NUMBER: US/09/881,823
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 07/378,577
; PRIOR FILING DATE: 1999-08-20
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Murine
; US-09-881-823-12

Query Match          58.3%; Score 35; DB 10; Length 144;
Best Local Similarity 71.4%; Pred. No. 17;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 NYGSFYY 10
Db 121 SYGSYY 127

RESULT 14
US-09-839-884-40
; Sequence 40, Application US/09839884
; Patent No. US20020076739A1
; GENERAL INFORMATION:
; APPLICANT: Aebersold, Rudolf H.
; APPLICANT: Gelb, Michael H.
; APPLICANT: Gygi, Steven
; APPLICANT: Scott, C R
; APPLICANT: Turecek, Frantisek
; APPLICANT: Gerber, Scott A
; APPLICANT: Rist, Beate
; TITLE OF INVENTION: Rapid Quantitative Analysis of Proteins or Protein
; FILE REFERENCE: 64-98A
; CURRENT APPLICATION NUMBER: US/09/839,884
; CURRENT FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: 09/383,062
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 60/097,788
; PRIOR FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40
; LENGTH: 30
; TYPE: PRT
; ORGANISM: yeast
; NAME/KEY: VARIANT
; LOCATION: (2)
; OTHER INFORMATION: C at position 2 is ICAT-labeled cysteinyl residue.
US-09-839-884-40

Query Match          56.7%; Score 34; DB 10; Length 30;
Best Local Similarity 83.3%; Pred. No. 5.2;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
Db 10 HNYGAF 15

RESULT 15
US-09-965-602-48
; Sequence 48, Application US/09965602
; Patent No. US20020103154A1
; GENERAL INFORMATION:
; APPLICANT: Dimster-Denk, Dago
; TITLE OF INVENTION: ESSENTIAL GENES IN YEAST AS TARGETS FOR ANTIFUNGAL
; TITLE OF INVENTION: AGENTS,
; TITLE OF INVENTION: HERBICIDES, INSECTICIDES AND ANTI-PROLIFERATION DRUGS
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; FILE REFERENCE: ACA-8
; CURRENT APPLICATION NUMBER: US/09/965,602
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/539,697
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 87
; TYPE: PRT
; ORGANISM: human
US-09-965-602-48

Query Match 56.7%; Score 34; DB 10; Length 87;
Best Local Similarity 44.4%; Pred. NO. 15;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 2 RHNYGSFY 10
||| :||
Db 17 RHNFSFY 25

Search completed: November 18, 2002, 18:45:16
Job time : 2.96078 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:01 ; Search time 4.2402 Seconds
(without alignments)
69.390 Million cell updates/sec

Title: US-09-016-061-66
Perfect score: 60
Sequence: 1 ARHNGSFY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	38	63.3	122	1	US-08-360-125-11
2	38	63.3	122	2	US-08-450-578-11
3	38	63.3	122	2	US-09-017-628-11
4	38	63.3	122	2	US-09-014-880-11
5	38	63.3	122	4	US-08-450-363-11
6	37	61.7	36	1	US-08-053-131-84
7	37	61.7	36	1	US-08-645-641-84
8	37	61.7	36	1	US-07-853-408B-84
9	37	61.7	36	2	US-08-096-762-84
10	37	61.7	36	2	US-08-308-865-84
11	37	61.7	36	4	US-09-042-353-281
12	37	61.7	36	4	US-08-758-417A-129
13	37	61.7	36	5	PCT-US92-10983-84
14	36	60.0	94	3	US-09-147-550-14
15	36	60.0	94	3	US-09-147-550-45
16	36	60.0	94	3	US-09-147-550-48
17	36	60.0	94	3	US-09-147-550-77
18	36	60.0	94	3	US-09-147-550-84
19	36	60.0	94	3	US-09-147-550-90
20	36	60.0	94	3	US-09-147-550-101
21	36	60.0	94	4	US-09-557-917-14
22	36	60.0	94	4	US-09-557-917-45
23	36	60.0	94	4	US-09-557-917-48
24	36	60.0	94	4	US-09-557-917-77
25	36	60.0	94	4	US-09-557-917-84
26	36	60.0	94	4	US-09-557-917-90
27	36	60.0	94	4	US-09-557-917-101

35 58.3 33 1 US-08-053-131-78 Sequence 78, Appl
29 35 58.3 33 1 US-08-645-641-78 Sequence 78, Appl
30 35 58.3 33 1 US-07-853-408B-78 Sequence 78, Appl
31 35 58.3 33 2 US-08-096-762-78 Sequence 78, Appl
32 35 58.3 33 2 US-08-308-865-78 Sequence 78, Appl
33 35 58.3 33 4 US-09-042-353-275 Sequence 123, App
34 35 58.3 33 4 US-08-758-417A-123 Sequence 78, Appl
35 35 58.3 33 5 PCT-US92-10983-78 Sequence 6, Appl
36 34 56.7 119 3 US-08-767-128-6 Sequence 1, Appl
37 34 56.7 123 2 US-08-652-816A-1 Sequence 6, Appl
38 34 56.7 123 2 US-08-652-816A-6 Sequence 8, Appl
39 34 56.7 123 2 US-08-652-816A-8 Sequence 24, Appl
40 34 56.7 191 4 US-09-443-041A-24 Sequence 30, Appl
41 34 56.7 236 4 US-09-443-041A-10 Sequence 10, Appl
42 34 56.7 260 4 US-09-443-041A-26 Sequence 26, Appl
43 34 56.7 261 4 US-09-443-041A-28 Sequence 28, Appl
44 34 56.7 269 4 US-09-443-041A-32 Sequence 32, Appl
45 34 56.7 271 4 US-09-443-041A-32

ALIGNMENTS

RESULT 1
US-08-360-125-11
; Sequence 11, Application US/08360125
; Patent No. 5767246
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA
; APPLICANT: Toshiaki TAGAWA
; APPLICANT: Yoko HIRAKAWA
; APPLICANT: No. 5767246hiko ITO
; TITLE OF INVENTION: Human Monoclonal Antibody
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
; TITLE OF INVENTION: Cell Membrane
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/360.125
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/905.534
; FILING DATE: June 29, 1992
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

;;
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE: Hybridoma producing human antibody 1-3-1
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
US-08-360-125-11

Query Match 63.3%; Score 38; DB 1; Length 122;
Best Local Similarity 60.0%; Pred. No. 19;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNGSEFY 10
Db 98 ARSGYGY 107

RESULT 2

US-08-450-578-11
; Sequence 11, Application US/08450578
; Patent No. 5837845
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA
; APPLICANT: Toshiaki TAGAWA
; APPLICANT: Yoko HIRAKAWA
; APPLICANT: No. 5837845shiko ITO
; APPLICANT: Kazuhiro NAGAIKE
; TITLE OF INVENTION: Human Monoclonal Antibody
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
; TITLE OF INVENTION: Cell Membrane
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS

;;
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,578
; FILING DATE: May 25, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/360,125
; FILING DATE: December 20, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/905,534
; FILING DATE: June 29, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE: Hybridoma producing human antibody 1-3-1
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
US-08-450-578-11

Query Match 63.3%; Score 38; DB 2; Length 122;
Best Local Similarity 60.0%; Pred. No. 19;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNGSEFY 10
Db 98 ARSGYGY 107

RESULT 3

US-09-017-628-11
; Sequence 11, Application US/09017628
; Patent No. 5990287
; GENERAL INFORMATION:
; APPLICANT: HOSOKAWA, Saiko
; APPLICANT: TAGAWA, Toshiaki
; APPLICANT: HIRAKAWA, Yoko
; APPLICANT: ITO, No. 5990287ihiko
; APPLICANT: NAGAIKE, Kazuhiro
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY BINDING TO
; TITLE OF INVENTION: SURFACE ANTIGEN OF CANCER CELL MEMBRANE
; FILE REFERENCE: 177/527361KH
; CURRENT APPLICATION NUMBER: US/09/017,628
; EARLIER FILING DATE: 1998-02-02
; EARLIER APPLICATION NUMBER: 08/360,125
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Hybridoma producing human antibody 1-3-1
US-09-017-628-11

Query Match 63.3%; Score 38; DB 2; Length 122;
Best Local Similarity 60.0%; Pred. No. 19;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSFY 10
|| :|| :||
Db 98 ARGSYGVY 107

RESULT 4

US-09-014-880-11
; Sequence 11, Application US/09014880
; Patent No. 5990297
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA et al.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY
; TITLE OF INVENTION: BINDING TO SURFACE ANTIGEN OF CANCER CELL MEMBRANE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
; STREET: 2033 K Street, N.W., #800
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/014,880
; FILING DATE: January 28, 1998
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/450,578
; FILING DATE: May 25, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/360,125
; FILING DATE: December 20, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/905,534
; FILING DATE: June 29, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.

; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-721-8200
; TELEFAX: 202-721-8250
; TELEX:

; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; CELL TYPE: Hybridoma producing human antibody 1-3-1
US-09-014-880-11

Query Match 63.3%; Score 38; DB 2; Length 122;
Best Local Similarity 60.0%; Pred. No. 19;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSFY 10
|| :|| :||
Db 98 ARGSYGVY 107

RESULT 5

US-08-450-363-11
; Sequence 11, Application US/08450363
; Patent No. 6436434
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA
; APPLICANT: Toshiaki TAGAWA
; APPLICANT: Yoko HIRAKAWA
; APPLICANT: No. 6436434ihiko ITO
; APPLICANT: Kazuhiro NAGAIKE
; TITLE OF INVENTION: Human Monoclonal Antibody
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,363
; FILING DATE: May 25, 1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/360,125
; FILING DATE: December 20, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/905,534
; FILING DATE: June 29, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids

;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; HYPOTHETICAL:
;; ANTI-SENSE:
;; FRAGMENT TYPE:
;; ORIGINAL SOURCE:
;; ORGANISM:
;; STRAIN:
;; INDIVIDUAL ISOLATE:
;; DEVELOPMENTAL STAGE:
;; HAPLOTYPE:
;; TISSUE TYPE:
;; CELL TYPE: Hybridoma producing human antibody 1-3-1
;; CELL LINE:
;; ORGANELLE:
;; IMMEDIATE SOURCE:
;; LIBRARY:
;; CLONE:
;; POSITION IN GENOME:
;; CHROMOSOME/SEGMENT:
;; MAP POSITION:
;; UNITS:
;; FEATURE:
;; NAME/KEY:
;; LOCATION:
;; IDENTIFICATION METHOD:
;; OTHER INFORMATION:
;; PUBLICATION INFORMATION:
;; AUTHORS:
;; TITLE:
;; JOURNAL:
;; VOLUME:
;; ISSUE:
;; PAGES:
;; DATE:
;; DOCUMENT NUMBER:
;; FILING DATE:
;; PUBLICATION DATE:
;; RELEVANT RESIDUES IN SEQ ID NO:
US-08-450-363-11

Query Match 63.3%; Score 38; DB 4; Length 122;
Best Local Similarity 60.0%; Pred. No. 19;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSFY 10
|| :|| :||
Db 98 ARGSGYGY 107

RESULT 6
US-08-053-131-84
; Sequence 84, Application US/08053131
; Patent No. 5661016
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 197
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 200
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/645,641
; FILING DATE: 20-MAY-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/904,068
; FILING DATE: 23-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14643-000913
; TELECOMMUNICATION INFORMATION:

;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/053,131
;; FILING DATE: 26-APR-1993
;; CLASSIFICATION: 800
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/990,860
;; FILING DATE: 16-DEC-1992
;; APPLICATION DATA:
;; APPLICATION NUMBER: US 07/810,279
;; FILING DATE: 17-DEC-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/853,408
;; FILING DATE: 18-MAR-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Smith, William M.
;; REGISTRATION NUMBER: 30,223
;; REFERENCE/DOCKET NUMBER: 14643-9-3
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-326-2400
;; TELEFAX: 415-326-2422
;; INFORMATION FOR SEQ ID NO: 84:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 36 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-053-131-84

Query Match 61.7%; Score 37; DB 1; Length 36;
Best Local Similarity 57.1%; Pred. No. 8.7;
Matches 8; Conservative 1; Mismatches 1; Indels 4; Gaps 1;

QY 1 ARHNYGS----FY 10
||| :|| :||
Db 3 ARHYGSGSYDY 16

RESULT 7
US-08-645-641-84
; Sequence 84, Application US/08645641
; Patent No. 5719032
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 5719032-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 150
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/645,641
; FILING DATE: 20-MAY-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/904,068
; FILING DATE: 23-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14643-000913
; TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-645-641-84

Query Match 61.7%; Score 37; DB 1; Length 36;
Best Local Similarity 57.1%; Pred. No. 8.7;
Matches 8; Conservative 1; Mismatches 1; Indels 4; Gaps 1;

QY 1 ARHNYGS----FYY 10
||| ||| :||
Db 3 ARHYGSGSYDYY 16

RESULT 8

US-07-853-408B-84

Sequence 84, Application US/07853408B
Patent No. 5789650
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
TITLE OF INVENTION: Transgenic No. 5789650-Human Animals for
Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 150
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/853,408B
FILING DATE: 19920318
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14643-9
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422

INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-853-408B-84

Query Match 61.7%; Score 37; DB 1; Length 36;
Best Local Similarity 57.1%; Pred. No. 8.7;
Matches 8; Conservative 1; Mismatches 1; Indels 4; Gaps 1;

QY 1 ARHNYGS----FYY 10
||| ||| :||
Db 3 ARHYGSGSYDYY 16

RESULT 9

US-08-096-762-84

Sequence 84, Application US/08096762

Patent No. 5814318

GENERAL INFORMATION:

APPLICANT: Lonberg, Nils

TITLE OF INVENTION: Transgenic No. 5814318-Human Animals for

Producing Heterologous Antibodies

NUMBER OF SEQUENCES: 210

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Kourie and Crew

STREET: One Market Plaza, Steuart Tower, Suite 200

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/096,762

FILING DATE: 22-JUL-1993

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/053,131

FILING DATE: 26-APR-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/990,860

FILING DATE: 16-DEC-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/904,068

FILING DATE: 23-JUN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/853,408

FILING DATE: 18-MAR-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/810,279

FILING DATE: 17-DEC-1991

ATTORNEY/AGENT INFORMATION:

NAME: Smith, William M.

REGISTRATION NUMBER: 30,223

REFERENCE/DOCKET NUMBER: 14643-9-4

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-326-2400

TELEFAX: 415-326-2422

INFORMATION FOR SEQ ID NO: 84:

SEQUENCE CHARACTERISTICS:

LENGTH: 36 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-096-762-84

Query Match 61.7%; Score 37; DB 2; Length 36;
Best Local Similarity 57.1%; Pred. No. 8.7;
Matches 8; Conservative 1; Mismatches 1; Indels 4; Gaps 1;

Qy 1 ARHNYGS----FYY 10
||| ||| :||
Db 3 ARHYGSGSYDYY 16

RESULT 10

US-08-308-865-84

Sequence 84, Application US/08308865
Patent No. 5877397
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
TITLE OF INVENTION: Transgenic No. 5877397-Human Animals for
Producing Heterologous Antibodies

;; NUMBER OF SEQUENCES: 150
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: William M. Smith
;; STREET: One Market Plaza, Steuart Tower, Suite 2000
;; CITY: San Francisco
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94105
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/308,865
;; FILING DATE:
;; CLASSIFICATION: 800
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/145,707
;; FILING DATE:
;; APPLICATION NUMBER: US 07/904,068
;; FILING DATE: 23-JUN-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Smith, William M.
;; REGISTRATION NUMBER: 30,223
;; REFERENCE/DOCKET NUMBER: 14643-9-1-1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-326-2400
;; TELEFAX: 415-326-2422
;; INFORMATION FOR SEQ ID NO: 84:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 36 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-08-308-865-84

Query Match 61.7%; Score 37; DB 2; Length 36;
Best Local Similarity 57.1%; Pred. No. 8.7;
Matches 8; Conservative 1; Mismatches 1; Indels 4; Gaps 1;

QY 1 ARHNYGS----FYY 10
||| ||| :||
Db 3 ARHYGSGSYDYY 16

RESULT 11
US-09-042-353-281
Sequence 281, Application US/09042353
Patent No. 6255458
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 421
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,353
FILING DATE: 13-MAR-1998
CLASSIFICATION: 800

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/810,279
;; FILING DATE: 17-DEC-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/853,408
;; FILING DATE: 18-MAR-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/904,068
;; FILING DATE: 23-JUN-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/990,860
;; FILING DATE: 16-DEC-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/053,131
;; FILING DATE: 26-APR-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/096,762
;; FILING DATE: 22-JUL-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/155,301
;; FILING DATE: 18-NOV-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/161,739
;; FILING DATE: 03-DEC-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/165,699
;; FILING DATE: 10-DEC-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/209,741
;; FILING DATE: 09-MAR-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/352,322
;; FILING DATE: 07-DEC-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/544,404
;; FILING DATE: 10-OCT-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/728,463
;; FILING DATE: 10-OCT-1996
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: WO PCT/US96/16433
;; FILING DATE: 10-OCT-1996
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/758,417
;; FILING DATE: 02-DEC-1996
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: WO PCT/US97/21803
;; FILING DATE: 01-DEC-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Apple, Randolph T.
;; REGISTRATION NUMBER: 36,429
;; REFERENCE/DOCKET NUMBER: 014643-009040US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 576-0200
;; TELEFAX: (415) 576-0300
;; INFORMATION FOR SEQ ID NO: 281:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 36 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-09-042-353-281

Query Match 61.7%; Score 37; DB 4; Length 36;
Best Local Similarity 57.1%; Pred. No. 8.7;
Matches 8; Conservative 1; Mismatches 1; Indels 4; Gaps 1;

QY 1 ARHNYGS----FYY 10
||| ||| :||
Db 3 ARHYGSGSYDYY 16

RESULT 12
US-08-758-417A-129
; Sequence 129, Application US/08758417A
; Patent No. 6300129
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for
; Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 417
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/758,417A
; FILING DATE: 02-Dec-1996
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/728,463
; FILING DATE: 10-OCT-1996
; APPLICATION NUMBER: US 08/544,404
; FILING DATE: 10-OCT-1995
; APPLICATION NUMBER: US 08/352,322
; FILING DATE: 07-DEC-1994
; APPLICATION NUMBER: US 08/209,741
; FILING DATE: 09-MAR-1994
; APPLICATION NUMBER: US 08/165,699
; FILING DATE: 10-DEC-1993
; APPLICATION NUMBER: US 08/161,739
; FILING DATE: 03-DEC-1993
; APPLICATION NUMBER: US 08/155,301
; FILING DATE: 18-NOV-1993
; APPLICATION NUMBER: US 08/096,762
; FILING DATE: 22-JUL-1993
; APPLICATION NUMBER: US 08/053,131
; FILING DATE: 26-APR-1993
; APPLICATION NUMBER: US 07/990,860
; FILING DATE: 16-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Serafini, Andrew T.
; REGISTRATION NUMBER: 41,303
; REFERENCE/DOCKET NUMBER: 014643-009030US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 129:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 129:
US-08-758-417A-129

Query Match 61.7%; Score 37; DB 4; Length 36;
Best Local Similarity 57.1%; Pred. No. 8.7;
Matches 8; Conservative 1; Mismatches 1; Indels 4; Gaps 1;
QY 1 ARHNYGS---FYI 10
||| ||| :||
Db 3 ARHYGSGSYDIY 16

RESULT 13
PCT-US92-10983-84
; Sequence 84, Application PC/TUS9210983
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic Non-Human Animals for
; Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 152
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10983
; FILING DATE: 19921217
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14643-9-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US92-10983-84

Query Match 61.7%; Score 37; DB 5; Length 36;
Best Local Similarity 57.1%; Pred. No. 8.7;
Matches 8; Conservative 1; Mismatches 1; Indels 4; Gaps 1;
QY 1 ARHNYGS---FYI 10
||| ||| :||
Db 3 ARHYGSGSYDIY 16

RESULT 14
US-09-147-550-14
; Sequence 14, Application US/09147550
; Patent No. 6090340
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 94
; TYPE: PNT
; ORGANISM: BOVINE

US-09-147-550-14

Query Match 60.0%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 32;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
| | | | |
Db 80 RHNYGVF 86

RESULT 15

US-09-147-550-45
; Sequence 45, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-45

Query Match 60.0%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 32;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
| | | | |
Db 80 RHNYGVF 86

Search completed: November 18, 2002, 17:43:37
Job time : 5.2402 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:01 : Search time 4.90196 Seconds
(without alignments)
196.114 Million cell updates/sec

Title: US-09-016-061-68

Perfect score: 54

Sequence: 1 ARHNYGSPAS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_73:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	40	74.1	446	2 T19625	hypothetical prote
2	39	72.2	89	2 S38688	MHC class II histo
3	39	72.2	89	2 S38683	MHC class II histo
4	39	72.2	89	2 S38684	MHC class II histo
5	39	72.2	225	2 I47095	MHC class II OVAR-
6	36	66.7	65	2 S17441	hypothetical prote
7	36	66.7	82	2 I51106	Major histocompati
8	36	66.7	360	2 S48566	hypothetical prote
9	35	64.8	85	2 I59634	MHC class II DR-be
10	35	64.8	89	2 S38676	MHC class II histo
11	35	64.8	89	2 S38680	MHC class II histo
12	35	64.8	89	2 S57512	MHC class II histo
13	35	64.8	98	1 WMBP72	gene 7 protein - p
14	35	64.8	98	1 WMBP72	MHC class II histo
15	35	64.8	123	2 C25239	conserved hypothet
16	35	64.8	195	2 G86742	class II histocomp
17	35	64.8	200	2 D32526	MHC cell surface g
18	35	64.8	221	2 I45939	class II histocomp
19	35	64.8	237	2 C27060	gene HLA-DRB1 prot
20	35	64.8	266	2 I54287	class II histocomp
21	35	64.8	266	2 A27618	lymphocyte antigen
22	35	64.8	266	2 I54295	cytochrome c-type
23	35	64.8	313	1 A05213	phosphatidylcholin
24	35	64.8	347	2 S43771	Ig heavy chain v r
25	34	63.0	108	2 S26316	Ig heavy chain v r
26	34	63.0	110	2 S26317	MHC class II histo
27	34	63.0	115	2 S37265	conserved hypothet
28	34	63.0	210	1 B69265	MHC class II histo
29	34	63.0	263	2 A45838	MHC class II histo

30	34	63.0	265	2 B39797	MHC class II histo
31	34	63.0	275	2 G75130	translation initia
32	34	63.0	275	2 D71087	probable translati
33	34	63.0	279	2 T05421	hypothetical prote
34	34	63.0	287	1 PMBY	inorganic diphosph
35	34	63.0	287	1 PMVKL	inorganic diphosph
36	34	63.0	550	2 AE1058	alpha, alpha-phosph
37	34	63.0	723	2 F83173	outer membrane pro
38	34	63.0	1052	2 AF2959	conserved hypothet
39	34	63.0	1341	2 H98323	hypothetical prote
40	33	61.1	80	2 I54469	MHC HLA-DR-beta-1
41	33	61.1	80	2 I68777	MHC HLA-DR-beta-1
42	33	61.1	81	2 I54550	HLA DRB1*1202 - hu
43	33	61.1	87	2 S38681	major histocompati
44	33	61.1	87	2 S38682	major histocompati
45	33	61.1	87	2 S38685	major histocompati

ALIGNMENTS

RESULT 1

T19625
hypothetical protein C31H5.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
C:Accession: T19625
R:Kershaw, J.
submitted to the EMBL Data Library, April 1997
A:Reference number: Z19153
A:Accession: T19625
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-446 <WIL>
A:Cross-references: EMBL:293778; PIDN:CA807846.1; GSPDB:GN00019; CESP:C31H5.6
A:Experimental source: clone C31H5
C:Genetics:
A:Gene: CESP:C31H5.6
A:Map position: 1
A:Introns: 49/2; 85/1; 120/2; 183/3; 218/3; 255/3; 285/2; 331/3; 360/3
C:Superfamily: Caenorhabditis elegans hypothetical protein W03D8.8

Query Match 74.1%; Score 40; DB 2; Length 446;
Best Local Similarity 77.8%; Pred. No. 6.6;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSPAS 10
Db 51 RHNYGSHAA 59
|||||

RESULT 2

S38688
MHC class II histocompatibility antigen HLA-DR-08 beta chain - northern lesser bushba
C:Species: Galago senegalensis (northern lesser bushbaby)
C:Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 19-May-2000
C:Accession: S38688
R:Figuerola, F.; O'Huigin, C.; Tichy, H.; Klein, J.
submitted to the EMBL Data Library, November 1993
A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduce
A:Reference number: S38676
A:Accession: S38688
A:Molecule type: DNA
A:Residues: 1-89 <FIG>
A:Cross-references: EMBL:Z27158
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 72.2%; Score 39; DB 2; Length 89;
Best Local Similarity 77.8%; Pred. No. 2.1;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RHNYGSPAS 10
|||||

Db 75 RHNYGVFES 83

RESULT 3

S38683

MHC class II histocompatibility antigen HLA-DR-03 beta chain - northern lesser bushbaby

C:Species: Galago senegalensis (northern lesser bushbaby)

C:Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 19-May-2000

C:Accession: S38683

R:Figueroa, F.; O'Huigin, C.; Tichy, H.; Klein, J.

A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduced from submitted to the EMBL Data Library, November 1993

A:Reference number: S38676

A:Accession: S38683

A:Molecule type: DNA

A:Residues: 1-89 <FIG>

A:Cross-references: EMBL:227153

C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 72.2%; Score 39; DB 2; Length 89;

Best Local Similarity 77.8%; Pred. No. 2.1;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAS 10

|||||

Db 75 RHNYGVFES 83

RESULT 4

S38684

MHC class II histocompatibility antigen HLA-DR-04 beta chain - northern lesser bushbaby

C:Species: Galago senegalensis (northern lesser bushbaby)

C:Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 19-May-2000

C:Accession: S38684

R:Figueroa, F.; O'Huigin, C.; Tichy, H.; Klein, J.

A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduced from submitted to the EMBL Data Library, November 1993

A:Reference number: S38676

A:Accession: S38684

A:Molecule type: DNA

A:Residues: 1-89 <FIG>

A:Cross-references: EMBL:227154

C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 72.2%; Score 39; DB 2; Length 89;

Best Local Similarity 77.8%; Pred. No. 2.1;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAS 10

|||||

Db 75 RHNYGVFES 83

RESULT 5

I47095

MHC class II OVAR-DR-beta-3 - sheep (fragment)

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C:Date: 15-Oct-1996 #sequence_revision 15-Oct-1996 #text_change 21-Jan-2000

C:Accession: I47095

R:Fabb, S.A.; Maddox, J.F.; Gogolin-Ewens, K.J.; Baker, L.; Wu, M.J.; Brandon, M.R.

A:Title: Isolation, characterization and evolution of ovine major histocompatibility complex genes

A:Reference number: I47075; MUID:94057592; PMID:7902039

A:Accession: I47095

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-225 <FAB>

A:Cross-references: GB:L04790; NID:g458880; PIDN:AAAL6562.1; PID:g458881

C:Genetics:

A:Gene: OVAR-DRB3

C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

F:98-163/Domain: immunoglobulin homology <IMM>

Query Match 72.2%; Score 39; DB 2; Length 225;

Best Local Similarity 77.8%; Pred. No. 5.2;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAS 10

|||||

Db 68 RHNYGVFES 76

RESULT 6

S17441

hypothetical protein (rpl2 5' region) - garden pea chloroplast (fragment)

C:Species: chloroplast Pisum sativum (garden pea)

C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 11-Jun-1999

C:Accession: S17441

R:Nagano, Y.; Ishikawa, H.; Matsuno, R.; Sasaki, Y.

A:Title: Nucleotide sequence and expression of the ribosomal protein L2 gene in pea chloroplast

A:Reference number: S17441; MUID:91355950; PMID:1884007

A:Accession: S17441

A:Molecule type: DNA

A:Residues: 1-65 <NAG>

A:Cross-references: EMBL:X59015; NID:g12175; PIDN:CAA41754.1; PID:g388252

C:Genetics:

A:Genome: chloroplast

C:Superfamily: cytochrome c-type synthesis protein

C:Keywords: chloroplast

Query Match 66.7%; Score 36; DB 2; Length 65;

Best Local Similarity 75.0%; Pred. No. 5.7;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFAS 10

|||||

Db 57 HSYGSFAS 64

RESULT 7

I51106

Major Histocompatibility Complex class IIB - ring-necked pheasant (fragment)

C:Species: Phasianus colchicus (ring-necked pheasant)

C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 23-Jul-1999

C:Accession: I51106

R:Wittzell, H.; von Schantz, T.; Zoorob, R.; Auffray, C.

A:Title: Molecular characterization of three Mhc class II B haplotypes in the ring-necked pheasant

A:Reference number: I51103; MUID:94245280; PMID:7910588

A:Accession: I51106

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-82 <WIT>

A:Cross-references: EMBL:X75406; NID:g496926; PIDN:CAA53160.1; PID:g496927

C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 66.7%; Score 36; DB 2; Length 82;

Best Local Similarity 85.7%; Pred. No. 7.2;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8

|||||

Db 75 RHNYGVF 81

RESULT 8

S48566

hypothetical protein YLR215c - yeast (Saccharomyces cerevisiae)

N:Alternate names: hypothetical protein L8167.23

C:Species: Saccharomyces cerevisiae

C:Date: 02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change 19-Apr-2002

C:Accession: S48566

R:Pauley, A.

A:Description: The sequence of S. cerevisiae cosmid 8167.

A:Reference number: S48545

A:Accession: S48566

A:Molecule type: DNA

A:Residues: 1-360 <PAU>

A:Cross-references: EMBL:U14913; NID:g544497; PIDN:AAB67444.1; PID:g544519; GSPDB:GN0001

C:Genetics:

A:Gene: SGD:CDIC23; MIPS:YLR215C

A:Cross-references: SGD:S0004205

A:Map position: 12R

C:Superfamily: Saccharomyces cerevisiae hypothetical protein YLR215C

Query Match

Best Local Similarity 66.7%; Score 36; DB 2; Length 360;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAS 10

|||||

Db 304 RHNTGRFAS 312

RESULT 9

I59634

MHC class II DR-beta-1 - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999

C:Accession: I59634

R:Lin, Y.N.; Ren, E.C.; Chan, S.H.

Tissue Antigens 41, 204-205, 1993

A:Title: A new DR11 allele in Singaporean Chinese.

A:Reference number: I59634; MUID:93369836; PMID:8362413

A:Accession: I59634

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-85 <RES>

A:Cross-references: GB:M98436; NID:gl87890; PIDN:AAA59693.1; PID:gl87891

C:Genetics:

A:Gene: HLA-DRB1-11

C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match

Best Local Similarity 64.8%; Score 35; DB 2; Length 85;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAS 10

|||||

Db 75 RHNYGAVES 83

RESULT 10

S38676

MHC class II histocompatibility antigen HLA-DR-01 beta chain - Galago moholi (fragment)

C:Species: Galago moholi

C:Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 20-Jun-2000

C:Accession: S38676

R:Figuerola, F.; O'Huigin, C.; Tichy, H.; Klein, J.

submitted to the EMBL Data Library, November 1993

A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduced

A:Reference number: S38676

A:Molecule type: DNA

A:Residues: 1-89 <FIG>

A:Cross-references: EMBL:227130; NID:g415801; PIDN:CAA81657.1; PID:gl132545

C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match

Best Local Similarity 64.8%; Score 35; DB 2; Length 89;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAS 10

|||||

Db 75 RHNYGAVES 83

RESULT 13

WMBP7Z

gene 7 protein - phage PZA

C:Species: phage PZA

A:Note: host Bacillus subtilis

C:Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 23-Jul-1999

C:Accession: A24831

R:Paces, V.; Vlcek, C.; Urbanek, P.

Gene 44, 107-114, 1986

A:Title: Nucleotide sequence of the late region of Bacillus subtilis phage PZA, a clo

RESULT 11

S38680

MHC class II histocompatibility antigen HLA-DR-05 beta chain - Galago moholi (fragment)

C:Species: Galago moholi

C:Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 20-Jun-2000

C:Accession: S38680

R:Figuerola, F.; O'Huigin, C.; Tichy, H.; Klein, J.

submitted to the EMBL Data Library, November 1993

A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduce

A:Reference number: S38676

A:Molecule type: DNA

A:Residues: 1-89 <FIG>

A:Cross-references: EMBL:227134; NID:g415805; PIDN:CAA81661.1; PID:gl132549

C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match

Best Local Similarity 64.8%; Score 35; DB 2; Length 89;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAS 10

|||||

Db 75 RHNYGAVES 83

RESULT 12

S57512

MHC class II histocompatibility antigen HLA-DR beta 1 chain DRB1*08 precursor - human

C:Species: Homo sapiens (man)

C:Date: 10-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 23-Jul-1999

C:Accession: S57512; I79647

R:Versluis, L.F.; Savelkoul, P.; van der Zwan, A.W.; van den Berg-Loonen, E.; Tilanus

submitted to the EMBL Data Library, June 1995

A:Reference number: S57512

A:Accession: S57512

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-89 <VER>

A:Cross-references: EMBL:X88854; NID:g887451; PIDN:CAA61324.1; PID:g887452

R:Gyllenstein, U.B.; Sundvall, M.; Erlich, H.A.

Proc. Natl. Acad. Sci. U.S.A. 88, 3686-3690, 1991

A:Title: Allelic diversity is generated by intraexon sequence exchange at the DRB1 lo

A:Reference number: I59196; MUID:91219437; PMID:2023919

A:Accession: I79647

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-73 <RES>

A:Cross-references: GB:M63196; NID:gl81762; PIDN:AAA52321.1; PID:gl81763

C:Genetics:

A:Gene: GDB:HLA-DRB1

A:Cross-references: GDB:I20642

A:Map position: 6p21.3-6p21.3

C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match

Best Local Similarity 64.8%; Score 35; DB 2; Length 89;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAS 10

|||||

Db 75 RHNYGAVES 83

A:Reference number: A91550; MUID:87031573; PMID:3095188

A:Accession: A24831

A:Molecule type: DNA

A:Residues: 1-98 <PAC>

A:Cross-references: GB:M11813; GB:M13904; GB:M13905; NID:g216046; PIDN:AAA88483.1; PID:g

C:Genetics:

A:Gene: 7

C:Superfamily: phage PZA gene 7 protein

C:Keywords: late protein

Query Match 64.8%; Score 35; DB 1; Length 98;

Best Local Similarity 77.8%; Pred. No. 13;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RHNYGSFAS 10

| | | | | | |

Db 33 RVNYGSFVS 41

RESULT 14

WMBPF9

gene 7 protein - phage phi-29

N:Alternate names: head morphogenesis protein

C:Species: phage phi-29

A:Note: host Bacillus subtilis

C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 23-Jul-1999

C:Accession: A28923; A25816

R:Innis, C.A.; Garvey, K.J.; Ito, J.

Nucleic Acids Res. 14, 7129, 1986

A:Title: Nucleotide sequence of phage phi-29 gene 7: structure of intergenic spacer betw

A:Reference number: A28923; MUID:87016351; PMID:3763399

A:Accession: A28923

A:Molecule type: DNA

A:Residues: 1-98 <IN>

A:Cross-references: GB:X04386; NID:g15522; PIDN:CAA27974.1; PID:g15524

R:Vicek, C.; Paces, V.

Gene 46, 215-225, 1986

A:Title: Nucleotide sequence of the late region of Bacillus phage phi-29 completes the 1

A:Reference number: A25816; MUID:87106857; PMID:3803926

A:Accession: A25816

A:Molecule type: DNA

A:Residues: 1-98 <VLC>

A:Cross-references: GB:M14782; NID:g215323; PIDN:AAA32279.1; PID:g215324

C:Genetics:

A:Gene: 7

C:Superfamily: phage PZA gene 7 protein

C:Keywords: head protein; late protein

Query Match 64.8%; Score 35; DB 1; Length 98;

Best Local Similarity 77.8%; Pred. No. 13;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RHNYGSFAS 10

| | | | | | |

Db 33 RVNYGSFVS 41

RESULT 15

C25239

MHC class II histocompatibility antigen HLA-DR-2-MN2-2 beta chain precursor - human (fra

C:Species: Homo sapiens (man)

C:Date: 28-Sep-1987 #sequence_revision 28-Sep-1987 #text_change 03-May-1996

C:Accession: C25239

R:Wu, S.; Saunders, T.L.; Bach, F.H.

Nature 324, 676-679, 1986

A:Title: Polymorphism of human Ia antigens generated by reciprocal intergenic exchange b

A:Reference number: A25239; MUID:87090380; PMID:3099214

A:Accession: C25239

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-123 <WUS>

C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 64.8%; Score 35; DB 2; Length 123;

Best Local Similarity 66.7%; Pred. No. 17;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RHNYGSFAS 10

| | | | | | |

Db 109 RHNYGAVES 117

Search completed: November 18, 2002, 17:47:05

Job time : 5.90196 secs

GenCore version 5.1.3

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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:00 ; Search time 2.45098 Seconds
(without alignments)
169.223 Million cell updates/sec

Title: us-09-016-061-68

Perfect score: 54

Sequence: 1 ARHNYGSFAS 10

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	75.9	323	1 CCSA_LOTJA	Q9bbp4 lotus japon
2	36	66.7	65	1 CCSA_PEA	P31172 pisum sativ
3	36	66.7	328	1 CCSA_ARATH	P56770 arabidopsis
4	35	64.8	98	1 VG7_BPPH2	P13848 bacterioph
5	35	64.8	98	1 VG7_BPPH2	P07533 bacterioph
6	35	64.8	313	1 CCSA_TOBAC	P12216 nicotiana t
7	34	63.0	275	1 IF2A_PVRAB	Q9v0e4 pyrococcus
8	34	63.0	275	1 IF2A_PVRAB	C58655 pyrococcus
9	34	63.0	284	1 IPYR_PICPA	Q13505 pichia past
10	34	63.0	286	1 IPYR_KLULA	P13998 kluyveromyc
11	34	63.0	286	1 IPYR_YEAST	P00817 saccharomyc
12	33	61.1	266	1 HB2D_CANFA	P18470 canis fami
13	33	61.1	322	1 FATE_VIBAN	P11460 vibrio angu
14	33	61.1	398	1 F221_ARATH	C04088 arabidopsis
15	33	61.1	448	1 NCAP_CVHOC	P33469 human coron
16	33	61.1	470	1 SYE2_RICPR	Q9zct8 rickettsia
17	33	61.1	473	1 SYE_AQAE	O67271 aquifex aeo
18	33	61.1	639	1 Y119_MYCTU	O50614 mycobacteri
19	33	61.1	682	1 VG50_BMFL5	Q05262 mycobacteri
20	33	61.1	1254	1 MDR3_CAEEL	P34713 caenorhabdi
21	32	59.3	65	1 CCSA_OENBE	P31565 oenothera b
22	32	59.3	196	1 WBBJ_ECOLI	P37750 escherichia
23	32	59.3	198	1 HB2G_HUMAN	P01914 homo sapien
24	32	59.3	213	1 PNCA_ECOLI	P21369 escherichia
25	32	59.3	251	1 SAST_ANAPL	P00633 anas platyr
26	32	59.3	266	1 HB2A_HUMAN	P01913 homo sapien
27	32	59.3	266	1 HB2B_HUMAN	P01912 homo sapien
28	32	59.3	266	1 HB2C_HUMAN	P01914 homo sapien
29	32	59.3	266	1 HB2D_HUMAN	P13759 homo sapien
30	32	59.3	266	1 HB2E_HUMAN	P04229 homo sapien
31	32	59.3	266	1 HB2F_HUMAN	P13758 homo sapien
32	32	59.3	266	1 HB2I_HUMAN	P13760 homo sapien
33	32	59.3	266	1 HB2J_HUMAN	P20039 homo sapien

34 32 59.3 266 1 HB2J_HUMAN P13761 homo sapien
35 32 59.3 305 1 YN45_DEIRA Q9rry7 deinococcus
36 32 59.3 319 1 CCSA_OENHO Q9mt12 oenothera h
37 32 59.3 321 1 CCSA_MAIZE P46659 zea mays (m
38 32 59.3 321 1 CCSA_ORYSA P12215 oryza sativ
39 32 59.3 322 1 CCSA_WHEAT P58266 triticum ae
40 32 59.3 323 1 CCSA_SPIOL Q9m3j1 spinacia ol
41 32 59.3 349 1 PTEL_YEAST P41903 saccharomyc
42 32 59.3 385 1 O65B_DROME P82983 drosophila
43 32 59.3 396 1 ALR_BRUME Q8vd03 bruceella me
44 32 59.3 464 1 DLDH_MYCTU O53747 mycobacteri
45 32 59.3 491 1 SYE_LISIN Q9zf38 listeria in

ALIGNMENTS

RESULT 1
CCSA_LOTJA STANDARD; PRT; 323 AA.
AC Q9BBP4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Cytochrome c biogenesis protein ccsc.
GN CCSA.
OS Lotus japonicus.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Lotaeae; Lotus.
OX NCBI_TaxID=34305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Accession MG-20;
RX MEDLINE=21082929; PubMed=11214967;
RA Kato T., Kaneko T., Sato S., Nakamura Y., Tabata S.;
RT "Complete structure of the chloroplast genome of a legume, Lotus japonicus.";
RL DNA Res. 7:323-330(2000).
CC -!- FUNCTION: REQUIRED DURING CYTOCHROME BIOGENESIS AT THE STEP OF
CC -!- HEME ATTACHMENT (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CCMF/CYCK/CCLL/NRFE/CCSA FAMILY.
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CC -----
CC EMBL: AP002983; BAB33244.1; -
DR InterPro: IPR002541; CytC_asm.
DR Pfam: PF01578; CytC_asm; 1.
KW Cytochrome c-type biogenesis; Chloroplast.
SQ SEQUENCE 323 AA; 37185 MW; 5A034E3E2829FE35 CRC64;
Query Match 75.9%; Score 41; DB 1; Length 323;
Best Local Similarity 87.5%; Pred. No. 0.63;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3 HNYGSFAS 10
Db 315 HNYGSFAS 322
|||||
RESULT 2
CCSA_PEA STANDARD; PRT; 65 AA.
AC P31172;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Cytochrome c biogenesis protein ccsa (Fragment).
GN CCSA.
OS Pisum sativum (Garden pea).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eusoids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
ON NCBI_TaxID=3888;
RX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Alaska;
RX MEDLINE=9135950; PubMed=1884007;
RA Nagano Y., Ishikawa H., Matsuno R., Sasaki Y.;
RT "Nucleotide sequence and expression of the ribosomal protein L2 gene
in pea chloroplasts.";
RL Plant Mol Biol 17:541-545(1991).
CC -!- FUNCTION: REQUIRED DURING CYTOCHROME BIOGENESIS AT THE STEP OF
HEME ATTACHMENT (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CCME/CYCK/CCLI/NRFE/CCSA FAMILY.
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CC -----
DR EMBL; X59015; CAA41754.1; -;
DR PIR; S17441; S17441.
DR InterPro; IPR002541; CytoC.asm.
DR Pfam; PF01578; CytoC.asm; 1.
KW Cytochrome c-type biogenesis; Chloroplast.
FT NON_TER
FT 1
SQ SEQUENCE 65 AA; 7396 MW; 9E523E0C70B102AA CRC64;

Query Match 66.7%; Score 36; DB 1; Length 65;
Best Local Similarity 75.0%; Pred. No. 1.2;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSPAS 10
Db 57 HSYGSFTS 64

RESULT 3
CCSA_ARATH
ID CCSA_ARATH STANDARD; PRT; 328 AA.
AC P56770;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cytochrome c biogenesis protein ccsa.
GN CCSA.
OS Arabidopsis thaliana (Mouse-ear cress).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eusoids II; Brassicales; Brassicaceae; Arabidopsi.
ON NCBI_TaxID=3702;
RX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20039611; PubMed=10574454;
RA Sato S., Nakamura Y., Kaneko T., Asamizu E., Tabata S.;
RT "Complete structure of the chloroplast genome of Arabidopsis
thaliana.";
RL DNA Res. 6:283-290(1999).
CC -!- FUNCTION: REQUIRED DURING CYTOCHROME BIOGENESIS AT THE STEP OF
HEME ATTACHMENT (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CCME/CYCK/CCLI/NRFE/CCSA FAMILY.
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CC -----
DR EMBL; AP000423; BAA84436.1; -;
DR InterPro; IPR002541; CytoC.asm.
DR Pfam; PF01578; CytoC.asm; 1.
KW Cytochrome c-type biogenesis; Chloroplast.
SQ SEQUENCE 328 AA; 37732 MW; C88D1508B2924D6F CRC64;

Query Match 66.7%; Score 36; DB 1; Length 328;
Best Local Similarity 75.0%; Pred. No. 6.5;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSPAS 10
Db 320 HSYGSFTS 327

RESULT 4
VG7_BPPH2
ID VG7_BPPH2 STANDARD; PRT; 98 AA.
AC P13848;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Head morphogenesis protein (Late protein GP7).
GN 7.
OS Bacteriophage phi-29.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;
OC phi-29-like viruses.
ON NCBI_TaxID=10736;
RX [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87106857; PubMed=3803926;
RA Vilek C., Paces V.;
RT "Nucleotide sequence of the late region of Bacillus phage phi 29
completes the 19,285-bp sequence of phi 29 genome. Comparison with
the homologous sequence of phage PZA.";
RL Gene 46:215-225(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87016351; PubMed=3763399;
RA Innis C.A., Garvey K.J., Ito J.;
RT "Nucleotide sequence of phage phi 29 gene 7: structure of intergenic
spacer between the major early and late genes.";
RL Nucleic Acids Res. 14:7129-7129(1986).
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CC -----
DR EMBL; M14782; AAA32279.1; -;
DR EMBL; X04386; CAA27974.1; -;
DR PIR; A28923; WMBPF9.
KW Late protein.
SQ SEQUENCE 98 AA; 11266 MW; FF2E7985D2266E14 CRC64;

Query Match 64.8%; Score 35; DB 1; Length 98;
Best Local Similarity 77.8%; Pred. No. 2.9;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYSFAS 10
Db 33 RNYGSFVS 41


```
RESULT 5
VG7_BPZA
ID VG7_BPZA STANDARD; PRT; 98 AA.
AC P07533;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Head morphogenesis protein (late protein GP7).
GN 7.
OS Bacteriophage PZA.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;
OC phi-29-like viruses.
OX NCBI_TaxID=10757;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87031573; PubMed=3095188;
RA Paces V., Vlcek C., Urbanek P.;
RT "Nucleotide sequence of the late region of Bacillus subtilis phage
RT PZA, a close relative of phi 29.";
RL Gene 44:107-114(1986).
CC -----
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CC -----
DR EMBL; M11813; AA88483.1; -.
DR PIR; A24831; WMBP72.
DR PIR; A05213; A05213.
DR InterPro; IPR002541; CytC_asm.
DR Pfam; PF01578; CytC_asm; 1.
KW Cytochrome c-type biogenesis; Chloroplast.
SQ SEQUENCE 98 AA; 11281 MW; 444408C39B606A25 CRC64;

Query Match 64.8%; Score 35; DB 1; Length 98;
Best Local Similarity 77.8%; Pred. No. 2.9;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RHNYGSFAS 10
Db 33 RVNYGSFVS 41

RESULT 6
CCSA_TOBAC
ID CCSA_TOBAC STANDARD; PRT; 313 AA.
AC P12216;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cytochrome c biogenesis protein ccsa.
GN CCSA.
OS Nicotiana tabacum (Common tobacco).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=cv. Bright Yellow 4;
RA Shinozaki K., Ohme M., Tanaka M., Wakasugi T., Hayashida N.,
RA Matsubayashi T., Zaita N., Chunwongse J., Obokata J.,
RA Yamaguchi-Shinozaki K., Ohto C., Torazawa K., Meng B.-y., Sugita M.,
RA Dena H., Kamogashira T., Yamada K., Kusuda J., Takaiwa F., Kato A.,
RA Tohdoh N., Shimada H., Sugiyama M.;
RT "The complete nucleotide sequence of the tobacco chloroplast genome:
RT its gene organization and expression.";
RL EMBO J. 5:2043-2049(1986).
CC -!- FUNCTION: REQUIRED DURING CYTOCHROME BIOGENESIS AT THE STEP OF
CC HEME ATTACHMENT (BY SIMILARITY).
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-!- SIMILARITY: BELONGS TO THE CCMF/CYCK/CCL1/NRFE/CCSA FAMILY.
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CC -----
DR EMBL; 200044; CAA77395.1; -.
DR PIR; A05213; A05213.
DR InterPro; IPR002541; CytC_asm.
DR Pfam; PF01578; CytC_asm; 1.
KW Cytochrome c-type biogenesis; Chloroplast.
SQ SEQUENCE 313 AA; 35558 MW; 0C93417F79C47A96 CRC64;

Query Match 64.8%; Score 35; DB 1; Length 313;
Best Local Similarity 75.0%; Pred. No. 9.9;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 HNYGSFAS 10
Db 303 HSYGSFVS 310

RESULT 7
IF2A_PVRAB
ID IF2A_PVRAB STANDARD; PRT; 275 AA.
AC Q9V0E4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable translation Initiation factor 2 alpha subunit (eIF-2-alpha).
GN EIF2A OR PAB0568.
OS Pyrococcus abyssi.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=29292;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=GE5 / Orsay;
RA Hellig R.;
RT "Pyrococcus abyssi genome sequence: insights into archaeal chromosome
RT structure and evolution.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: EIF-2 FUNCTIONS IN THE EARLY STEPS OF PROTEIN SYNTHESIS
CC BY FORMING A TERNARY COMPLEX WITH GTP AND INITIATOR TRNA
CC (BY SIMILARITY).
CC -!- SUBUNIT: HETEROTRIMER COMPOSED OF AN ALPHA, A BETA, AND A GAMMA
CC CHAIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE EIF-2-ALPHA FAMILY.
CC -!- SIMILARITY: CONTAINS 1 SI MOTIF DOMAIN.
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CC -----
DR EMBL; AJ248285; CAB49760.1; -.
DR HSSP; P05055; ISRO.
DR InterPro; IPR003029; S1.
DR Pfam; PF00575; S1; 1.
DR SMART; SM00316; S1; 1.
DR PROSITE; PS50126; S1; 1.
KW Initiation factor; Protein biosynthesis; RNA-binding;
KW Complete proteome.
FT DOMAIN 12 83 S1 MOTIF.
SQ SEQUENCE 275 AA; 31912 MW; B2659F3A49879B4F CRC64;
```

Query Match 63.0%; Score 34; DB 1; Length 275;
 Best Local Similarity 83.3%; Pred. No. 14;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
 |||||:|
 Db 23 HNYGAF 28

RESULT 8

IF2A_PVRHO STANDARD; PRT; 275 AA.
 AC 058655;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Probable translation initiation factor 2 alpha subunit (eIF-2-alpha).
 GN EIF2A OR PH0961.
 OS Pyrococcus horikoshii.
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 OC Pyrococcus.
 OX NCBI_TaxID=53953;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=OT3;
 RX MEDLINE=9834137; PubMed=9679194;
 RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
 RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
 RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
 RA Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
 RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
 RA Masuchi Y., Shizuya H., Kikuchi H.;
 RT "Complete sequence and gene organization of the genome of a hyper-
 thermophilic archaeobacterium, Pyrococcus horikoshii OT3";
 RL DNA Res. 5:55-76(1998).
 CC -!- FUNCTION: EIF-2 FUNCTIONS IN THE EARLY STEPS OF PROTEIN SYNTHESIS
 CC BY FORMING A TERNARY COMPLEX WITH GTP AND INITIATOR TRNA
 CC (BY SIMILARITY).
 CC -!- SUBUNIT: HETEROTRIMER COMPOSED OF AN ALPHA, A BETA, AND A GAMMA
 CC CHAIN (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE EIF-2-ALPHA FAMILY.
 CC -!- SIMILARITY: CONTAINS 1 SI MOTIF DOMAIN.
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 CC -----
 CC EMBL; AF000004; BAA30058.1; -;
 CC HSP; P05055; LSRO.
 CC InterPro: IPR003029; S1.
 CC Pfam: PF00575; S1; 1.
 CC SMART: SM00316; S1; 1.
 CC PROSITE: PS0126; S1; 1.
 CC Initiation factor; Protein biosynthesis; RNA-binding;
 KW Complete proteome.
 FT DOMAIN 12 83
 SQ SEQUENCE 275 AA; 31980 MW; 6AAD15F10FFB436 CRC64;

Query Match 63.0%; Score 34; DB 1; Length 275;
 Best Local Similarity 83.3%; Pred. No. 14;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
 |||||:|
 Db 23 HNYGAF 28

RESULT 9

IPYR_PICPA

ID IPYR_PICPA STANDARD; PRT; 284 AA.
 AC 013505;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Inorganic pyrophosphatase (EC 3.6.1.1) (Pyrophosphate phospho-
 DE hydrolase) (PPase).
 GN IPP1.
 OS Pichia pastoris (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Pichia.
 OX NCBI_TaxID=4922;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL Y-11430;
 RX MEDLINE=99034033; PubMed=9818724;
 RA Cosano I.C., Alvarez P., Molina M., Nombela C.;
 RT "Cloning and sequence analysis of the Pichia pastoris TRP1, IPP1 and
 RT HIS3 genes";
 RL Yeast 14:861-867(1998).
 CC -!- CATALYTIC ACTIVITY: Diphosphate + H(2)O = 2 phosphate.
 CC -!- COFACTOR: REQUIRES THE PRESENCE OF DIVALENT METAL CATION.
 CC MAGNESIUM CONFERS THE HIGHEST ACTIVITY.
 CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: BELONGS TO THE PPASE FAMILY.
 CC -----
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 CC -----
 CC EMBL; AJ001000; CAA04453.1; -;
 CC HSP; P00817; IWGI.
 CC InterPro: IPR001596; Pyrophosphatase.
 CC Pfam: PF00719; Pyrophosphatase; 1.
 CC PROSITE: PS00387; PPASE; 1.
 CC Hydrolase; Magneslum.
 FT INIT_MET 0 0 BY SIMILARITY.
 FT ACT_SITE 56 56 PROBABLE.
 FT BINDING 78 78 INORGANIC PYROPHOSPHATE (BY SIMILARITY).
 SQ SEQUENCE 284 AA; 31937 MW; 3DAD27970D775D6 CRC64;
 Query Match 63.0%; Score 34; DB 1; Length 284;
 Best Local Similarity 83.3%; Pred. No. 14;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 3 HNYGSF 8
 |||||:|
 Db 91 HNYGAF 96
 RESULT 10
 ID IPYR_KLULA STANDARD; PRT; 286 AA.
 AC P13998;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 01-OCT-1994 (Rel. 30, Last annotation update)
 DE Inorganic pyrophosphatase (EC 3.6.1.1) (Pyrophosphate phospho-
 DE hydrolase) (PPase).
 GN IPP1 OR IPP.
 OS Kluyveromyces lactis (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
 OX NCBI_TaxID=28985;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89189093; PubMed=2538971;
 RA Stark M.J.R., Milner J.S.;

RT "Cloning and analysis of the Kluyveromyces lactis TRP1 gene: a
RT chromosomal locus flanked by genes encoding inorganic pyrophosphatase
RT and histone H3.";
RL Yeast 5:35-50(1989).
RN [2]
RN SIMILARITY TO E.COLI AND YEAST PPASES.
RX MEDLINE=90254161; PubMed=2160278;
RA Lahti R., Kolakowski L.F. Jr., Heinonen J., Vihinen M., Pohjanoksa K.,
RA Cooperman B.S.;
RT "Conservation of functional residues between yeast and E. coli
RT inorganic pyrophosphatases.";
RL Biochim. Biophys. Acta 1038:338-345(1990).
CC -|- CATALYTIC ACTIVITY: Diphosphate + H(2)O = 2 phosphate.
CC -|- COFACTOR: REQUIRES THE PRESENCE OF DIVALENT METAL CATION.
CC MAGNESIUM CONFERS THE HIGHEST ACTIVITY.
CC -|- SUBUNIT: HOMODIMER.
CC -|- SUBCELLULAR LOCATION: Cytoplasmic.
CC -|- SIMILARITY: BELONGS TO THE PPASE FAMILY.
CC -----
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CC -----
DR EMBL; X14230; CAA32446.1; -;
DR PIR; S07894; PNVKL.
DR HSSP; P00817; LWGI.
DR InterPro; IPR001596; Pyrophosphatase.
DR Pfam; PF00719; Pyrophosphatase; 1.
DR PROSITE; PS00387; PPASE; 1.
KW Hydrolyase; Magnesium.
FT INIT_MET 0 BY SIMILARITY.
FT ACT_SITE 56 56 PROBABLE.
FT BINDING 78 78 INORGANIC PYROPHOSPHATE (BY SIMILARITY).
SQ SEQUENCE 286 AA; 32034 MW; 11647F4ABD916A2F CRC64;

Query Match 63.0%; Score 34; DB 1; Length 286;
Best Local Similarity 83.3%; Pred. No. 14;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
DB 91 HNYGAF 96

RESULT 11
ID IPYR_YEAST STANDARD; PRT; 286 AA.
AC P00817;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Inorganic pyrophosphatase (EC 3.6.1.1) (Pyrophosphate phospho-
DE hydrolase) (PPase).
DE IPPI OR PPAL OR PPA OR YBR011C OR YBR0202.
GN Saccharomyces cerevisiae (Baker's yeast).
OS Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RN SEQUENCE FROM N.A.
RP STRAIN=X2180;
RX MEDLINE=90083474; PubMed=2849749;
RA Kolakowski L.F. Jr., Schloesser M., Cooperman B.S.;
RT "Cloning, molecular characterization and chromosome localization of
RT the inorganic pyrophosphatase (ppa) gene from S. cerevisiae.";
RL Nucleic Acids Res. 16:10441-10452(1988).
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=S288C;

RA Entian K.-D., Koetter P., Rose M., Li Z., Thermann R., Brendel M.,
RA Baur A., Boles E., Miosga T., Schaaff-Gerstenschlaeger I.,
RA Zimmermann F.K.;
RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
RN [3]
RN SEQUENCE.
RX MEDLINE=78087552; PubMed=340461;
RA Cohen S.A., Sterner R., Keim P.S., Heinrichson R.L.;
RT "Covalent structural analysis of yeast inorganic pyrophosphatase.";
RL J. Biol. Chem. 253:889-897(1978).
RN [4]
RN SEQUENCE OF 25-35 AND 239-251.
RC STRAIN=S288C;
RX MEDLINE=95203288; PubMed=7895733;
RA Garels J.I., Fitcher B., Kobayashi R., Latter G.I., Schwender B.,
RA Volpe T., Warner J.R., McLaughlin C.S.;
RT "Protein identifications for a Saccharomyces cerevisiae protein
RT database.";
RL Electrophoresis 15:1466-1486(1994).
RN [5]
RN SEQUENCE OF 239-249.
RC STRAIN=ATCC 38531 / Y41;
RX MEDLINE=97089742; PubMed=8935650;
RA Norbeck J., Blomberg A.;
RT "Protein expression during exponential growth in 0.7 M NaCl medium of
RT Saccharomyces cerevisiae";
RL FEMS Microbiol. Lett. 137:1-8(1996).
RN [6]
RN ACTIVE SITE.
RX MEDLINE=80109718; PubMed=6101539;
RA Bond M.W., Chiu N.Y., Cooperman B.S.;
RT "Identification of an arginine important for enzymatic activity
RT within the covalent structure of yeast inorganic pyrophosphatase.";
RL Biochemistry 19:94-102(1980).
RN [7]
RN X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
RA Arutiunian E.G., Terzian S., Voronova A.A., Kuranova I.P.,
RA Smirnova E.A., Vainstein B.K., Hohne W.E., Hansen G.;
RT "X-ray diffraction study of inorganic pyrophosphatase from baker's
RT yeast at the 3-A resolution.";
RL Dokl. Akad. Nauk SSSR 258:1481-1492(1981).
RN [8]
RN X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE=97148342; PubMed=8994974;
RA Heikinheimo P., Lehtonen J., Baykov A., Lahti R., Cooperman B.S.,
RA Goldman A.;
RT "The structural basis for pyrophosphatase catalysis.";
RL Structure 4:1491-1508(1996).
RN [9]
RN X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
RA Swaminathan K., Cooperman B.S., Lahti R., Voet D.;
RL Submitted (DEC-1997) to the PDB data bank.
RN [10]
RN X-RAY CRYSTALLOGRAPHY (2.15 ANGSTROMS) OF MUTANTS LYS-78 AND LYS-117.
RX MEDLINE=99096888; PubMed=9878371;
RA Tuominen V., Heikinheimo P., Kajander T., Torkkel T., Hyytiä T.,
RA Kapyla J., Lahti R., Cooperman B.S., Goldman A.;
RT "The 78K and D117E active-site variants of Saccharomyces cerevisiae
RT soluble inorganic pyrophosphatase: structural studies and mechanistic
RT implications.";
RL J. Mol. Biol. 284:1565-1580(1998).
RN [11]
RN SIMILARITY TO E.COLI AND K.LACTIS PPASES.
RX MEDLINE=90254161; PubMed=2160278;
RA Lahti R., Kolakowski L.F. Jr., Heinonen J., Vihinen M., Pohjanoksa K.,
RA Cooperman B.S.;
RT "Conservation of functional residues between yeast and E. coli
RT inorganic pyrophosphatases.";
RL Biochim. Biophys. Acta 1038:338-345(1990).
CC -|- CATALYTIC ACTIVITY: Diphosphate + H(2)O = 2 phosphate.
CC -|- COFACTOR: REQUIRES THE PRESENCE OF DIVALENT METAL CATION.
CC MAGNESIUM CONFERS THE HIGHEST ACTIVITY. IT BINDS UP TO 4 DIVALENT
CC CATIONS PER SUBUNIT, WITH THREE REQUIRED FOR ACTIVITY.

CC -!- SUBUNIT: HOMODIMER.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO THE PPASE FAMILY.
CC -----
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CC -----

DR EMBL: X13253; CAA31629.1; -.
DR EMBL: 235880; CAA84949.1; -.
DR PIR: S45864; PMBY.
DR PDB: 1YYP; 15-OCT-91.
DR PDB: 1YPP; 07-DEC-96.
DR PDB: 1WGI; 19-NOV-97.
DR PDB: 1WGU; 19-NOV-97.
DR PDB: 1HUJ; 08-APR-98.
DR PDB: 1HUK; 08-APR-98.
DR PDB: 117E; 23-DEC-98.
DR PDB: 8PRK; 23-DEC-98.
DR SWISS-2DPAGE; P00817; YEAST.
DR COMPUYEAST-2DPAGE; P00817; -.
DR SGD: S0000215; IPPI.
DR InterPro: IPR001596; Pyrophosphatase.
DR Pfam: PF00719; Pyrophosphatase; 1.
DR PROSITE: PS00387; PPASE; 1.
KW Hydrolyase; Magnesium; 3D-structure.
FT INIT_MET 0 0
FT ACT_SITE 56 56 PROBABLE.
FT BINDING 78 78 INORGANIC PYROPHOSPHATE.
FT CONFLICT 40 40 N -> D (IN REF. 3).
FT CONFLICT 71 71 D -> N (IN REF. 3).
FT CONFLICT 74 74 MISSING (IN REF. 3).
FT CONFLICT 123 123 E -> Q (IN REF. 3).
FT CONFLICT 136 136 Q -> E (IN REF. 3).
FT CONFLICT 186 186 N -> D (IN REF. 3).
FT CONFLICT 224 224 D -> N (IN REF. 3).
FT CONFLICT 266 266 L -> P (IN REF. 2).
FT STRAND 4 7
FT STRAND 16 20
FT STRAND 25 25
FT TURN 28 30
FT TURN 38 41
FT STRAND 45 45
FT STRAND 55 55
FT STRAND 79 79
FT TURN 97 98
FT TURN 111 112
FT STRAND 121 123
FT STRAND 131 132
FT STRAND 135 135
FT STRAND 138 146
FT STRAND 151 158
FT TURN 160 161
FT TURN 165 167
FT HELIX 172 175
FT TURN 176 177
FT TURN 179 180
FT TURN 182 197
FT STRAND 203 203
FT HELIX 205 207
FT STRAND 210 210
FT HELIX 212 230
FT TURN 231 231
FT TURN 245 246
FT TURN 248 249
FT TURN 251 252
FT TURN 255 260
FT TURN 274 275
SQ SEQUENCE , 286 AA; 32184 MW; F29390260B60C8B2 CRC64;

Query Match 63.08; Score 34; DB 1; Length 286;
Best Local Similarity 83.3%; Pred. No. 14;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
DB 91 HNYGAF 96
|||||

RESULT 12
HB2D_CANFA STANDARD; PRT; 266 AA.
ID HB2D_CANFA
AC P18470;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE DLA class II histocompatibility antigen, DR-1 beta chain precursor.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-90316610; PubMed-2370085;
RT Sarmiento U.M., Storb R.;
RT "Nucleotide sequence of a dog DRB cDNA clone.";
RL Immunogenetics 31:396-399(1990).
CC -----
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CC -----

DR EMBL: M29611; AAA30874.1; -.
DR PIR: A45844; A45844.
DR HSSP: P13760; 2SEB.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003597; Ig_cl.
DR InterPro: IPR000353; MHC_II_beta.
DR Pfam: PF00047; Ig; 1.
DR Pfam: PF00969; MHC_II_beta; 1.
DR ProDom: PD000328; MHC_II_beta; 1.
DR SMART: SM00407; IGcl; 1.
DR PROSITE: PS00290; IG_MHC; 1.
KW MHC II; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 29
FT CHAIN 30 266 DLA CLASS II HISTOCOMPATIBILITY ANTIGEN,
FT DR-1 BETA CHAIN.
FT DOMAIN 30 124 EXTRACELLULAR BETA-1.
FT DOMAIN 125 227 EXTRACELLULAR BETA-2.
FT TRANSMEM 228 250
FT DOMAIN 251 266 CYTOPLASMIC TAIL.
FT DISULFID 44 108 BY SIMILARITY.
FT DISULFID 146 202 BY SIMILARITY.
FT CARBOHYD 48 48 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 266 AA; 30151 MW; 4E8297BBF1ACDD67 CRC64;

Query Match 61.1%; Score 33; DB 1; Length 266;
Best Local Similarity 66.7%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 RHNYGSFAS 10
DB 109 RHNYGVIES 117
|||||

RESULT 13
FATB_VIBAN STANDARD; PRT; 322 AA.
ID FATB_VIBAN

AC P11460;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ferric anguibactin-binding protein precursor.
 GN FATB.
 OS Vibrio anguillarum (Listonella anguillarum).
 OG Plasmid pJMI.
 OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Listonella.
 OX NCBI_TaxID=55601;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=775;
 RX MEDLINE=88139336; PubMed=2830268;
 RA Actis L.A., Tolmasky M.E., Farrell D.H., Crosa J.H.;
 RT "Genetic and molecular characterization of essential components of
 the Vibrio anguillarum plasmid-mediated iron-transport system.";
 RL J. Biol. Chem. 263:2853-2860(1988).
 RN [2]
 RP SEQUENCE OF 1-154 FROM N.A.
 RC STRAIN=775;
 RX MEDLINE=92084677; PubMed=1748657;
 RA Koester W.L., Actis L.A., Waldbeser L.S., Tolmasky M.E., Crosa J.H.;
 RT "Molecular characterization of the iron transport system mediated by
 the pJMI plasmid in Vibrio anguillarum 775.";
 RL J. Biol. Chem. 266:23829-23833(1991).
 CC -1- FUNCTION: BINDS FERRIC ANGUIBACTIN; PART OF THE BINDING-PROTEIN-
 DEPENDENT TRANSPORT SYSTEM FOR UPTAKE OF FERRIC ANGUIBACTIN.
 CC -1- SUBCELLULAR LOCATION: Attached to the inner membrane by a lipid
 anchor (Potential).
 CC -1- SIMILARITY: BELONGS TO THE BACTERIAL EXTRACELLULAR SOLUTE-BINDING
 PROTEIN FAMILY 8.
 CC -----
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 CC -----
 DR EMBL; J03529; AAA91580.1; -;
 DR EMBL; M74068; AAA25643.1; ALT_INIT.
 DR PIR; A29928; A29928.
 DR InterPro; IPR002491; Peripla_BP.
 DR Pfam; PF01487; Peripla_BP_2; 1.
 DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
 KW Transport; Iron transport; Signal; Inner membrane; Lipoprotein;
 KW Plasmid.
 FT SIGNAL 1 22 POTENTIAL.
 FT CHAIN 23 322 FERRIC ANGUIBACTIN-BINDING PROTEIN.
 FT LIPID 23 23 N-ACYL DIGLYCERIDE (POTENTIAL).
 SQ SEQUENCE 322 AA; 35635 MW; FB8674EED5CF73F7 CRC64;
 Query Match 61.1%; Score 33; DB 1; Length 322;
 Best Local Similarity 75.0%; Pred. No. 26;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 3 HNYGSFAS 10
 II IIII I
 Db 203 HNYGSFSS 210
 RESULT 14
 PF21_ARATH
 ID PF21_ARATH STANDARD; PRT; 398 AA.
 AC Q04088;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Possible transcription factor PosF21.
 GN POSF21 OR AT2G31370 OR T28P16.14.
 OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Zurich; TISSUE=Leaf;
 RX MEDLINE=93251100; PubMed=1844885;
 RA Aeschbacher R.A., Schrott M., Potrykus I., Saul M.W.;
 RT "Isolation and molecular characterization of PosF21, an Arabidopsis
 thaliana gene which shows characteristics of a b-zip class
 transcription factor.";
 RL Plant J. 1:303-316(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=20083487; PubMed=10617197;
 RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
 RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
 RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
 RA Moffat K.S., Cronin L.A., Shen M., Pal G., Van Aken S., Mayam L.,
 RA Tallon L.J., Gill J.E., Adams M.D., Carter A.J., Creasy T.H.,
 RA Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
 RA Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
 RA Venter J.C.;
 RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
 thaliana.";
 RL Nature 402:761-768(1999).
 CC -1- FUNCTION: PUTATIVE TRANSCRIPTION FACTOR WITH AN ACTIVATORY
 ROLE.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED CONSTITUTIVELY AT A LOW LEVEL IN
 YOUNG SEEDLINGS AND IN ROOTS, STEMS AND LEAVES OF MATURE
 ARABIDOPSIS PLANTS.
 CC -1- SIMILARITY: BELONGS TO THE BZIP FAMILY.
 CC -----
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 CC -----
 DR EMBL; X61031; CAA43366.1; -;
 DR EMBL; AC007169; AAD26486.1; -;
 DR InterPro; IPR004827; TF_bZIP.
 DR Pfam; PF00170; bZIP; 1.
 DR SMART; SM00338; BRLZ; 1.
 DR PROSITE; PS00036; BZIP_BASIC; FALSE_NEG.
 KW Transcription regulation; DNA-binding; Nuclear protein.
 FT DNA_BIND 203 222 BASIC MOTIF.
 FT DOMAIN 229 264 LEUCINE-ZIPPER.
 FT DOMAIN 340 372 POLY-GLN.
 SQ SEQUENCE 398 AA; 44689 MW; 2DAA9EC9B9C14D11 CRC64;
 Query Match 61.1%; Score 33; DB 1; Length 398;
 Best Local Similarity 85.7%; Pred. No. 33;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 4 NYGSFAS 10
 IIII I
 Db 305 NYGSFSGS 311
 RESULT 15
 NCAP_CVHOC
 ID NCAP_CVHOC STANDARD; PRT; 448 AA.
 AC P33469;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DE Possible transcription factor PosF21.
 GN POSF21 OR AT2G31370 OR T28P16.14.
 OS Arabidopsis thaliana (Mouse-ear cress).

```

GN N.
OS Human coronavirus (strain OC43).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=31631;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89243809; PubMed=2541577;
RA Kamahora T., Soe L.H., Lai M.M.C.;
RT "Sequence analysis of nucleocapsid gene and leader RNA of human
RT coronavirus OC43.";
RL Virus Res. 12:1-9(1989).
DR PIR; A60003; A60003.
DR InterPro; IPR001218; Corona_nucleocap.
DR Pfam; PF00937; Corona_nucleoca; 1.
KW Nucleocapsid.
SQ SEQUENCE 448 AA; 49316 MW; 5193AB1AE0D75626 CRC64;

Query Match 61.1%; Score 33; DB 1; Length 448;
Best Local Similarity 85.7%; Pred. No. 37;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 103 RHNRGSF 109

```

Search completed: November 18, 2002, 17:33:26
Job time : 2.45098 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:01 ; Search time 10.4412 Seconds
(without alignments)
197.341 Million cell updates/sec

Title: US-09-016-061-68
Perfect score: 54
Sequence: 1 ARHNYGSFAS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp_archea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	43	79.6	839	10	Q9LIE5
2	41	75.9	89	7	O19495
3	40	74.1	276	7	Q9GJN0
4	40	74.1	446	5	O62086
5	39	72.2	39	7	P79474
6	39	72.2	39	7	P79477
7	39	72.2	39	7	P79478
8	39	72.2	39	7	P79479
9	39	72.2	67	7	Q8SP02
10	39	72.2	76	7	Q9TPC2
11	39	72.2	82	7	O19287
12	39	72.2	82	7	O19288
13	39	72.2	82	7	Q9MXN1
14	39	72.2	82	7	Q9TPC9
15	39	72.2	82	7	Q30606
16	39	72.2	82	7	Q30608

17	39	72.2	82	7	Q30637	Q30637 macaca mula
18	39	72.2	82	7	Q30638	Q30638 macaca mula
19	39	72.2	82	7	Q30658	Q30658 macaca mula
20	39	72.2	82	7	Q30659	Q30659 macaca mula
21	39	72.2	82	7	Q30666	Q30666 macaca mula
22	39	72.2	82	7	Q30667	Q30667 macaca mula
23	39	72.2	82	7	Q30668	Q30668 macaca mula
24	39	72.2	83	6	O9TSS5	O9TSS5 bos indicus
25	39	72.2	83	7	O98002	O98002 ovis aries
26	39	72.2	83	7	O9BDA9	O9BDA9 ovis canad
27	39	72.2	83	7	O9BDA8	O9BDA8 ovis canad
28	39	72.2	83	7	O9BDA6	O9BDA6 ovis canad
29	39	72.2	83	7	O9BD98	O9BD98 ovis canad
30	39	72.2	83	7	O9BD97	O9BD97 ovis canad
31	39	72.2	83	7	O9BD95	O9BD95 ovis canad
32	39	72.2	83	7	O9BD93	O9BD93 ovis canad
33	39	72.2	83	7	O9BD91	O9BD91 ovis canad
34	39	72.2	83	7	O9BD90	O9BD90 ovis canad
35	39	72.2	83	7	O9BD89	O9BD89 ovis canad
36	39	72.2	85	7	P79966	P79966 capra aegag
37	39	72.2	85	7	P79967	P79967 capra aegag
38	39	72.2	85	7	P79968	P79968 capra aegag
39	39	72.2	85	7	Q30796	Q30796 ovis aries
40	39	72.2	85	7	Q30800	Q30800 ovis aries
41	39	72.2	85	7	Q30803	Q30803 ovis aries
42	39	72.2	85	7	Q30812	Q30812 ovis aries
43	39	72.2	86	7	Q30326	Q30326 bos taurus
44	39	72.2	89	7	O19210	O19210 capra hircu
45	39	72.2	89	7	O19212	O19212 capra hircu

ALIGNMENTS

RESULT 1

Q9LIE5

ID Q9LIE5 PRELIMINARY; PRT; 839 AA.

AC Q9LIE5;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE Far-red impaired response protein, mutator-like transposase-like

DE protein, phytochrome A signaling protein-like.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=COLUMBIA;

RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;

RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=COLUMBIA;

RX MEDLINE=20363099; PubMed=10907853;

RA Nakamura Y.;

RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.

RT Sequence features of the regions of 4,251,695 bp covered by ninety pl,

RT TAC and BAC clones."

RL DNA Res. 7:217-221(2000).

DR EMBL; AP001306; BAB03065.1; -

DR InterPro; IPR004330; FARI.

DR InterPro; IPR001000; Glyco_hydro_10.

DR Pfam; PF03101; FARI; 1.

DR PROSITE; PS00591; GLYCOSYL_HYDROL_F10; UNKNOWN1.

SQ SEQUENCE 839 AA; 95996 MW; CBBF60DF8B6797F8 CRC64;

Query Match 79.6%; Score 43; DB 10; Length 839;
Best Local Similarity 87.5%; Pred. No. 4.5;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSF 8
Db 274 SRHNYGSF 281

RESULT 2

ID O19495 PRELIMINARY; PRT; 89 AA.
AC O19495;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II beta 1 domain (Fragment).
GN B-LBI.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=15.15I-5; TISSUE=BURSA;
RX MEDLINE=98179131; PubMed=9510552;
RA Pharr G.T., Dodgson J.B., Hunt H.D., Bacon L.D.;
RT "Class II MHC cDNAs in 1515 B-congenic chickens.";
RL Immunogenetics 47:350-354(1998).
DR EMBL; U91532; AAC15813.1; -;
DR InterPro; IPR000353; MHC_II_beta.
DR Pfam; PF00969; MHC_II_beta.1.
DR ProDom; PD000328; MHC_II_beta; 1.
KW Glycoprotein; MHC II; Transmembrane.
FT NON_TER 1
FT TER 89
SQ SEQUENCE 89 AA; 10724 MW; BC7D558B6AEB1379 CRC64;

Query Match 75.9%; Score 41; DB 7; Length 89;

Best Local Similarity 77.8%; Pred. No. 0.89;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAS 10
Db 75 RHNYGDFES 83

RESULT 3

ID Q9GJNO PRELIMINARY; PRT; 276 AA.
AC Q9GJNO;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II beta chain.
GN HClIBETA.
OS Caiman crocodilus (Spectacled caiman) (Caiman sclerops).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Crocodylidae; Alligatorinae; Caiman.
OX NCBI_TaxID=8499;
RN [1]
RP SEQUENCE FROM N.A.
RA Voldby J., Vitved L., Due M., Gronlund J., Holmskov U., Teisner B.,
RA Salomonsen J., Brusgaard K., Skjold K.;
RT "Cloning, sequence and genomic structure of MHC class II antigens from
the spectacled caiman, Caiman crocodilus.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF256651; AAF99283.1; -;
DR HSSP; P13760; 2SEB.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR000353; MHC_II_beta.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00969; MHC_II_beta; 1.
DR ProDom; PD000328; MHC_II_beta; 1.
DR SMART; SM00407; IGc1; 1.

DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Glycoprotein; MHC II; Transmembrane.
SQ SEQUENCE 276 AA; 30366 MW; EA8A4684986AEA6A CRC64;

Query Match 74.1%; Score 40; DB 7; Length 276;

Best Local Similarity 87.5%; Pred. No. 5.2;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFA 9
Db 108 RHNYGVFA 115

RESULT 4

ID O62086 PRELIMINARY; PRT; 446 AA.
AC O62086;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE C31H5.6 protein.
GN C31H5.6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Kershaw J.K.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RX none;
RT "Genome sequence of the nematode C.elegans: A platform for
investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; Z93778; CAB07846.1; -;
DR InterPro; IPR000379; Ser_estrs_site.
SQ SEQUENCE 446 AA; 50763 MW; 82AD969CDAD753DE CRC64;

Query Match 74.1%; Score 40; DB 5; Length 446;

Best Local Similarity 77.8%; Pred. No. 8.9;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFAS 10
Db 51 RHNYGSFAA 59

RESULT 5

ID P79474 PRELIMINARY; PRT; 39 AA.
AC P79474;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II DRB (Fragment).
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervioidea;
OC Cervidae; Cervinae; Cervus.
OX NCBI_TaxID=9860;
RN [1]
RP SEQUENCE FROM N.A.
RA Swarbrick P.A., Crawford A.M.;
RT "The MHC class II DRB intron 2 microsatellite of red deer.";
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U63077; AAB37777.1; -;
DR InterPro; IPR000353; MHC_II_beta.
DR Pfam; PF00969; MHC_II_beta; 1.
DR ProDom; PD000328; MHC_II_beta; 1.
KW Glycoprotein; MHC II; Transmembrane.

FT NON_TER 1 1
 SQ SEQUENCE 39 AA; 4767 MW; CAF3680999733D1D CRC64;

Query Match 72.2%; Score 39; DB 7; Length 39;
 Best Local Similarity 77.8%; Pred. No. 0.88;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAS 10
 Db | | | | | | | | | |
 25 RHNYGVFES 33

RESULT 6

P79477 PRELIMINARY; PRT; 39 AA.
 AC P79477;
 DT 01-MAY-1997 (T-EMBLrel. 03, Created)
 DT 01-MAY-1997 (T-EMBLrel. 03, Last sequence update)
 DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)
 DE MHC class II DRB (Fragment).
 OS Cervus elaphus (Red deer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
 OC Cervidae; Cervinae; Cervus.
 OX NCBI_TaxID=9860;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Swarbrick P.A., Crawford A.M.;
 RT "The MHC class II DRB intron 2 microsatellite of red deer.";
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U63080; AAB37780.1; -.
 DR InterPro; IPR000353; MHC_II_beta.
 DR Pfam; PF00969; MHC_II_beta; 1.
 DR ProDom; PD000328; MHC_II_beta; 1.
 KW Glycoprotein; MHC II; Transmembrane.
 FT NON_TER 1 1
 FT NON_TER 39 39
 SQ SEQUENCE 39 AA; 4806 MW; C2188A16752A3C1D CRC64;

Query Match 72.2%; Score 39; DB 7; Length 39;
 Best Local Similarity 77.8%; Pred. No. 0.88;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAS 10
 Db | | | | | | | | | |
 25 RHNYGVFES 33

RESULT 7

P79478 PRELIMINARY; PRT; 39 AA.
 AC P79478;
 DT 01-MAY-1997 (T-EMBLrel. 03, Created)
 DT 01-MAY-1997 (T-EMBLrel. 03, Last sequence update)
 DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)
 DE MHC class II DRB (Fragment).
 OS Cervus elaphus (Red deer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
 OC Cervidae; Cervinae; Cervus.
 OX NCBI_TaxID=9860;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Swarbrick P.A., Crawford A.M.;
 RT "The MHC class II DRB intron 2 microsatellite of red deer.";
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U63081; AAB37781.1; -.
 DR InterPro; IPR000353; MHC_II_beta.
 DR Pfam; PF00969; MHC_II_beta; 1.
 DR ProDom; PD000328; MHC_II_beta; 1.
 KW Glycoprotein; MHC II; Transmembrane.
 FT NON_TER 1 1

FT NON_TER 39 39
 SQ SEQUENCE 39 AA; 4806 MW; C2188A16752A3C1D CRC64;

Query Match 72.2%; Score 39; DB 7; Length 39;
 Best Local Similarity 77.8%; Pred. No. 0.88;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAS 10
 Db | | | | | | | | | |
 25 RHNYGVFES 33

RESULT 8

P79479 PRELIMINARY; PRT; 39 AA.
 AC P79479;
 DT 01-MAY-1997 (T-EMBLrel. 03, Created)
 DT 01-MAY-1997 (T-EMBLrel. 03, Last sequence update)
 DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)
 DE MHC class II DRB (Fragment).
 OS Cervus elaphus (Red deer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
 OC Cervidae; Cervinae; Cervus.
 OX NCBI_TaxID=9860;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Swarbrick P.A., Crawford A.M.;
 RT "The MHC class II DRB intron 2 microsatellite of red deer.";
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U63082; AAB37782.1; -.
 DR InterPro; IPR000353; MHC_II_beta.
 DR Pfam; PF00969; MHC_II_beta; 1.
 DR ProDom; PD000328; MHC_II_beta; 1.
 KW Glycoprotein; MHC II; Transmembrane.
 FT NON_TER 1 1
 FT NON_TER 39 39
 SQ SEQUENCE 39 AA; 4806 MW; C2188A16752A3C1D CRC64;

Query Match 72.2%; Score 39; DB 7; Length 39;
 Best Local Similarity 77.8%; Pred. No. 0.88;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAS 10
 Db | | | | | | | | | |
 25 RHNYGVFES 33

RESULT 9

Q8SP02 PRELIMINARY; PRT; 67 AA.
 AC Q8SP02;
 DT 01-JUN-2002 (T-EMBLrel. 21, Created)
 DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
 DE MHC class II antigen (Fragment).
 GN HAGG-DRB.
 OS Hapalemur griseus griseus.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Strepsirhini; Lemuridae; Hapalemur.
 OX NCBI_TaxID=122219;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Go Y., Satta Y., Kawamoto Y., Rakotoarisoa G., Randrianja A.,
 RA Koyama N., Hirai H.;
 RT "Mhc-DRB genes evolution in lemurs.";
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB078220; BAB88434.1; -.
 FT NON_TER 1 1
 FT NON_TER 67 67
 SQ SEQUENCE 67 AA; 8083 MW; 559300839F0EFA52 CRC64;

Query Match 72.2%; Score 39; DB 7; Length 67;

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Best Local Similarity 77.8%; Pred. No. 1.6; Mismatches 0; Indels 2; Gaps 0;
Matches 7; Conservative 0;

QY 2 RHNYGSFAS 10
Db 59 RHNYGVFES 67

RESULT 10
Q9TPC2 PRELIMINARY; PRT; 76 AA.
AC Q9TPC2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II antigen (Fragment).
GN MAMU-DRBI.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Sauerbmann U., Khazand M., Nagy M., Peiberg C.;
RT "Mhc-DO-DRB-haplotype analysis in the rhesus macaque: evidence for a
RT number of different haplotypes displaying a low allelic
RT polymorphism.";
RL Tissue Antigens 0:0-0(1999).
DR EMBL; AF175315; AAF07040.1; -.
DR HSSP; P13758; IDLH.
DR InterPro; IPR000353; MHC_II_beta.
DR Pfam; PF00969; MHC_II_beta; 1.
DR ProDom; PD000328; MHC_II_beta; 1.
KW Glycoprotein; MHC II; Transmembrane.
FT NON_TER 1
FT NON_TER 76
FT SEQUENCE 76 AA; 9315 MW; 1DC073E1B87A9AD0 CRC64;

Query Match 72.2%; Score 39; DB 7; Length 76;
Best Local Similarity 77.8%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 0; Indels 2; Gaps 0;

QY 2 RHNYGSFAS 10
Db 67 RHNYGVFES 75

RESULT 11
O19287 PRELIMINARY; PRT; 82 AA.
AC O19287;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II DR beta 1 (Fragment).
GN HLA-DRBI.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE OF 3-30 FROM N.A.
RA Slierendregt B.L., Otting N., van Besouw N., Jonker M., Bontrop R.E.;
RT "Expansion and contraction of rhesus macaque DRB regions by
RT duplication and deletion.";
RL J. Immunol. 152:2298-2307(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-BLOOD;
RA de Groot N.N.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF031264; AAB87436.1; -.
DR InterPro; IPR000353; MHC_II_beta.
DR Pfam; PF00969; MHC_II_beta; 1.
DR ProDom; PD000328; MHC_II_beta; 1.
KW Glycoprotein; MHC II; Transmembrane.
FT NON_TER 1
FT NON_TER 82
FT SEQUENCE 82 AA; 9910 MW; C0A61E39A7F37FBA CRC64;

Query Match 72.2%; Score 39; DB 7; Length 82;
Best Local Similarity 77.8%; Pred. No. 2.1;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAS 10
Db 73 RHNYGVFES 81

RESULT 12
O19288 PRELIMINARY; PRT; 82 AA.
AC O19288;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II DR beta (Fragment).
GN HLA-DRB.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE OF 3-30 FROM N.A.
RC TISSUE-BLOOD;
RA Slierendregt B.L., Otting N., van Besouw N., Jonker M., Bontrop R.E.;
RT "Expansion and contraction of rhesus macaque DRB regions by
RT duplication and deletion.";
RL J. Immunol. 152:2298-2307(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-BLOOD;
RA de Groot N.N.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF031264; AAB87436.1; -.
DR InterPro; IPR000353; MHC_II_beta.
DR Pfam; PF00969; MHC_II_beta; 1.
DR ProDom; PD000328; MHC_II_beta; 1.
KW Glycoprotein; MHC II; Transmembrane.
FT NON_TER 1
FT NON_TER 82
FT SEQUENCE 82 AA; 9910 MW; C0A61E39A7F37FBA CRC64;

Query Match 72.2%; Score 39; DB 7; Length 82;
Best Local Similarity 77.8%; Pred. No. 2.1;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAS 10
Db 73 RHNYGVFES 81

RESULT 13
Q9MXN1 PRELIMINARY; PRT; 82 AA.
AC Q9MXN1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II antigen (Fragment).

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RA de Groot N.N.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF031263; AAB87435.1; -.
DR InterPro; IPR000353; MHC_II_beta.
DR Pfam; PF00969; MHC_II_beta; 1.
DR ProDom; PD000328; MHC_II_beta; 1.
KW Glycoprotein; MHC II; Transmembrane.
FT NON_TER 1
FT NON_TER 82
FT SEQUENCE 82 AA; 9940 MW; BF90C7F17DAD7AE1 CRC64;

Query Match 72.2%; Score 39; DB 7; Length 82;
Best Local Similarity 77.8%; Pred. No. 2.1;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAS 10
Db 73 RHNYGVFES 81

RESULT 12
O19288 PRELIMINARY; PRT; 82 AA.
AC O19288;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II DR beta (Fragment).
GN HLA-DRB.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE OF 3-30 FROM N.A.
RC TISSUE-BLOOD;
RA Slierendregt B.L., Otting N., van Besouw N., Jonker M., Bontrop R.E.;
RT "Expansion and contraction of rhesus macaque DRB regions by
RT duplication and deletion.";
RL J. Immunol. 152:2298-2307(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-BLOOD;
RA de Groot N.N.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF031264; AAB87436.1; -.
DR InterPro; IPR000353; MHC_II_beta.
DR Pfam; PF00969; MHC_II_beta; 1.
DR ProDom; PD000328; MHC_II_beta; 1.
KW Glycoprotein; MHC II; Transmembrane.
FT NON_TER 1
FT NON_TER 82
FT SEQUENCE 82 AA; 9910 MW; C0A61E39A7F37FBA CRC64;

Query Match 72.2%; Score 39; DB 7; Length 82;
Best Local Similarity 77.8%; Pred. No. 2.1;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAS 10
Db 73 RHNYGVFES 81

RESULT 13
Q9MXN1 PRELIMINARY; PRT; 82 AA.
AC Q9MXN1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II antigen (Fragment).

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GN MAMU-DRB.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=8612; TISSUE=BLOOD;
RX MEDLINE=20412562; PubMed=10958357;
RA Otting N., de Groot N.G., Noort M.C., Doxiadis G.G.M., Bontrop R.E.;
RT "Allelic diversity of Mhc-DRB alleles in rhesus macaques.";
RL Tissue Antigens 56:58-68(2000).
DR EMBL: AF163286; AAF71683.1; -.
DR HSSP: P13758; IDLH.
DR InterPro: IPR000353; MHC_II_beta.
DR Pfam: PF00969; MHC_II_beta; 1.
DR ProDom: PD000328; MHC_II_beta; 1.
KW Glycoprotein; MHC II; Transmembrane.
FT NON_TER 1
FT NON_TER 82
SQ SEQUENCE 82 AA; 9891 MW; CC75E9B4BA35EEC2 CRC64;

Query Match 72.2%; Score 39; DB 7; Length 82;
Best Local Similarity 77.8%; Pred. No. 2.1;
Matches 7; Conservative 0; Mismatches 0; Indels 2; Gaps 0;

QY 2 RHNYGSPAS 10
DB 73 RHNYGVFES 81
|||||

RESULT 14
Q9TPC9 PRELIMINARY; PRT; 82 AA.
ID Q9TPC9
AC Q9TPC9
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE MHC class II antigen (Fragment).
GN CAMO-DRB1.
OS Calliobus moloch (Dusky titi).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Calliobinae;
OC Calliobus.
OX NCBI_TaxID=9523;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20214299; PubMed=10752625;
RA Kriener K., O'Huigin C., Tichy H., Klein J.;
RT "Convergent evolution of major histocompatibility complex molecules in
humans and New World monkeys.";
RL Immunogenetics 51:169-178(2000).
DR EMBL: AF173347; AAD56876.1; -.
DR InterPro: IPR000353; MHC_II_beta.
DR Pfam: PF00969; MHC_II_beta; 1.
DR ProDom: PD000328; MHC_II_beta; 1.
KW Glycoprotein; MHC II; Transmembrane.
FT NON_TER 1
FT NON_TER 82
SQ SEQUENCE 82 AA; 10015 MW; 68070C02D7C32202 CRC64;

Query Match 72.2%; Score 39; DB 7; Length 82;
Best Local Similarity 77.8%; Pred. No. 2.1;
Matches 7; Conservative 0; Mismatches 0; Indels 2; Gaps 0;

QY 2 RHNYGSPAS 10
DB 68 RHNYGVFES 76
|||||

RESULT 15
Q30606 PRELIMINARY; PRT; 82 AA.
ID Q30606
AC Q30606
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE Major histocompatibility complex class II (Fragment).
GN MAMU-DRB.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97152405; PubMed=8995183;
RA Knapp L.A., Cadavid L.F., Eberle M.E., Knechtle S.J., Bontrop R.E.;
RT "Identification of new mamu-DRB alleles using DGGE and direct
sequencing.";
RL Immunogenetics 45:171-179(1997).
DR EMBL: U57948; AAC50981.1; -.
DR HSSP: P13758; IDLH.
DR InterPro: IPR000353; MHC_II_beta.
DR Pfam: PF00969; MHC_II_beta; 1.
DR ProDom: PD000328; MHC_II_beta; 1.
KW Glycoprotein; MHC II; Transmembrane.
FT NON_TER 1
FT NON_TER 82
SQ SEQUENCE 82 AA; 9921 MW; CC75FCF5EE35EEC2 CRC64;

Query Match 72.2%; Score 39; DB 7; Length 82;
Best Local Similarity 77.8%; Pred. No. 2.1;
Matches 7; Conservative 0; Mismatches 0; Indels 2; Gaps 0;

QY 2 RHNYGSPAS 10
DB 73 RHNYGVFES 81
|||||

Search completed: November 18, 2002, 17:40:46
Job time : 11.4912 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:21:57 ; Search time 13.8235 Seconds
(without alignments)
96.394 Million cell updates/sec

Title: US-09-016-061-68
Perfect score: 54
Sequence: 1 ARHNGSFAS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_101002.*

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23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	54	100.0	10	19	AAW76024
2	54	100.0	10	22	AA861382
3	51	94.4	10	19	AAW76025
4	51	94.4	10	19	AAW76030
5	51	94.4	10	22	AA861383
6	51	94.4	10	22	AA861388
7	50	92.6	10	19	AAW76026
8	50	92.6	10	19	AAW76027
9	50	92.6	10	19	AAW76028
10	50	92.6	10	19	AAW76029

11	50	92.6	10	19	AAW76010
12	50	92.6	10	22	AA861368
13	50	92.6	10	22	AA861384
14	50	92.6	10	22	AA861385
15	50	92.6	10	22	AA861386
16	50	92.6	10	22	AA861387
17	50	92.6	117	19	AAW76001
18	50	92.6	117	19	AAW76003
19	50	92.6	117	20	AA861381
20	50	92.6	117	20	AA861387
21	50	92.6	117	22	AA861387
22	50	92.6	117	22	AA861388
23	50	92.6	117	22	AA861389
24	50	92.6	117	22	AA861391
25	50	92.6	118	20	AA861384
26	50	92.6	118	20	AA861385
27	50	92.6	118	20	AA861386
28	50	92.6	118	20	AA861383
29	50	92.6	130	20	AA861379
30	49	90.7	10	19	AAW76037
31	49	90.7	10	22	AA861395
32	48	88.9	10	19	AAW76040
33	48	88.9	10	22	AA861398
34	47	87.0	10	19	AAW76021
35	47	87.0	10	22	AA861379
36	46	85.2	10	19	AAW76039
37	46	85.2	10	19	AAW76022
38	46	85.2	10	19	AAW76023
39	46	85.2	10	22	AA861380
40	46	85.2	10	22	AA861381
41	46	85.2	10	22	AA861397
42	45	83.3	10	19	AAW76020
43	45	83.3	10	22	AA861378
44	43	79.6	10	19	AAW76038
45	43	79.6	10	22	AA861396

ALIGNMENTS

RESULT 1
AAW76024
ID AAW76024 standard; Protein; 10 AA.
XX
AC AAW76024;
XX
DT 02-NOV-1998 (first entry)
XX
DE LM609 grafted antibody V-H region CDR3 protein fragment #6.

KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.

XX Mus sp.

XX WO9833919-A2.

XX 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

XX (IXSV-) IXSYS INC.

XX Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

DR N-PSDB; AAV49861.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
PS Claim 62; Page 41; 129pp; English.
XX
CC AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
CC antibodies contain non-murine framework regions so are suitable for use
CC in humans. Enhanced types of LM609 have affinity more than 90 times
CC greater than that of parent the parent antibody.
XX
XX Sequence 10 AA;
SQ

Query Match 100.0%; Score 54; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0049;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFAS 10
| | | | | | | | | |
Db 1 ARHNYGSFAS 10

RESULT 2
AAB61382
ID AAB61382 standard; peptide; 10 AA.
XX
AC AAB61382;
XX
DT 03-APR-2001 (first entry)
XX
DE Mutant VH CDR3 peptide #5.
XX
XX LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
KW inflammatory; cancer; retina; restenosis; osteoporosis.
XX
OS Unidentified.
XX
XX WO200078815-A1.
XX
XX 28-DEC-2000.
XX
XX 23-JUN-2000; 2000WO-US17454.
XX
XX 24-JUN-1999; 99US-0339922.
XX
XX (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX
XX Huse WD, Wu H;
XX
XX WPI; 2001-050110/06.
XX
XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
PT osteoporosis -
XX
XX Disclosure; Page 41; 132pp; English.
XX
XX The present invention relates to enhanced LM609 grafted antibodies
CC exhibiting selective binding affinity to alphavbeta_3 integrin or
CC their functional fragments. The antibodies or their functional
CC fragments can be used in the diagnosis and treatment of
CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory

CC diseases (such as psoriasis and chronic articular rheumatism),
CC disorders associated with inappropriate or inopportune invasion of
CC vessels (such as diabetic retinopathy, neovascular glaucoma and
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
CC diseases (such as macular degeneration), restenosis and
CC osteoporosis.
XX
XX Sequence 10 AA;
SQ

Query Match 100.0%; Score 54; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0049;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFAS 10
| | | | | | | | | |
Db 1 ARHNYGSFAS 10

RESULT 3
AAW76025
ID AAW76025 standard; Protein; 10 AA.
XX
AC AAW76025;
XX
XX 02-NOV-1998 (first entry)
DT
XX
DE LM609 grafted antibody V-H region CDR3 protein fragment #7.
XX
XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
XX
XX Mus sp.
XX
XX WO9833919-A2.
XX
XX 06-AUG-1998.
XX
XX 30-JAN-1998; 98WO-US01826.
XX
XX 30-JAN-1997; 97US-0791391.
XX
XX (IXSY-) IXSYS INC.
XX
XX Glaser SM, Huse WD;
XX
XX WPI; 1998-437472/37.
XX
XX N-PSDB; AAV49862.
XX
XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
XX Claim 62; Page 41; 129pp; English.
XX
XX AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
CC antibodies contain non-murine framework regions so are suitable for use
CC in humans. Enhanced types of LM609 have affinity more than 90 times
CC greater than that of parent the parent antibody.
XX
XX Sequence 10 AA;
SQ

Query Match 94.4%; Score 51; DB 19; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.016; Indels 0; Gaps 0;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFAS 10
 DB 1 ARHNYGSFAT 10
 |||||

RESULT 4
 AAW76030
 ID AAW76030 standard; Protein; 10 AA.
 XX
 AC AAW76030;
 XX
 DT 02-NOV-1998 (first entry)
 XX
 DE LM609 grafted antibody V-H region CDR3 protein fragment #12.
 XX
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 XX
 OS Mus sp.
 XX
 PN WO9833919-A2.
 XX
 PD 06-AUG-1998.
 XX
 PF 30-JAN-1998; 98WO-US01826.
 XX
 PR 30-JAN-1997; 97US-0791391.
 XX
 PA (IXSY-) IXSYS INC.
 XX
 PI Glaser SM, Huse WD;
 XX
 DR WPI; 1998-437472/37.
 DR N-PSDB; AAV49867.
 XX
 XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 PS Claim 62; Page 41; 129pp; English.
 XX
 CC AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
 CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
 CC antibodies contain non-murine framework regions so are suitable for use
 CC in humans. Enhanced types of LM609 have affinity more than 90 times
 CC greater than that of parent the parent antibody.
 XX
 SQ Sequence 10 AA;

Query Match 94.4%; Score 51; DB 19; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.016; Indels 0; Gaps 0;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFAS 10
 DB 1 ARHNYGSFAA 10
 |||||

RESULT 5
 AAB61383
 ID AAB61383 standard; peptide; 10 AA.
 XX
 AC AAB61383;
 XX
 DT 03-APR-2001 (first entry)
 XX
 DE Mutant VH CDR3 peptide #6.
 XX
 KW LM609; grafted antibody; alphaVbeta3 integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis.
 XX
 OS Unidentified.
 XX
 PN WO200078815-A1.
 XX
 PD 28-DEC-2000.
 XX
 PF 23-JUN-2000; 2000WO-US17454.
 XX
 PR 24-JUN-1999; 99US-0339922.
 XX
 PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
 XX
 PI Huse WD, Wu H;
 XX
 DR WPI; 2001-050110/06.
 XX
 PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -
 XX
 PS Disclosure; Page 41; 132pp; English.
 XX
 CC The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphavbeta3 integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphavbeta3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.
 XX
 SQ Sequence 10 AA;

Query Match 94.4%; Score 51; DB 22; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.016;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFAS 10
 DB 1 ARHNYGSFAT 10
 |||||

RESULT 6
 AAB61388
 ID AAB61388 standard; peptide; 10 AA.
 XX
 AC AAB61388;
 XX
 DT 03-APR-2001 (first entry)
 XX
 DE Mutant VH CDR3 peptide #11.
 XX
 KW LM609; grafted antibody; alphavbeta3 integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis.

[illegible]

PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
PS Claim 62; Page 41; 129pp; English.
XX
CC AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
CC antibodies contain non-murine framework regions so are suitable for use
CC in humans. Enhanced types of LM609 have affinity more than 90 times
CC greater than that of parent the parent antibody.
XX
SQ Sequence 10 AA;
Query Match 92.6%; Score 50; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ARHNYGSFA 9
| | | | | | | |
DB 1 ARHNYGSFA 9
| | | | | | | |
RESULT 9
AAW76028
ID AAW76028 standard; Protein; 10 AA.
AC AAW76028;
XX
DT 02-NOV-1998 (first entry)
XX
DE LM609 grafted antibody V-H region CDR3 protein fragment #10.
XX
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
XX
OS Mus sp.
XX
PN WO9833919-A2.
XX
PD 06-AUG-1998.
XX
PF 30-JAN-1998; 98WO-US01826.
XX
PR 30-JAN-1997; 97US-0791391.
XX
PA (IXSY-) IXSYS INC.
XX
PI Glaser SM, Huse WD;
XX
DR WPI: 1998-437472/37.
DR N-PSDB; AAV49865.
XX
XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
XX integrin - and related grafted antibodies based on murine monoclonal
XX LM609, also related nucleic acid, used to treat, prevent or diagnose
XX angiogenesis or restenosis
XX
PS Claim 62; Page 41; 129pp; English.
XX
CC AAW76007-W76040 are protein fragments of the grafted monoclonal antibody

CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
CC antibodies contain non-murine framework regions so are suitable for use
CC in humans. Enhanced types of LM609 have affinity more than 90 times
CC greater than that of parent the parent antibody.
XX
SQ Sequence 10 AA;
Query Match 92.6%; Score 50; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ARHNYGSFA 9
| | | | | | | |
DB 1 ARHNYGSFA 9
| | | | | | | |
RESULT 10
AAW76029
ID AAW76029 standard; Protein; 10 AA.
AC AAW76029;
XX
DT 02-NOV-1998 (first entry)
XX
DE LM609 grafted antibody V-H region CDR3 protein fragment #11.
XX
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
XX
OS Mus sp.
XX
PN WO9833919-A2.
XX
PD 06-AUG-1998.
XX
PF 30-JAN-1998; 98WO-US01826.
XX
PR 30-JAN-1997; 97US-0791391.
XX
PA (IXSY-) IXSYS INC.
XX
PI Glaser SM, Huse WD;
XX
DR WPI: 1998-437472/37.
DR N-PSDB; AAV49866.
XX
XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
XX integrin - and related grafted antibodies based on murine monoclonal
XX LM609, also related nucleic acid, used to treat, prevent or diagnose
XX angiogenesis or restenosis
XX
PS Claim 62; Page 41; 129pp; English.
XX
CC AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
CC antibodies contain non-murine framework regions so are suitable for use
CC in humans. Enhanced types of LM609 have affinity more than 90 times
CC greater than that of parent the parent antibody.
XX
SQ Sequence 10 AA;
Query Match 92.6%; Score 50; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ARHNYGSFA 9
| | | | | | | |
DB 1 ARHNYGSFA 9
| | | | | | | |
RESULT 10
AAW76029
ID AAW76029 standard; Protein; 10 AA.
AC AAW76029;
XX
DT 02-NOV-1998 (first entry)
XX
DE LM609 grafted antibody V-H region CDR3 protein fragment #11.
XX
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
XX
OS Mus sp.
XX
PN WO9833919-A2.
XX
PD 06-AUG-1998.
XX
PF 30-JAN-1998; 98WO-US01826.
XX
PR 30-JAN-1997; 97US-0791391.
XX
PA (IXSY-) IXSYS INC.
XX
PI Glaser SM, Huse WD;
XX
DR WPI: 1998-437472/37.
DR N-PSDB; AAV49866.
XX
XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
XX integrin - and related grafted antibodies based on murine monoclonal
XX LM609, also related nucleic acid, used to treat, prevent or diagnose
XX angiogenesis or restenosis
XX
PS Claim 62; Page 41; 129pp; English.
XX
CC AAW76007-W76040 are protein fragments of the grafted monoclonal antibody

CC antibodies contain non-murine framework regions so are suitable for use
 CC in humans. Enhanced types of LM609 have affinity more than 90 times
 CC greater than that of parent the parent antibody.

SQ Sequence 10 AA;

Query Match 92.6%; Score 50; DB 19; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.024;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9

|||||

Db 1 ARHNYGSFA 9

RESULT 11

AAW76010

ID AAW76010 standard; Protein; 10 AA.

AC AAW76010;

DT 02-NOV-1998 (first entry)

DE LM609 grafted antibody V-H region CDR3 protein fragment #1.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.

OS Mus sp.

XX WO9833919-A2.

PN 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

PR 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

XX Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

DR N-PSDB; AAV49847.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

XX Disclosure; Page 40; 129pp; English.

XX AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
 CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
 CC antibodies contain non-murine framework regions so are suitable for use
 CC in humans. Enhanced types of LM609 have affinity more than 90 times
 CC greater than that of parent the parent antibody.

XX Sequence 10 AA;

Query Match

Best Local Similarity 92.6%; Score 50; DB 19; Length 10;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9

|||||

Db 1 ARHNYGSFA 9

RESULT 12

AAB61368

ID AAB61368 standard; peptide; 10 AA.

XX AAB61368;

AC AAB61368;

DT 03-APR-2001 (first entry)

DE LM609 VH CDR3 peptide.

XX LM609; grafted antibody; alphaVbeta_3 integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis.

XX Unidentified.

OS WO200078815-A1.

XX 28-DEC-2000.

XX 23-JUN-2000; 2000WO-US17454.

XX 24-JUN-1999; 99US-0339922.

XX (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX Huse WD, Wu H;

PI WPI; 2001-050110/06.

XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -

XX Disclosure; Page 39; 132pp; English.

XX The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphavbeta_3 integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.

XX Sequence 10 AA;

Query Match

Best Local Similarity 92.6%; Score 50; DB 22; Length 10;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9

|||||

Db 1 ARHNYGSFA 9

RESULT 13

AAB61384

ID AAB61384 standard; peptide; 10 AA.

XX AAB61384;

AC AAB61384;

DT 03-APR-2001 (first entry)

XX DE Mutant VH CDR3 peptide #7.
 XX LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis.
 XX OS Unidentified.
 XX PN WO200078815-A1.
 XX PD 28-DEC-2000.
 XX PF 23-JUN-2000; 2000WO-US17454.
 XX PR 24-JUN-1999; 99US-0339922.
 XX PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
 XX PI Huse WD, Wu H;
 XX DR WPI; 2001-050110/06.
 XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -
 XX PS Disclosure; Page 41; 132pp; English.
 XX The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphavbeta_3 integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.
 XX SQ Sequence 10 AA;
 XX Query Match 92.6%; Score 50; DB 22; Length 10;
 XX Best Local Similarity 100.0%; Pred. No. 0.024;
 XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ARHNYGSFA 9
 Db | | | | | | | | | |
 1 ARHNYGSFA 9
 RESULT 14
 AAB61385
 ID AAB61385 standard; peptide; 10 AA.
 XX AC AAB61385;
 XX DT 03-APR-2001 (first entry)
 XX DE Mutant VH CDR3 peptide #8.
 XX LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis.
 XX OS Unidentified.
 XX PN WO200078815-A1.
 XX PD 28-DEC-2000.
 XX PF 23-JUN-2000; 2000WO-US17454.
 XX PR 24-JUN-1999; 99US-0339922.
 XX PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
 XX PI Huse WD, Wu H;
 XX DR WPI; 2001-050110/06.
 XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -
 XX PS Disclosure; Page 41; 132pp; English.

PR 24-JUN-1999; 99US-0339922.
 XX (MOLE-) APPLIED MOLECULAR EVOLUTION.
 XX Huse WD, Wu H;
 XX WPI; 2001-050110/06.
 XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -
 XX PS Disclosure; Page 41; 132pp; English.
 XX The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphavbeta_3 integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.
 XX SQ Sequence 10 AA;
 XX Query Match 92.6%; Score 50; DB 22; Length 10;
 XX Best Local Similarity 100.0%; Pred. No. 0.024;
 XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ARHNYGSFA 9
 Db | | | | | | | | | |
 1 ARHNYGSFA 9
 RESULT 15
 AAB61386
 ID AAB61386 standard; peptide; 10 AA.
 XX AC AAB61386;
 XX DT 03-APR-2001 (first entry)
 XX DE Mutant VH CDR3 peptide #9.
 XX LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis.
 XX OS Unidentified.
 XX PN WO200078815-A1.
 XX PD 28-DEC-2000.
 XX PF 23-JUN-2000; 2000WO-US17454.
 XX PR 24-JUN-1999; 99US-0339922.
 XX PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
 XX PI Huse WD, Wu H;
 XX DR WPI; 2001-050110/06.
 XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -
 XX PS Disclosure; Page 41; 132pp; English.

XX CC CC CC CC CC CC CC CC CC CC XX SQ

Sequence 10 AA;

Query Match 92.6%; Score 50; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1 ARHNYGSFA 9
Db	1 ARHNYGSFA 9

Search completed: November 18, 2002, 17:31:37
Job time : 13.8235 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:54:45 ; Search time 1.96078 Seconds
(without alignments)
76.811 Million cell updates/sec

Title: US-09-016-061-68

Perfect score: 54

Sequence: 1 ARHNYGSFAS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 97044 seqs, 15060890 residues

Total number of hits satisfying chosen parameters: 97044

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_AA:*

1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
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8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	92.6	117	8	US-08-790-540A-2
2	50	92.6	117	8	US-08-790-540A-6
3	50	92.6	117	8	US-08-791-391A-2
4	50	92.6	117	8	US-08-791-391A-6
5	36	66.7	14	1	US-08-677-599B-22
6	36	66.7	101	10	US-09-764-853-432
7	35	64.8	742	10	US-09-801-368-26
8	34	63.0	30	10	US-09-839-884-40
9	34	63.0	287	10	US-09-415-540-5
10	33	61.1	14	1	US-08-677-599B-21
11	33	61.1	28	10	US-09-864-761-41603
12	33	61.1	123	9	US-09-144-886-60
13	33	61.1	123	9	US-09-144-886-61
14	32	59.3	14	1	US-08-677-599B-11
15	32	59.3	14	1	US-08-677-599B-12
16	32	59.3	14	1	US-08-677-599B-13
17	32	59.3	14	1	US-08-677-599B-14
18	32	59.3	14	1	US-08-677-599B-15
19	32	59.3	14	1	US-08-677-599B-16

Sequence 17, Appl
Sequence 18, Appl
Sequence 19, Appl
Sequence 20, Appl
Sequence 23, Appl
Sequence 11, Appl
Sequence 8, Appl
Sequence 121, Appl
Sequence 37, Appl
Sequence 103, Appl
Sequence 16, Appl
Sequence 15, Appl
Sequence 13, Appl
Sequence 14, Appl
Sequence 17, Appl
Sequence 19, Appl
Sequence 20, Appl
Sequence 21, Appl
Sequence 22, Appl
Sequence 23, Appl
Sequence 24, Appl
Sequence 368, Appl
Sequence 376, Appl
Sequence 56, Appl
Sequence 60, Appl

14 1 US-08-677-599B-17
14 1 US-08-677-599B-18
14 1 US-08-677-599B-19
14 1 US-08-677-599B-20
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14 1 US-08-677-599B-23
15 10 US-09-756-983-11
15 1 US-08-677-599B-8
15 12 US-10-081-281-121
15 12 US-09-766-378A-37
15 10 US-09-815-837-103
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15 10 US-09-815-837-24
15 10 US-09-741-669-368
15 10 US-09-912-020-376
15 10 US-09-815-837-56
15 10 US-09-815-837-60

ALIGNMENTS

RESULT 1
US-08-790-540A-2
; Sequence 2, Application US/08790540A
; Patent No. US20010011125A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; Sequence 2, Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,540A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-8949
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-790-540A-2

Query Match 92.6%; Score 50; DB 8; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.0064;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSPA 9
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Db 97 ARHNYGSPA 105

RESULT 2
US-08-790-540A-6
; Sequence 6, Application US/08790540A
; Patent No. US20010011125A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TELECOMMUNICATION INFORMATION:
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,540A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TELECOMMUNICATION INFORMATION:
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122

Query Match 92.6%; Score 50; DB 8; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.0064;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSPA 9
|||||

Db 97 ARHNYGSPA 105

RESULT 3
US-08-791-391A-2
; Sequence 2, Application US/08791391A
; Patent No. US20010016645A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TELECOMMUNICATION INFORMATION:
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,391A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-391A-2

Query Match 92.6%; Score 50; DB 8; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.0064;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSPA 9
|||||

Db 97 ARHNYGSPA 105

RESULT 4
US-08-791-391A-6
; Sequence 6, Application US/08791391A
; Patent No. US20010016645A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TELECOMMUNICATION INFORMATION:
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,391A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-391A-6

Query Match 92.6%; Score 50; DB 8; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.0064;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
| | | | | | | |
Db 97 ARHNYGSFA 105

RESULT 5

US-08-677-599B-22
; Sequence 22, Application US/08677599B
; Patent No. US20020155117A1
; GENERAL INFORMATION:
; APPLICANT: Sucia-Foca, Nicole
; TITLE OF INVENTION: METHODS FOR DETECTING ORGAN ALLOGRAFT
; TITLE OF INVENTION: REJECTION AND USES THEREOF
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/677,599B
; FILING DATE: 08-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq., John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 50161-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212/278/0400
; TELEFAX: 212/391/0525
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-677-599B-22

Query Match 66.7%; Score 36; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYG 6
| | | | |
Db 9 ARHNYG 14

RESULT 6

US-09-764-853-432
; Sequence 432, Application US/09764853
; Patent No. US20020090672A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJ206
; CURRENT APPLICATION NUMBER: US/09/764,853
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 939
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 432
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-853-432

Query Match 66.7%; Score 36; DB 10; Length 101;
Best Local Similarity 85.7%; Pred. No. 2.5;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
| | | | |
Db 64 RHNYSSF 70

RESULT 7

US-09-801-368-26
; Sequence 26, Application US/09801368
; Patent No. US20020128250A1
; GENERAL INFORMATION:
; APPLICANT: Busby, Robert
; APPLICANT: Cali, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Milne, Todd
; APPLICANT: NO. US20020128250A1man, Thea
; APPLICANT: Royer, John
; APPLICANT: Salama, Sofie
; APPLICANT: Sherman, Amir
; APPLICANT: Silva, Jeff
; APPLICANT: Summers, Eric
; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
; FILE REFERENCE: 109272.147
; CURRENT APPLICATION NUMBER: US/09/801,368
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 09/487,558
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/160,587
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 742
; TYPE: PRT
; ORGANISM: Aspergillus terreus
US-09-801-368-26

Query Match 64.8%; Score 35; DB 10; Length 742;
Best Local Similarity 75.0%; Pred. No. 33;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 HNYGSFAS.10
| | | | |
Db 124 HGYGFSVS 131

RESULT 8

US-09-839-884-40
; Sequence 40, Application US/09839884
; Patent No. US20020076739A1
; GENERAL INFORMATION:
; APPLICANT: Aebersold, Rudolf H.
; APPLICANT: Gelb, Michael H
; APPLICANT: Gygi, Steven
; APPLICANT: Scott, C R
; APPLICANT: Turecek, Frantisek
; APPLICANT: Gerber, Scott A
; APPLICANT: Rist, Beate
; TITLE OF INVENTION: Rapid Quantitative Analysis of Proteins or Protein
; TITLE OF INVENTION: Function in Complex Mixture
; FILE REFERENCE: 64-98A

; CURRENT APPLICATION NUMBER: US/09/839,884
; CURRENT FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: 09/383,062
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 60/097,788
; PRIOR FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40
; LENGTH: 30
; TYPE: PRT
; ORGANISM: yeast
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (2)
; OTHER INFORMATION: C at position 2 is ICAT-labeled cysteinyl residue.
US-09-839-884-40

Query Match 63.0%; Score 34; DB 10; Length 30;
Best Local Similarity 83.3%; Pred. No. 1.7;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
| | | | |
DB 10 HNYGAF 15

RESULT 9
US-09-415-540-5
; Sequence 5, Application US/09415540
; Patent No. US2001001091A1
; GENERAL INFORMATION:
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: A NOVEL HUMAN PYROPHOSPHATASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/741,437
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0148 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 853-0555
; TELEFAX: (415) 845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 287 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONING: 4199

US-09-415-540-5

Query Match 63.0%; Score 34; DB 10; Length 287;
Best Local Similarity 83.3%; Pred. No. 19;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
| | | | |
DB 92 HNYGAF 97

RESULT 10
US-08-677-599B-21
; Sequence 21, Application US/08677599B
; Patent No. US20020155117A1
; GENERAL INFORMATION:
; APPLICANT: Sucia-Foca, Nicole
; TITLE OF INVENTION: METHODS FOR DETECTING ORGAN ALLOGRAFT
; TITLE OF INVENTION: REJECTION AND USES THEREOF
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/677,599B
; FILING DATE: 08-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq., John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 50161-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212/278/0400
; TELEFAX: 212/391/0525
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-677-599B-21

Query Match 61.1%; Score 33; DB 1; Length 14;
Best Local Similarity 83.3%; Pred. No. 1.2;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYG 6
: | | | | |
DB 9 SRHNYG 14

RESULT 11
US-09-864-761-41603
; Sequence 41603, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aecomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23

; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 41603
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC008506.4
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 20
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 22
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 17
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 16
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 20
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 20
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 32
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 20
US-09-864-761-41603

Query Match 61.1%; Score 33; DB 10; Length 28;
Best Local Similarity 55.6%; Pred. No. 2.4;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RHNYGSFAS 10
|||::|
Db 6 RHNSAYS 14

RESULT 12
US-09-144-886-60
; Sequence 60, Application US/09144886
; Patent No. US20020155114A1
; GENERAL INFORMATION:
; APPLICANT: Marks, James D
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; TITLE OF INVENTION: Botulinum Neurotoxins
; FILE REFERENCE: 2500.117USO

; CURRENT APPLICATION NUMBER: US/09/144.886
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone
; OTHER INFORMATION: IAL region VH epitope 2
US-09-144-886-60

Query Match 61.1%; Score 33; DB 9; Length 123;
Best Local Similarity 55.6%; Pred. No. 12;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RHNYGSFAS 10
|||::|
Db 98 RHGYGNVPS 106

RESULT 13
US-09-144-886-61
; Sequence 61, Application US/09144886
; Patent No. US20020155114A1
; GENERAL INFORMATION:
; APPLICANT: Marks, James D
; APPLICANT: Amersdorfer, Peter
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; TITLE OF INVENTION: Botulinum Neurotoxins
; FILE REFERENCE: 2500.117USO
; CURRENT APPLICATION NUMBER: US/09/144.886
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 61
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone
; OTHER INFORMATION: IFL region VH epitope 2
US-09-144-886-61

Query Match 61.1%; Score 33; DB 9; Length 123;
Best Local Similarity 55.6%; Pred. No. 12;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RHNYGSFAS 10
|||::|
Db 98 RHGYGNVPS 106

RESULT 14
US-08-677-599B-11
; Sequence 11, Application US/08677599B
; Patent No. US20020155117A1
; GENERAL INFORMATION:
; APPLICANT: Sucia-Foca, Nicole
; TITLE OF INVENTION: METHODS FOR DETECTING ORGAN ALLOGRAFT
; TITLE OF INVENTION: REJECTION AND USES THEREOF
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/677,599B
FILING DATE: 08-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White Esq., John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 50161-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212/278/0400
TELEFAX: 212/391/0525
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-677-599B-11

Query Match 59.3%; Score 32; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHNYG 6
|||||
Db 10 RHNYG 14

RESULT 15

US-08-677-599B-12
Sequence 12, Application US/08677599B
Patent No. US2002015517A1
GENERAL INFORMATION:
APPLICANT: Sucia-Foca, Nicole
TITLE OF INVENTION: METHODS FOR DETECTING ORGAN ALLOGRAFT
TITLE OF INVENTION: REJECTION AND USES THEREOF
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/677,599B
FILING DATE: 08-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White Esq., John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 50161-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212/278/0400
TELEFAX: 212/391/0525
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-677-599B-12

Query Match 59.3%; Score 32; DB 1; Length 14;

Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHNYG 6
|||||
Db 10 RHNYG 14

Search completed: November 18, 2002, 18:45:16
Job time : 1.96078 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:01 ; Search time 4.2402 Seconds
(without alignments)
69.390 Million cell updates/sec

Title: US-09-016-061-68
Perfect score: 54
Sequence: 1 ARHNYGSFAS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 2942292 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A.COMB.pap:*
2: /cgn2_6/ptodata/1/iaa/5B.COMB.pap:*
3: /cgn2_6/ptodata/1/iaa/6A.COMB.pap:*
4: /cgn2_6/ptodata/1/iaa/6B.COMB.pap:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pap:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	39	72.2	94	3	US-09-147-550-14
2	39	72.2	94	3	US-09-147-550-45
3	39	72.2	94	3	US-09-147-550-48
4	39	72.2	94	3	US-09-147-550-77
5	39	72.2	94	3	US-09-147-550-84
6	39	72.2	94	3	US-09-147-550-90
7	39	72.2	94	3	US-09-147-550-101
8	39	72.2	94	4	US-09-557-917-14
9	39	72.2	94	4	US-09-557-917-45
10	39	72.2	94	4	US-09-557-917-48
11	39	72.2	94	4	US-09-557-917-77
12	39	72.2	94	4	US-09-557-917-84
13	39	72.2	94	4	US-09-557-917-90
14	39	72.2	94	4	US-09-557-917-101
15	36	66.7	119	3	US-08-767-128-6
16	35	64.8	94	3	US-09-147-550-39
17	35	64.8	94	3	US-09-147-550-59
18	35	64.8	94	3	US-09-147-550-63
19	35	64.8	94	4	US-09-557-917-39
20	35	64.8	94	4	US-09-557-917-59
21	35	64.8	94	4	US-09-557-917-63
22	35	64.8	742	4	US-09-215-694-12
23	34	63.0	94	3	US-09-147-550-55
24	34	63.0	94	3	US-09-147-550-62
25	34	63.0	94	3	US-09-147-550-87
26	34	63.0	94	3	US-09-147-550-108
27	34	63.0	94	4	US-09-557-917-55

28	34	63.0	94	4	US-09-557-917-62	Sequence 62, Appl
29	34	63.0	94	4	US-09-557-917-87	Sequence 87, Appl
30	34	63.0	94	4	US-09-557-917-108	Sequence 108, App
31	34	63.0	191	4	US-09-443-041A-24	Sequence 24, Appl
32	34	63.0	236	4	US-09-443-041A-30	Sequence 30, Appl
33	34	63.0	260	4	US-09-443-041A-10	Sequence 10, Appl
34	34	63.0	261	4	US-09-443-041A-26	Sequence 26, Appl
35	34	63.0	269	4	US-09-443-041A-28	Sequence 28, Appl
36	34	63.0	271	4	US-09-443-041A-32	Sequence 32, Appl
37	34	63.0	271	4	US-09-443-041A-33	Sequence 33, Appl
38	34	63.0	286	2	US-08-809-267-3	Sequence 3, Appl
39	34	63.0	286	5	PCT-US95-13662A-3	Sequence 5, Appl
40	34	63.0	287	2	US-08-741-437-5	Sequence 5, Appl
41	34	63.0	287	2	US-09-134-593-5	Sequence 5, Appl
42	33	61.1	94	3	US-09-147-550-19	Sequence 19, Appl
43	33	61.1	94	3	US-09-147-550-30	Sequence 30, Appl
44	33	61.1	94	3	US-09-147-550-83	Sequence 83, Appl
45	33	61.1	94	3	US-09-147-550-85	Sequence 85, Appl

ALIGNMENTS

RESULT 1

US-09-147-550-14
; Sequence 14, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: BOVINE LEUKEMIA AND THE RESISTANCE THEREO
; CURRENT FILING DATE: 1999-04-23
; EARLIER FILING DATE: 1997-07-17
; EARLIER FILING DATE: 1997-07-17
; EARLIER FILING DATE: 1996-07-19
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-14

Query Match 72.2%; Score 39; DB 3; Length 94;
Best Local Similarity 77.8%; Pred. No. 4.7;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAS 10
Db 80 RHNYGVFES 88
|||||

RESULT 2

US-09-147-550-45
; Sequence 45, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: BOVINE LEUKEMIA AND THE RESISTANCE THEREO
; CURRENT FILING DATE: 1999-04-23
; EARLIER FILING DATE: 1997-07-17
; EARLIER FILING DATE: 1996-07-19
; EARLIER FILING DATE: 1997-07-19
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER APPLICATION NUMBER: JP 9-77979

; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-45

Query Match 72.2%; Score 39; DB 3; Length 94;
Best Local Similarity 77.8%; Pred. No. 4.7;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RHNYGSFAS 10
| | | | |
Db 80 RHNYGVFES 88

RESULT 3
US-09-147-550-48
; Sequence 48, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-48

Query Match 72.2%; Score 39; DB 3; Length 94;
Best Local Similarity 77.8%; Pred. No. 4.7;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RHNYGSFAS 10
| | | | |
Db 80 RHNYGVFES 88

RESULT 4
US-09-147-550-77
; Sequence 77, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 77
; LENGTH: 94

; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-77

Query Match 72.2%; Score 39; DB 3; Length 94;
Best Local Similarity 77.8%; Pred. No. 4.7;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RHNYGSFAS 10
| | | | |
Db 80 RHNYGVFES 88

RESULT 5
US-09-147-550-84
; Sequence 84, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-84

Query Match 72.2%; Score 39; DB 3; Length 94;
Best Local Similarity 77.8%; Pred. No. 4.7;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RHNYGSFAS 10
| | | | |
Db 80 RHNYGVFES 88

RESULT 6
US-09-147-550-90
; Sequence 90, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 90
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-90

Query Match 72.2%; Score 39; DB 3; Length 94;

Best Local Similarity 77.8%; Pred. No. 4.7;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAS 10
| | | | | | | |
Db 80 RHNYGVFES 88

RESULT 7
US-09-147-550-101
; Sequence 101, Application US/09147550
; Patent No. 6090340
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; EARLIER FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-101

Query Match 72.2%; Score 39; DB 3; Length 94;
Best Local Similarity 77.8%; Pred. No. 4.7;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAS 10
| | | | | | | |
Db 80 RHNYGVFES 88

RESULT 8
US-09-557-917-14
; Sequence 14, Application US/09557917
; Patent No. 6284457
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/557,917
; EARLIER FILING DATE: 2000-04-21
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-14

Query Match 72.2%; Score 39; DB 4; Length 94;
Best Local Similarity 77.8%; Pred. No. 4.7;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAS 10
| | | | | | | |
Db 80 RHNYGVFES 88

RESULT 9
US-09-557-917-45
; Sequence 45, Application US/09557917
; Patent No. 6284457
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/557,917
; EARLIER FILING DATE: 2000-04-21
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-45

Query Match 72.2%; Score 39; DB 4; Length 94;
Best Local Similarity 77.8%; Pred. No. 4.7;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAS 10
| | | | | | | |
Db 80 RHNYGVFES 88

RESULT 10
US-09-557-917-48
; Sequence 48, Application US/09557917
; Patent No. 6284457
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/557,917
; EARLIER FILING DATE: 2000-04-21
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-48

Query Match 72.2%; Score 39; DB 4; Length 94;
Best Local Similarity 77.8%; Pred. No. 4.7;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAS 10

```
Db      80 RHNYGVFES 88
||||| | |
RESULT 11
US-09-557-917-77
; Sequence 77, Application US/09557917
; Patent No. 6284457
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 77
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-77

Query Match      72.2%; Score 39; DB 4; Length 94;
Best Local Similarity 77.8%; Pred. No. 4.7;
Matches 7; Conservative 0; Mismatches 0; Indels 2; Gaps 0;

Qy      2 RHNYGSFAS 10
||||| | |
Db      80 RHNYGVFES 88

RESULT 12
US-09-557-917-84
; Sequence 84, Application US/09557917
; Patent No. 6284457
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-84

Query Match      72.2%; Score 39; DB 4; Length 94;
Best Local Similarity 77.8%; Pred. No. 4.7;
Matches 7; Conservative 0; Mismatches 0; Indels 2; Gaps 0;

Qy      2 RHNYGSFAS 10
||||| | |
Db      80 RHNYGVFES 88

RESULT 13
US-09-557-917-90
; Sequence 90, Application US/09557917
; Patent No. 6284457
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 90
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-90

Query Match      72.2%; Score 39; DB 4; Length 94;
Best Local Similarity 77.8%; Pred. No. 4.7;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 RHNYGSFAS 10
||||| | |
Db      80 RHNYGVFES 88

RESULT 14
US-09-557-917-101
; Sequence 101, Application US/09557917
; Patent No. 6284457
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-101

Query Match      72.2%; Score 39; DB 4; Length 94;
Best Local Similarity 77.8%; Pred. No. 4.7;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 RHNYGSFAS 10
||||| | |
Db      80 RHNYGVFES 88
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Search completed: November 18, 2002, 17:43:37
Job time : 4.2402 secs

RESULT 15
US-08-767-128-6
; Sequence 6: Application US/08767128
; Patent No. 611079
; GENERAL INFORMATION:
; APPLICANT: WYLIE, DWANE E.
; APPLICANT: LOPEZ, OSVALDO
; APPLICANT: MURRAY, PETER JOSEPH
; APPLICANT: GOEBEL, PETER
; TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
; TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
; STREET: 3100 No. 611079west Center, 90 South Seventh St
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/767,128
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE: 04-DEC-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/09258
; FILING DATE: 05-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/541,373
; FILING DATE: 10-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/462,798
; FILING DATE: 05-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G.
; REGISTRATION NUMBER: 35,093
; REFERENCE/DOCKET NUMBER: 8648.49USF1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/371-5278
; TELEFAX: 612/332-9081
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
US-08-767-128-6

Query Match 66.7%; Score 36; DB 3; Length 119;
Best Local Similarity 66.7%; Pred. No. 20;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ARHNYGSEA 9
|||:|:|
Db 97 ARHHYGYA 105

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:01 ; Search time 4.90196 Seconds
(without alignments)
196.114 Million cell updates/sec

Title: US-09-016-061-70

Perfect score: 55

Sequence: 1 ARHNYGSPAT 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: pir1:*
- 2: pir2:*
- 3: pir3:*
- 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	39	70.9	446	2 T19625	hypothetical prote
2	37	67.3	448	1 A60003	nucleocapsid prote
3	36	65.5	82	2 I51106	Major Histocompati
4	36	65.5	89	2 S38688	MHC class II histo
5	36	65.5	89	2 S38683	MHC class II histo
6	36	65.5	89	2 S38684	MHC class II histo
7	36	65.5	225	2 I47095	MHC class II OVAR-
8	36	65.5	399	2 AE3556	alanine racemase (
9	35	63.6	31	2 S00685	hypothetical prote
10	35	63.6	195	2 G86742	conserved hypotet
11	35	63.6	201	1 S55040	C 3.4.25.1 proteas
12	35	63.6	201	2 S38725	C 3.4.25.1 proteas
13	35	63.6	262	2 G69040	translation initia
14	35	63.6	270	2 AH1188	transporters (form
15	35	63.6	270	2 AH1546	transporters (form
16	35	63.6	347	2 S43771	phosphatidylcholin
17	35	63.6	1101	2 T16840	hypothetical prote
18	34	61.8	108	2 S26316	Ig heavy chain v r
19	34	61.8	110	2 S26317	Ig heavy chain v r
20	34	61.8	210	1 B69265	conserved hypotet
21	34	61.8	275	2 G75130	translation initia
22	34	61.8	275	2 D71087	probable translati
23	34	61.8	287	1 PWBV	inorganic diphosph
24	34	61.8	287	1 PWVKL	inorganic diphosph
25	34	61.8	347	2 C87326	hypothetical prote
26	34	61.8	527	2 T39741	ars binding protei
27	34	61.8	548	2 T25424	hypothetical prote
28	34	61.8	723	2 F83173	outer membrane pro
29	34	61.8	1052	2 AF2959	conserved hypotet

30	34	61.8	1341	2 H98323	hypothetical prote
31	33	60.0	65	2 S17441	hypothetical prote
32	33	60.0	80	2 I54469	MHC HLA-DR-beta-1
33	33	60.0	80	2 I68777	MHC HLA-DR-beta-1
34	33	60.0	81	2 I54550	HLA DRB1*1202 - hu
35	33	60.0	85	2 I59634	MHC class II DR-be
36	33	60.0	89	2 S38676	MHC class II histo
37	33	60.0	89	2 S38680	MHC class II histo
38	33	60.0	89	2 S57512	MHC class II histo
39	33	60.0	123	2 C25239	MHC class II histo
40	33	60.0	167	2 T16454	hypothetical prote
41	33	60.0	200	2 D32526	class II histocomp
42	33	60.0	220	2 T46055	hypothetical prote
43	33	60.0	237	2 C27060	class II histocomp
44	33	60.0	266	2 I54287	gene HLA-DRB1 prot
45	33	60.0	266	2 A27618	class II histocomp

ALIGNMENTS

RESULT 1

T19625

hypothetical protein C31H5.6 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000

C:Accession: T19625

R:Kershaw, J.

submitted to the EMBL Data Library, April 1997

A:Reference number: Z19153

A:Accession: T19625

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-446 <WIL>

A:Cross-references: EMBL:Z93778; PIDN:CAB07846.1; GSPDB:GN00019; CESP:C31H5.6

A:Experimental source: clone C31H5

C:Genetics:

A:Gene: CESP:C31H5.6

A:Map position: 1

A:Introns: 49/2; 85/1; 120/2; 183/3; 218/3; 255/3; 285/2; 331/3; 360/3

C:Superfamily: Caenorhabditis elegans hypothetical protein W03D8.8

Query Match 70.9%; Score 39; DB 2; Length 446;

Best Local Similarity 87.5%; Pred. No. 11;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 RHNYGSFA 9

Db 51 RHNYGSHA 58

RESULT 2

A60003

nucleocapsid protein - human coronavirus (strain OC43)

C:Species: human coronavirus

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 26-Feb-1999

C:Accession: A60003

R:Kamahora, T.; Soe, L.H.; Lai, M.M.C.

Virus Res. 12, 1-9, 1989

A:Title: Sequence analysis of nucleocapsid gene and leader RNA of human coronavirus O

A:Reference number: A60003; MUID:89243809; PMID:2541577

A:Accession: A60003

A:Molecule type: genomic RNA

A:Residues: 1-448 <KAM>

C:Genetics:

A:Gene: N

C:Superfamily: coronavirus nucleocapsid protein

C:Keywords: glycoprotein; nucleocapsid

F:17,221,336,388,408,421/Binding site: carbohydrate (Asn) (covalent) #status predi

Query Match 67.3%; Score 37; DB 1; Length 448;

Best Local Similarity 77.8%; Pred. No. 26;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAT 10
| | | | |
Db 103 RHNRGSFKT 111

RESULT 3

IS1106
Major Histocompatibility Complex class IIB - ring-necked pheasant (fragment)
C:Species: Phasianus colchicus (ring-necked pheasant)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 23-Jul-1999

C:Accession: IS1106
R:Witzell, H.; von Schantz, T.; Zoorob, R.; Auffray, C.
Immunogenetics 39, 395-403, 1994
A:Title: Molecular characterization of three Mhc class II B haplotypes in the ring-necked pheasant
A:Reference number: IS1103; MUID:94245280; PMID:7910588
A:Accession: IS1106
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-82 <WIT>
A:Cross-references: EMBL:X75406; NID:g496926; PIDN:CAA53160.1; PID:g496927
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 65.5%; Score 36; DB 2; Length 82;

Best Local Similarity 85.7%; Pred. No. 7.6;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
| | | | |
Db 75 RHNYGVF 81

RESULT 4

S38688
MHC class II histocompatibility antigen HLA-DR-08 beta chain - northern lesser bushbaby
C:Species: Galago senegalensis (northern lesser bushbaby)
C:Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 19-May-2000

C:Accession: S38688
R:Figuerola, F.; O'Huigin, C.; Tichy, H.; Klein, J.
submitted to the EMBL Data Library, November 1993
A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduced from GB/EMBL/DBDJ
A:Reference number: S38676
A:Accession: S38688
A:Molecule type: DNA
A:Residues: 1-89 <FIG>
A:Cross-references: EMBL:Z27158
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 65.5%; Score 36; DB 2; Length 89;

Best Local Similarity 85.7%; Pred. No. 8.3;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
| | | | |
Db 75 RHNYGVF 81

RESULT 5

S38683
MHC class II histocompatibility antigen HLA-DR-03 beta chain - northern lesser bushbaby
C:Species: Galago senegalensis (northern lesser bushbaby)
C:Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 19-May-2000

C:Accession: S38683
R:Figuerola, F.; O'Huigin, C.; Tichy, H.; Klein, J.
submitted to the EMBL Data Library, November 1993
A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduced from GB/EMBL/DBDJ
A:Reference number: S38676
A:Accession: S38683
A:Molecule type: DNA
A:Residues: 1-89 <FIG>
A:Cross-references: EMBL:Z27153
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 65.5%; Score 36; DB 2; Length 89;
Best Local Similarity 85.7%; Pred. No. 8.3;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
| | | | |
Db 75 RHNYGVF 81

RESULT 6

S38684
MHC class II histocompatibility antigen HLA-DR-04 beta chain - northern lesser bushbaby
C:Species: Galago senegalensis (northern lesser bushbaby)
C:Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 19-May-2000
C:Accession: S38684
R:Figuerola, F.; O'Huigin, C.; Tichy, H.; Klein, J.
submitted to the EMBL Data Library, November 1993
A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduced from GB/EMBL/DBDJ
A:Reference number: S38676
A:Accession: S38684
A:Molecule type: DNA
A:Residues: 1-89 <FIG>
A:Cross-references: EMBL:Z27154
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 65.5%; Score 36; DB 2; Length 89;

Best Local Similarity 85.7%; Pred. No. 8.3;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
| | | | |
Db 75 RHNYGVF 81

RESULT 7

I47095
MHC class II OVAR-DR-beta-3 - sheep (fragment)
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 15-Oct-1996 #sequence_revision 15-Oct-1996 #text_change 21-Jan-2000
C:Accession: I47095
R:Fabb, S.A.; Maddox, J.F.; Gogollin-Ewens, K.J.; Baker, L.; Wu, M.J.; Brandon, M.R.
Anim. Genet. 24, 249-255, 1993
A:Title: Isolation, characterization and evolution of ovine major histocompatibility antigen (MHC) class II OVAR-DRB3 gene
A:Reference number: I47075; MUID:94057592; PMID:7902039
A:Accession: I47095
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-225 <FAB>
A:Cross-references: GB:L04790; NID:g458880; PIDN:AAA16562.1; PID:g458881
C:Genetics:
A:Gene: OVAR-DRB3
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

F;98-163/Domain: immunoglobulin homology <IMM>

Query Match 65.5%; Score 36; DB 2; Length 225;

Best Local Similarity 85.7%; Pred. No. 21;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
| | | | |
Db 68 RHNYGVF 74

RESULT 8

AE3556
alanine racemase (EC 5.1.1.1) [imported] - Brucella melitensis (strain 16M)
C:Species: Brucella melitensis
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 03-Jun-2002
C:Accession: AE3556
R:DelVecchio, V.G.; Kapetral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanov
; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Let
proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melit


```
A:Reference number: AD3252; PMID:11756688
A:Accession: AE3556
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-399 <KUR>
A:Cross-references: GB:AE008918; PIDN:AAL53616.1; PID:g17984530; GSPDB:GN00191
A:Experimental source: strain 16M
C:Genetics:
A:Gene: BMEI10374
A:Map position: II
A:Superfamily: alanine racemase
C:Keywords: isomerase

Query Match      65.5%; Score 36; DB 2; Length 399;
Best Local Similarity 66.7%; Pred. No. 37;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy  2 RHNYGSFAT 10
    |||| : ||
Db  29 RHNYSAIAT 37

RESULT 9
S00685
hypothetical protein 3 - phage P1
C:Species: phage P1
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 08-Oct-1999
C:Accession: S00685
R:Eliason, J.L.; Sternberg, N.
J. Mol. Biol. 198, 281-293, 1987
A:Title: Characterization of the binding sites of cl repressor of bacteriophage P1. Evid
A:Reference number: S00684; MUID:88118929; PMID:3430609
A:Accession: S00685
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-31 <ELI>
A:Cross-references: EMBL:X06561; NID:g15128; PIDN:CAA29805.1; PID:g15130

Query Match      63.6%; Score 35; DB 2; Length 31;
Best Local Similarity 66.7%; Pred. No. 4.5;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy  2 RHNYGSFAT 10
    |||| : |
Db  18 RHNYGFHST 26

RESULT 10
G86742
conserved hypothetical protein yjgF [imported] - Lactococcus lactis subsp. lactis (strain
C:Species: Lactococcus lactis subsp. lactis
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 17-May-2002
C:Accession: G86742
R:Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarre, K.; Weissenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s
A:Reference number: A86625; MUID:21235186; PMID:11337471
A:Accession: G86742
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-195 <STO>
A:Cross-references: GB:AE005176; PID:g12723879; PIDN:AAK05041.1; GSPDB:GN00146
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: yjgF
C:Superfamily: hypothetical protein bl011

Query Match      63.6%; Score 35; DB 2; Length 195;
Best Local Similarity 62.5%; Pred. No. 28;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy  1 ARHNYGSF 8
    |::|::|::|
```

```
Db  103 AKHNWGAF 110

RESULT 11
S55040
C 3.4.25.1 proteasome endopeptidase complex ( ) beta chain C7-I - human
N:Alternate names: proteasome beta-2; proteasome chain C7-I
C:Species: Homo sapiens (man)
C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 03-Jun-2002
C:Accession: S55040; PC2323; S50148
R:Nothwang, H.G.; Tamura, T.; Tanaka, K.; Ichihara, A.
Biochim. Biophys. Acta 1219, 361-368, 1994
A:Title: Sequence analyses and inter-species comparisons of three novel human proteas
A:Reference number: S50147; MUID:95002149; PMID:7918633
A:Accession: S55040
A:Molecule type: mRNA
A:Residues: 1-201 <NOT>
A:Cross-references: GB:D26599; NID:g565648; PIDN:BAA05646.1; PID:g565649
R:Kristensen, P.; Johnsen, A.H.; Uerkvitz, W.; Tanaka, K.; Hendill, K.B.
Biochem. Biophys. Res. Commun. 205, 1785-1789, 1994
A:Title: Human proteasome subunits from 2-dimensional gels identified by partial sequ
A:Reference number: PC2315; MUID:95110324; PMID:7811265
A:Accession: PC2323
A:Molecule type: protein
A:Residues: 72-85 <KRI>
A:Experimental source: placenta
C:Comment: The proteasome consists of subunits of 21K-30K arranged in 4 stacked rings
C:Genetics:
A:Gene: GDB:PSMB2; HC7-I
A:Cross-references: GDB:567222
A:Superfamily: human multicatalytic endopeptidase complex beta chain C7
C:Keywords: hydrolase; proteinase

Query Match      63.6%; Score 35; DB 1; Length 201;
Best Local Similarity 60.0%; Pred. No. 29;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy  1 ARHNYGSFAT 10
    | | | | |
Db  130 AAHGYGAFLT 139

RESULT 12
S38725
C 3.4.25.1 proteasome endopeptidase complex ( ) beta chain C7-I - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 19-May-1994 #sequence_revision 10-Nov-1995 #text_change 03-Jun-2002
C:Accession: S38725; S38726
R:Nishimura, C.; Tamura, T.; Tokunaga, F.; Tanaka, K.; Ichihara, A.
FEBS Lett. 332, 52-56, 1993
A:Title: cDNA cloning of rat proteasome subunit RC7-I, a homologue of yeast PREL esse
A:Reference number: S38725; MUID:94009687; PMID:8405448
A:Accession: S38725
A:Molecule type: mRNA
A:Residues: 1-201 <NIS>
A:Cross-references: GB:D21799; NID:g436780; PIDN:BAA04823.1; PID:g436781
A:Accession: S38726
A:Molecule type: protein
A:Residues: 42-62,69,'L',71-80,'V',82-90,'P',92-98,'G',100-119,'X',121-122,'X',124,12
C:Superfamily: human multicatalytic endopeptidase complex beta chain C7
C:Keywords: hydrolase

Query Match      63.6%; Score 35; DB 2; Length 201;
Best Local Similarity 60.0%; Pred. No. 29;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy  1 ARHNYGSFAT 10
    | | | | |
Db  130 AAHGYGAFLT 139

RESULT 13
G69040
```

translation initiation factor eIF-2, alpha subunit - Methanobacterium thermoautotrophicum
 C:Species: Methanobacterium thermoautotrophicum
 C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 26-Aug-1999
 C:Accession: G69040
 R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N. K.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
 J. Bacteriol. 179, 7135-7155, 1997
 A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: function
 A:Reference number: A69000; MUID:98037514; PMID:9371463
 A:Accession: G69040
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-262 <MTH>
 A:Cross-references: GB:AE000895; GB:AE000666; NID:g2622403; PIDN:AAB85786.1; PID:g262241
 A:Experimental source: strain Delta H
 C:Genetics:
 A:Gene: MTH1308
 A:Start codon: GTG
 C:Superfamily: translation initiation factor eIF-2 alpha chain

Query Match 63.6%; Score 35; DB 2; Length 262;
 Best Local Similarity 85.7%; Pred. No. 37;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 NYGSFAT 10
 | : |||||
 Db 27 NYGAFAT 33

RESULT 14
 AH1188
 transporters (formate) homolog lmo0912 [imported] - Listeria monocytogenes (strain EGD-e)
 C:Species: Listeria monocytogenes
 C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
 C:Accession: AH1188
 R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
 ; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
 D.; Jones, L.M.; Karst, U.
 Science 294, 849-852, 2001
 A:Authors: Kref, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
 ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla
 A:Title: Comparative genomics of Listeria species.
 A:Reference number: AB1077; MUID:21537279; PMID:11679669
 A:Accession: AH1188
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-270 <GLA>
 A:Cross-references: GB:NC_003210; PIDN:CAC98990.1; PID:g16410315; GSPDB:GN00177
 A:Experimental source: strain EGD-e
 C:Genetics:
 A:Gene: lmo0912
 C:Superfamily: formate dehydrogenase fcbB

Query Match 63.6%; Score 35; DB 2; Length 270;
 Best Local Similarity 75.0%; Pred. No. 39;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFAT 10
 | : |||||
 Db 55 HEWGSFAT 62

RESULT 15
 AH1546
 transporters (formate) homolog lin0912 [imported] - Listeria innocua (strain Clp11262)
 C:Species: Listeria innocua
 C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
 C:Accession: AH1546
 R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
 ; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
 D.; Jones, L.M.; Karst, U.
 Science 294, 849-852, 2001

A:Authors: Kref, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
 ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla
 A:Title: Comparative genomics of Listeria species.
 A:Reference number: AB1077; MUID:21537279; PMID:11679669
 A:Accession: AH1546
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-270 <GLA>
 A:Cross-references: GB:AL592022; PIDN:CAC96144.1; PID:g16413361; GSPDB:GN00178
 A:Experimental source: strain Clp11262
 C:Genetics:
 A:Gene: lin0912
 C:Superfamily: formate dehydrogenase fcbB

Query Match 63.6%; Score 35; DB 2; Length 270;
 Best Local Similarity 75.0%; Pred. No. 39;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFAT 10
 | : |||||
 Db 55 HEWGSFAT 62

Search completed: November 18, 2002, 17:47:06
 Job time : 5.90196 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:00 ; Search time 2.45098 Seconds
(without alignments)
169.223 Million cell updates/sec

Title: US-09-016-061-70

Perfect score: 55

Sequence: 1 ARHNYGSFAT 10

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	38	69.1	323	1	CCSA_LOTJA
2	37	67.3	448	1	NCAP_CVHOC
3	36	65.5	396	1	ALR_BRUNE
4	35	63.6	201	1	PSB2_HUMAN
5	35	63.6	201	1	PSB2_MOUSE
6	35	63.6	201	1	PSB2_RAT
7	35	63.6	262	1	IF2A_METH
8	34	61.8	275	1	IF2A_PYRAB
9	34	61.8	275	1	IF2A_PYRHO
10	34	61.8	284	1	IPYR_PICPA
11	34	61.8	286	1	IPYR_KLULA
12	34	61.8	286	1	IPYR_YEAST
13	34	61.8	527	1	ABP2_SCHPO
14	33	60.0	65	1	CCSA_PEA
15	33	60.0	328	1	CCSA_ARATH
16	33	60.0	467	1	VL2_HPV33
17	33	60.0	470	1	SYE2_RICPR
18	33	60.0	473	1	SYE_AQUAE
19	33	60.0	512	1	PNTA_HAEIN
20	33	60.0	625	1	TRF5_YEAST
21	33	60.0	682	1	VF50_BPML5
22	32	58.2	65	1	CCSA_OENBE
23	32	58.2	96	1	YT16_STRCO
24	32	58.2	98	1	VG7_BPPI2
25	32	58.2	98	1	VG7_BPPI2
26	32	58.2	196	1	WBBJ_ECOLI
27	32	58.2	198	1	HB2G_HUMAN
28	32	58.2	214	1	DPOL_ADET1
29	32	58.2	266	1	HB2A_HUMAN
30	32	58.2	266	1	HB2B_HUMAN
31	32	58.2	266	1	HB2C_HUMAN
32	32	58.2	266	1	HB2D_HUMAN
33	32	58.2	266	1	HB2D_HUMAN

34	32	58.2	266	1	HB2E_HUMAN	P04229	homo sapien
35	32	58.2	266	1	HB2F_HUMAN	P13758	homo sapien
36	32	58.2	266	1	HB2H_HUMAN	P13760	homo sapien
37	32	58.2	266	1	HB2I_HUMAN	P20039	homo sapien
38	32	58.2	266	1	HB2J_HUMAN	P13761	homo sapien
39	32	58.2	281	1	HXA5_MORSA	Q9pww3	morone saxa
40	32	58.2	305	1	YMA5_DEIRA	Q9rrv7	deinococcus
41	32	58.2	313	1	CCSA_TOBAC	P12216	nicotiana t
42	32	58.2	319	1	CCSA_OENHO	Q9mti2	oenothera h
43	32	58.2	321	1	CCSA_MAIZE	P46659	zea mays h
44	32	58.2	321	1	CCSA_ORYSA	P12215	oryza sativ
45	32	58.2	322	1	CCSA_WHEAT	P58366	triticum ae

ALIGNMENTS

RESULT 1

CCSA_LOTJA

ID CCSA_LOTJA STANDARD; PRT; 323 AA.

AC Q9BBP4;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Cytochrome c biogenesis protein ccsc.

GN CCSA.

OS Lotus japonicus.

OG Chloroplast.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids I; Fabales; Fabaceae; Papilionoideae; Lotaeae; Lotus.

OX NCBI_TaxID=34305;

[1]

RP SEQUENCE FROM N.A.

RC STRAIN=Accession MG-20;

RA MEDLINE=21082929; PubMed=11214967;

RA Kato T., Kaneko T., Sato S., Nakamura Y., Tabata S.;

RT "Complete structure of the chloroplast genome of a legume, Lotus japonicus."

RL DNA Res. 7:323-330(2000).

CC -!- FUNCTION: REQUIRED DURING CYTOCHROME BIOGENESIS AT THE STEP OF HEME ATTACHMENT (BY SIMILARITY).

CC -!- SIMILARITY: BELONGS TO THE CCMF/CYCK/CCL1/NRFE/CCSA FAMILY.

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DR EMBL; AP002983; BAB33244.1; .

DR InterPro; IPR002541; CytoC_asm.

DR Pfam; PF01578; CytoC_asm; 1.

KW Cytochrome c-type biogenesis; Chloroplast.

SQ SEQUENCE 323 AA: 37185 MW; 5A034E3E2829FE35 CRC64;

Query Match 69.1%; Score 38; DB 1; Length 323;

Best Local Similarity 75.0%; Pred. No. 2.9;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFAT 10

Db 315 HNYGSFAT 322

|||||:

RESULT 2

NCAP_CVHOC

ID NCAP_CVHOC STANDARD; PRT; 448 AA.

AC P33469;

DT 01-FEB-1994 (Rel. 28, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE Nucleocapsid protein.
GN N.
OS Human coronavirus (strain OC43).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=31631;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89243809; PubMed=2541577;
RA Kamahora T., Soe L.H., Lai M.M.C.;
RT "Sequence analysis of nucleocapsid gene and leader RNA of human
RT coronavirus OC43";
RL Virus Res. 12:1-9(1989).
DR PIR; A60003; A60003.
DR InterPro; IPR001218; Corona_nucleocap.
DR Pfam; PF00937; Corona_nucleoca; 1.
KW Nucleocapsid.
SQ SEQUENCE 448 AA; 49316 MW; 5193ABIAE0D75626 CRC64;
Query Match 67.3%; Score 37; DB 1; Length 448;
Best Local Similarity 77.8%; Pred. No. 6.5;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 RHNYGSFAT 10
Db 103 RHNRGSFKT 111
RESULT 3
ALR_BRUME STANDARD; PRT; 396 AA.
AC Q8YD03;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Alanine racemase (EC 5.1.1.1).
GN ALR OR BMEII0374.
OS Brucella melitensis.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29459;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=16M / ATCC 23456 / Biotype 1;
RX MEDLINE=20020109; PubMed=11756688;
RA DelVecchio V.G., Kapatal V., Redkar R.J., Patra G., Muijer C., Los T.,
RA Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,
RA Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,
RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
RA Haselkorn R., Kyrpides N., Overbeek R.;
RT "The genome sequence of the facultative intracellular pathogen
RT Brucella melitensis";
RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
CC -!- FUNCTION: Provides the D-alanine required for cell wall
CC biosynthesis (By similarity).
CC -!- CATALYTIC ACTIVITY: L-alanine = D-alanine.
CC -!- COFACTOR: Pyridoxal phosphate (By similarity).
CC -!- PATHWAY: Along with D-alanine-D-alanine ligase, it makes up the
CC D-alanine branch of the peptidoglycan biosynthetic route.
CC -!- SIMILARITY: BELONGS TO THE ALANINE RACEMASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AE009674; AAL53616.1; ALT_INIT.
DR InterPro; IPR000821; Ala_racemase.
DR Pfam; PF00842; Ala_racemase; 1.

DR PROSITE; PS00395; ALANINE_RACEMASE; 1.
KW Isomerase; Pyridoxal phosphate; Cell wall; Peptidoglycan synthesis;
FT ACT_SITE 46 CATALYTIC BASE SPECIFIC TO D-ALANINE
FT ACT_SITE 280 CATALYTIC BASE SPECIFIC TO L-ALANINE
FT BINDING 46 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
SQ SEQUENCE 396 AA; 42367 MW; 3BA10919EB0066A CRC64;
Query Match 65.5%; Score 36; DB 1; Length 396;
Best Local Similarity 66.7%; Pred. No. 9;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 2 RHNYGSFAT 10
Db 26 RHNYSAIAT 34
RESULT 4
PSB2_HUMAN STANDARD; PRT; 201 AA.
ID PSB2_HUMAN
AC P49721; P31145;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Proteasome subunit beta type 2 (EC 3.4.25.1) (Proteasome component
DE C7-I) (Macropain subunit C7-I) (Multicatalytic endopeptidase complex
DE subunit C7-I).
GN PSMB2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95002149; PubMed=7918633;
RA Nothwang H.G., Tamura T., Tanaka K., Ichihara A.;
RT "Sequence analyses and inter-species comparisons of three novel human
RT proteasomal subunits, HsN3, Hsc7-I and Hsc10-II, confine potential
RT proteolytic active-site residues";
RL Biochim. Biophys. Acta 1219:361-368(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RA Strausberg R.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 172-177 AND 186-193.
RX TISSUE=Keratinocytes;
RC MEDLINE=93162043; PubMed=1286667;
RA Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E.,
RA Vandekerckhove J.;
RT "Microsequences of 145 proteins recorded in the two-dimensional gel
RT protein database of normal human epidermal keratinocytes";
RL Electrophoresis 13:960-969(1992).
CC -!- FUNCTION: THE PROTEASOME IS A MULTICATALYTIC PROTEINASE COMPLEX
CC WHICH IS CHARACTERIZED BY ITS ABILITY TO CLEAVE PEPTIDES WITH ARG,
CC PHE, TYR, LEU, AND GLU ADJACENT TO THE LEAVING GROUP AT NEUTRAL OR
CC SLIGHTLY BASIC PH. THE PROTEASOME HAS AN ATP-DEPENDENT PROTEOLYTIC
CC ACTIVITY. THIS SUBUNIT HAS A CHYMOTRYPSIN-LIKE ACTIVITY.
CC -!- CATALYTIC ACTIVITY: Cleavage at peptide bonds with very broad
CC specificity.
CC -!- PATHWAY: Involved in an ATP/ubiquitin-dependent non-lysosomal
CC proteolytic pathway.
CC -!- SUBUNIT: THE PROTEASOME IS COMPOSED OF AT LEAST 15 NON IDENTICAL
CC SUBUNITS WHICH FORM A HIGHLY ORDERED RING-SHAPED STRUCTURE.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY T1B.
CC -----
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EMBL; D26599; BAA05646.1; -.
DR HSSP; P22141; 1RYP.
DR MEROPS; T01.984; -.
DR MGD; MGI:1347045; PsmB2.
DR InterPro; IPR000243; Proteasome_B.
DR InterPro; IPR001353; Proteasome; 1.
DR Pfam; PF00227; proteasome; 1.
DR PROSITE; PS00854; PROTEASOME_B; 1.
KW: Proteasome; Hydrolase; Protease.
SQ SEQUENCE 201 AA; 22836 MW; 04D085D7BAA76130 CRC64;

Query Match 63.6%; Score 35; DB 1; Length 201;
Best Local Similarity 60.0%; Pred. No. 7;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARHNYGSFAT 10
| | | | |
DB 130 AHNGYGAFLT 139

RESULT 5
PSB2_MOUSE STANDARD; PRT; 201 AA.
AC Q9R1P3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Proteasome subunit beta type 2 (EC 3.4.25.1) (Proteasome component C7-1) (Macropain subunit C7-I) (Multicatalytic endopeptidase complex subunit C7-I).
GN PSMB2.

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B10.BR;
RX MEDLINE=99367391; PubMed=10436176;
RA Elenich L.A., Nandi D., Kent E.A., McCluskey T.S., Cruz M., Iyer M.N., Woodward E.C., Conn C.W., Ochoa A.L., Ginsburg D.B., Monaco J.J.;
RT "The complete primary structure of mouse 20S proteasomes";
RL Immunogenetics 49:835-842(1999).

CC -!- FUNCTION: THE PROTEASOME IS A MULTICATALYTIC PROTEINASE COMPLEX WHICH IS CHARACTERIZED BY ITS ABILITY TO CLEAVE PEPTIDES WITH ARG, PHE, TYR, LEU, AND GLU ADJACENT TO THE LEAVING GROUP AT NEUTRAL OR SLIGHTLY BASIC PH. THE PROTEASOME HAS AN ATP-DEPENDENT PROTEOLYTIC ACTIVITY. THIS SUBUNIT HAS A CHYMOTRYPSIN-LIKE ACTIVITY.
CC -!- CATALYTIC ACTIVITY: Cleavage at peptide bonds with very broad specificity.

CC -!- PATHWAY: Involved in an ATP/ubiquitin-dependent non-lysosomal proteolytic pathway.
CC -!- SUBUNIT: THE PROTEASOME IS COMPOSED OF AT LEAST 15 NON IDENTICAL SUBUNITS WHICH FORM A HIGHLY ORDERED RING-SHAPED STRUCTURE.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY T1B.

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DR EMBL; AF060090; AAD50535.1; -.
DR HSSP; P22141; 1RYP.
DR MEROPS; T01.984; -.
DR MGD; MGI:1347045; PsmB2.
DR InterPro; IPR000243; Proteasome_B.
DR InterPro; IPR001353; Proteasome; 1.
DR Pfam; PF00227; proteasome; 1.
DR PROSITE; PS00854; PROTEASOME_B; 1.
KW: Proteasome; Hydrolase; Protease.
SQ SEQUENCE 201 AA; 22906 MW; E9B3121974777958 CRC64;

Query Match 63.6%; Score 35; DB 1; Length 201;
Best Local Similarity 60.0%; Pred. No. 7;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARHNYGSFAT 10
| | | | |
DB 130 AHNGYGAFLT 139

RESULT 6
PSB2_RAT STANDARD; PRT; 201 AA.
AC P40307;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Proteasome subunit beta type 2 (EC 3.4.25.1) (Proteasome component C7-1) (Macropain subunit C7-I) (Multicatalytic endopeptidase complex subunit C7-I).
GN PSMB2.

OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=94009687; PubMed=8405448;
RA Nishimura C., Tamura T., Tokunaga F., Tanaka K., Ichihara A.;
RT "cDNA cloning of rat proteasome subunit RC7-I, a homologue of yeast PRE1 essential for chymotrypsin-like activity";
RL FEBS Lett. 332:52-56(1993).

CC -!- FUNCTION: THE PROTEASOME IS A MULTICATALYTIC PROTEINASE COMPLEX WHICH IS CHARACTERIZED BY ITS ABILITY TO CLEAVE PEPTIDES WITH ARG, PHE, TYR, LEU, AND GLU ADJACENT TO THE LEAVING GROUP AT NEUTRAL OR SLIGHTLY BASIC PH. THE PROTEASOME HAS AN ATP-DEPENDENT PROTEOLYTIC ACTIVITY. THIS SUBUNIT HAS A CHYMOTRYPSIN-LIKE ACTIVITY.
CC -!- CATALYTIC ACTIVITY: Cleavage at peptide bonds with very broad specificity.
CC -!- PATHWAY: Involved in an ATP/ubiquitin-dependent non-lysosomal proteolytic pathway.
CC -!- SUBUNIT: THE PROTEASOME IS COMPOSED OF AT LEAST 15 NON IDENTICAL SUBUNITS WHICH FORM A HIGHLY ORDERED RING-SHAPED STRUCTURE.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY T1B.

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DR EMBL; D21799; BAA04823.1; -.
DR PIR; S38725; S38725.
DR HSSP; P22141; 1RYP.
DR MEROPS; T01.984; -.
DR InterPro; IPR000243; Proteasome_B.
DR InterPro; IPR001353; Proteasome; 1.
DR Pfam; PF00227; proteasome; 1.
DR PROSITE; PS00854; PROTEASOME_B; 1.

KW Proteasome; Hydrolase; Protease.
 FT CONFLICT 70 70 R -> L (IN REF. 1; AA SEQUENCE).
 FT CONFLICT 81 81 A -> V (IN REF. 1; AA SEQUENCE).
 FT CONFLICT 91 91 C -> P (IN REF. 1; AA SEQUENCE).
 SQ SEQUENCE 201 AA; 22912 MW; E9AC021972B76528 CRC64;

Query Match 63.6%; Score 35; DB 1; Length 201;
 Best Local Similarity 60.0%; Pred. No. 7;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARHNGSFAT 10
 |||||
 DB 130 AAHGYGAFLT 139

RESULT 7

IF2A_METTH STANDARD; PRT; 262 AA.
 AC 027363;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Probable translation initiation factor 2 alpha subunit (eIF-2-alpha).
 GN EIF2A OR MTH1308.
 OS Methanobacterium thermoautotrophicum.
 OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
 OC Methanobacteriaceae; Methanothermobacter.
 OX NCBI_TaxID=187420;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Delta H;
 RX MEDLINE=98037514; PubMed=9371463;
 RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,
 RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
 RA Harrison D., Hoang L., Keagle P., Lum W., Pothier B., Qiu D.,
 RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
 RA Jiwni N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
 RA McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,
 RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
 RT "Complete genome sequence of Methanobacterium thermoautotrophicum
 delah: functional analysis and comparative genomics.";
 RL J. Bacteriol. 179:7135-7155(1997).
 CC -!- FUNCTION: EIF-2 FUNCTIONS IN THE EARLY STEPS OF PROTEIN SYNTHESIS
 CC BY FORMING A TERNARY COMPLEX WITH GTP AND INITIATOR TRNA
 CC (BY SIMILARITY).
 CC -!- SUBUNIT: HETEROTRIMER COMPOSED OF AN ALPHA, A BETA, AND A GAMMA
 CC CHAIN (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE EIF-2-ALPHA FAMILY.
 CC -!- SIMILARITY: CONTAINS 1 SI MOTIF DOMAIN.

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DR EMBL; AE000895; AAB85786.1;
 DR InterPro; IPR003029; SI.
 DR Pfam; PF00575; S1; 1.
 DR SMART; SM00316; S1; 1.
 DR PROSITE; PS0126; S1; 1.
 KW Initiation factor; Protein biosynthesis; RNA-binding;
 KW Complete proteome.
 FT DOMAIN 15 86 SI MOTIF.
 SQ SEQUENCE 262 AA; 29780 MW; D7324B76DAFD5AA7 CRC64;

Query Match 63.6%; Score 35; DB 1; Length 262;
 Best Local Similarity 85.7%; Pred. No. 9.2;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 NYGSFAT 10

Db 27 NYGAFAT 33
 |||||

RESULT 8

IF2A_PVRAB STANDARD; PRT; 275 AA.
 ID IF2A_PVRAB
 AC Q9V0B4;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Probable translation initiation factor 2 alpha subunit (eIF-2-alpha).
 GN EIF2A OR PAB0568.
 OS Pyrococcus abyssi.
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 OC Pyrococcus.
 OX NCBI_TaxID=29292;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GE5 / Orsay;
 RA Heilig R.;
 RT "Pyrococcus abyssi genome sequence: insights into archaeal chromosome
 structure and evolution";
 RT Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: EIF-2 FUNCTIONS IN THE EARLY STEPS OF PROTEIN SYNTHESIS
 CC BY FORMING A TERNARY COMPLEX WITH GTP AND INITIATOR TRNA
 CC (BY SIMILARITY).
 CC -!- SUBUNIT: HETEROTRIMER COMPOSED OF AN ALPHA, A BETA, AND A GAMMA
 CC CHAIN (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE EIF-2-ALPHA FAMILY.
 CC -!- SIMILARITY: CONTAINS 1 SI MOTIF DOMAIN.

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 CC -----

DR EMBL; AJ248285; CAB49760.1;
 DR HSSP; P05055; ISRO.
 DR InterPro; IPR003029; SI.
 DR Pfam; PF00575; S1; 1.
 DR SMART; SM00316; S1; 1.
 DR PROSITE; PS0126; S1; 1.
 KW Initiation factor; Protein biosynthesis; RNA-binding;
 KW Complete proteome.
 FT DOMAIN 12 83 SI MOTIF.
 SQ SEQUENCE 275 AA; 31912 MW; B2659F3A49879B4F CRC64;

Query Match

Best Local Similarity 61.8%; Score 34; DB 1; Length 275;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8

|||||

Db 23 HNYGAF 28

RESULT 9

IF2A_PVRHO STANDARD; PRT; 275 AA.
 ID IF2A_PVRHO
 AC O58655;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Probable translation initiation factor 2 alpha subunit (eIF-2-alpha).
 GN EIF2A OR PH0961.
 OS Pyrococcus horikoshii.
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 OC Pyrococcus.
 OX NCBI_TaxID=53953;

```

RN  (1)
RP  SEQUENCE FROM N.A.
RC  STRAIN=OT3;
RA  MEDLINE=98344137; PubMed=9679194;
RA  Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
RA  Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
RA  Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
RA  Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kishida N., Oguchi A.,
RA  Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RA  Masuchi Y., Shizuya H., Kikuchi H.;
RT  "Complete sequence and gene organization of the genome of a hyper-
RT  thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
RL  DNA Res. 5:55-76(1998).
CC  -!- FUNCTION: EIF-2 FUNCTIONS IN THE EARLY STEPS OF PROTEIN SYNTHESIS
CC  BY FORMING A TERNARY COMPLEX WITH GTP AND INITIATOR TRNA
CC  (BY SIMILARITY).
CC  -!- SUBUNIT: HETEROTRIMER COMPOSED OF AN ALPHA, A BETA, AND A GAMMA
CC  CHAIN (BY SIMILARITY).
CC  -!- SIMILARITY: BELONGS TO THE EIF-2-ALPHA FAMILY.
CC  -!- SIMILARITY: CONTAINS 1 SL MOTIF DOMAIN.
CC  -----
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CC  -----
DR  EMBL; AP000004; BAA30058.1; -.
DR  HSP; P05055; LSRO.
DR  InterPro; IPR003029; S1.
DR  Pfam; PF00575; S1; 1.
DR  SMART; SM00316; S1; 1.
DR  PROSITE; PS50126; S1; 1.
KW  Initiation factor; Protein biosynthesis; RNA-binding;
KW  Complete proteome.
FT  DOMAIN 12 83 SL MOTIF.
SQ  SEQUENCE 275 AA; 31980 MW; 6AAAD15F10FFB436 CRC64;

Query Match 61.8%; Score 34; DB 1; Length 275;
Best Local Similarity 83.3%; Pred. No. 15;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
Db 23 HNYGAF 28

RESULT 10
IPYR_PICPA
ID IPYR_PICPA STANDARD; PRT; 284 AA.
AC O13505;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Inorganic pyrophosphatase (EC 3.6.1.1) (Pyrophosphate phospho-
DE hydrolase) (PPase).
GN IPPI.
OS Pichia pastoris (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Pichia.
OX NCBI_TaxID=4922;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL Y-11430;
RX MEDLINE=99034033; PubMed=9818724;
RA Cosano I.C., Alvarez P., Molina M., Nombela C.;
RT "Cloning and sequence analysis of the Pichia pastoris TRP1 and
RT HIS3 genes.";
RL Yeast 14:861-867(1998).
CC -!- CATALYTIC ACTIVITY: Diphosphate + H(2)O = 2 phosphate.
CC -!- COFACTOR: REQUIRES THE PRESENCE OF DIVALENT METAL CATION.

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CC  -----
CC  MAGNESIUM CONFERS THE HIGHEST ACTIVITY.
CC  -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC  -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC  -!- SIMILARITY: BELONGS TO THE PPASE FAMILY.
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; AJ001000; CAA04453.1; -.
DR  HSP; P00817; IWGI.
DR  InterPro; IPR001596; Pyrophosphatase.
DR  Pfam; PF00719; Pyrophosphatase; 1.
DR  PROSITE; PS00387; PPASE; 1.
KW  Hydrolase; Magnesium.
FT  INIT_MET 0 BY SIMILARITY.
FT  ACT_SITE 56 56 PROBABLE.
FT  BINDING 78 78 INORGANIC PYROPHOSPHATE (BY SIMILARITY).
SQ  SEQUENCE 284 AA; 31937 MW; 3DAD27970D7775D6 CRC64;

Query Match 61.8%; Score 34; DB 1; Length 284;
Best Local Similarity 83.3%; Pred. No. 16;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
Db 91 HNYGAF 96

RESULT 11
IPYR_KLULA
ID IPYR_KLULA STANDARD; PRT; 286 AA.
AC P13998;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE Inorganic pyrophosphatase (EC 3.6.1.1) (Pyrophosphate phospho-
DE hydrolase) (PPase).
GN IPPI OR IPP.
OS Kluyveromyces lactis (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
OX NCBI_TaxID=28985;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89189093; PubMed=2538971;
RA Stark M.J.R., Milner J.S.;
RT "Cloning and analysis of the Kluyveromyces lactis TRP1 gene: a
RT chromosomal locus flanked by genes encoding inorganic pyrophosphatase
RT and histone H3.";
RL Yeast 5:35-50(1989).
RN [2]
RP SIMILARITY TO E.COLI AND YEAST PPASES.
RX MEDLINE=90254161; PubMed=2160278;
RA Lahti R., Kollakowski L.F. Jr., Heinonen J., Vihinen M., Pohjanoksa K.,
RA Cooperman B.S.;
RT "Conservation of functional residues between yeast and E. coli
RT inorganic pyrophosphatases.";
RL Biochim. Biophys. Acta 1038:338-345(1990).
CC -!- CATALYTIC ACTIVITY: Diphosphate + H(2)O = 2 phosphate.
CC -!- COFACTOR: REQUIRES THE PRESENCE OF DIVALENT METAL CATION.
CC  MAGNESIUM CONFERS THE HIGHEST ACTIVITY.
CC  -!- SUBUNIT: HOMODIMER.
CC  -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC  -!- SIMILARITY: BELONGS TO THE PPASE FAMILY.
CC  -----
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 CC -----

DR EMBL; X14230; CAA32446.1; -;
 DR PIR; S07894; PWKL.
 DR HSSP; P00817; IWGI.
 DR InterPro; IPR001596; Pyrophosphatase.
 DR Pfam; PF00719; Pyrophosphatase; 1.
 DR PROSITE; PS00387; PPASe; 1.
 KW Hydrolase; Magnesium.
 FT INIT_MET 0 BY SIMILARITY.
 FT ACT_SITE 56 56 PROBABLE.
 FT BINDING 78 78 INORGANIC PYROPHOSPHATE (BY SIMILARITY).
 SQ SEQUENCE 286 AA; 32034 MW; 11647F4ABD916A2F CRC64;

Query Match 61.8%; Score 34; DB 1; Length 286;
 Best Local Similarity 83.3%; Pred. No. 16;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
 |||||
 Db 91 HNYGAF 96

RESULT 12

ID IPYR_YEAST STANDARD; PRT; 286 AA.
 AC P00817;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Inorganic pyrophosphatase (EC 3.6.1.1) (Pyrophosphate phospho-
 DE hydrolase) (PPase);
 GN IPPI OR PPAL OR PPA OR YBR011C OR YBR0202.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=X2180;
 RX MEDLINE=89083474; PubMed=2849749;
 RA Kolakowski L.F. Jr., Schloesser M., Cooperman B.S.;
 RT "Cloning, molecular characterization and chromosome localization of
 RT the inorganic pyrophosphatase (PPA) gene from *S. cerevisiae*.";
 RL Nucleic Acids Res. 16:10441-10452(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288c;
 RA Entian K.-D., Koetter P., Rose M., Li Z., Thermann R., Brendel M.,
 RA Baur A., Boles E., Miosga T., Schaaff-Gerstenschlaeger I.,
 RA Zimmermann F.K.;
 RA Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE
 RX MEDLINE=78087552; PubMed=340461;
 RA Cohen S.A., Sterner R., Keim P.S., Heinrichson R.L.;
 RA "Covalent structural analysis of yeast inorganic pyrophosphatase.";
 RL J. Biol. Chem. 253:889-897(1978).
 RN [4]
 RP SEQUENCE OF 25-35 AND 239-251.
 RC STRAIN=S288c;
 RX MEDLINE=95203288; PubMed=7895733;
 RA Garrels J.I., Futter B., Kobayashi R., Latter G.I., Schwender B.,
 RA Volpe T., Warner J.R., McLaughlin C.S.;
 RT "Protein identifications for a Saccharomyces cerevisiae protein
 RT database.";
 RL Electrophoresis 15:1466-1486(1994).
 RN [5]
 RP SEQUENCE OF 239-249.
 RC STRAIN=ATCC 38531 / Y41;

RX MEDLINE=97089742; PubMed=8935650;
 RA Norbeck J., Blomberg A.;
 RT "Protein expression during exponential growth in 0.7 M NaCl medium of
 RT Saccharomyces cerevisiae.";
 RL FEMS Microbiol. Lett. 137:1-8(1996).
 RN [6]
 RP ACTIVE SITE.
 RX MEDLINE=80109718; PubMed=6101539;
 RA Bond M.W., Chiu N.Y., Cooperman B.S.;
 RT "Identification of an arginine important for enzymatic activity
 RT within the covalent structure of yeast inorganic pyrophosphatase.";
 RL Biochemistry 19:94-102(1980).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
 RA Arutunian E.G., Terzian S.S., Voronova A.A., Kuranova I.P.,
 RA Smirnova E.A., Valstein B.K., Hohne W.E., Hansen G.;
 RT "X-ray diffraction study of inorganic pyrophosphatase from baker's
 RT yeast at the 3-A resolution.";
 RL Dokl. Akad. Nauk SSSR 258:1481-1492(1981).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RX MEDLINE=97148342; PubMed=8994974;
 RA Heikinheimo P., Lehtonen J., Baykov A., Lahti R., Cooperman B.S.,
 RA Goldman A.;
 RT "The structural basis for pyrophosphatase catalysis.";
 RL Structure 4:1491-1508(1996).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
 RA Swaminathan K., Cooperman B.S., Lahti R., Voet D.;
 RL Submitted (DEC-1997) to the PDB data bank.
 RN [10]
 RP X-RAY CRYSTALLOGRAPHY (2.15 ANGSTROMS) OF MUTANTS LYS-78 AND LYS-117.
 RX MEDLINE=99096888; PubMed=9878371;
 RA Tuominen V., Heikinheimo P., Kallander T., Torkkel T., Hyttia T.,
 RA Kapyla J., Lahti R., Cooperman B.S., Goldman A.;
 RT "The R78K and D117E active-site variants of Saccharomyces cerevisiae
 RT soluble inorganic pyrophosphatase: structural studies and mechanistic
 RT implications.";
 RL J. Mol. Biol. 284:1565-1580(1998).
 RN [11]
 RP SIMILARITY TO E.COLI AND K.LACTIS PPASES.
 RX MEDLINE=90254161; PubMed=2160278;
 RA Lahti R., Kolakowski L.F. Jr., Heinonen J., Vihinen M., Pohjanoksa K.,
 RA Cooperman B.S.;
 RT "Conservation of functional residues between yeast and *E. coli*.
 RT inorganic pyrophosphatases.";
 RL Biochim. Biophys. Acta 1038:338-345(1990).
 CC -|- CATALYTIC ACTIVITY: Diphosphate + H(2)O = 2 phosphate.
 CC -|- COFACTOR: REQUIRES THE PRESENCE OF DIVALENT METAL CATION.
 CC MAGNESIUM CONFERS THE HIGHEST ACTIVITY. IT BINDS UP TO 4 DIVALENT
 CC CATIONS PER SUBUNIT, WITH THREE REQUIRED FOR ACTIVITY.
 CC -|- SUBUNIT: HOMODIMER.
 CC -|- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -|- SIMILARITY: BELONGS TO THE PPASE FAMILY.
 CC -----
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 CC -----
 DR EMBL; X13253; CAA31629.1; -;
 DR EMBL; Z35880; CAA84949.1; -;
 DR PIR; S45864; PWBY.
 DR PDB; 1PYP; 15-OCT-91.
 DR PDB; 1YPP; 07-DEC-96.
 DR PDB; 1WGI; 19-NOV-97.
 DR PDB; 1WUJ; 19-NOV-97.
 DR PDB; 1HUJ; 08-APR-98.
 DR PDB; 1HUK; 08-APR-98.
 DR PDB; 117E; 23-DEC-98.

DR PDB; 6PRK; 23-DEC-98.
 DR SWISS-2DPAGE: P00817; YEAST.
 DR COMPLEYEAST-2DPAGE: P00817; -
 DR SGD: S0000215; IPPI.
 DR InterPro: IP001596; Pyrophosphatase.
 DR Pfam: PF00719; Pyrophosphatase; 1.
 DR PROSITE: PS00387; PPASE; 1.
 KW Hydrolase; Magnesium; 3D-structure.
 FT INIT_MEF 0 0
 FT ACT_SITE 56 56 PROBABLE.
 FT BINDING 78 78 INORGANIC PYROPHOSPHATE.
 FT CONFLICT 40 40 N -> D (IN REF. 3).
 FT CONFLICT 71 71 D -> N (IN REF. 3).
 FT CONFLICT 74 74 MISSING (IN REF. 3).
 FT CONFLICT 123 123 E -> Q (IN REF. 3).
 FT CONFLICT 136 136 Q -> E (IN REF. 3).
 FT CONFLICT 186 186 N -> D (IN REF. 3).
 FT CONFLICT 224 224 D -> N (IN REF. 3).
 FT CONFLICT 266 266 L -> P (IN REF. 2).
 FT STRAND 4 7
 FT STRAND 16 20
 FT STRAND 25 25
 FT TURN 28 30
 FT TURN 38 41
 FT STRAND 45 45
 FT STRAND 55 55
 FT TURN 79 79
 FT TURN 111 112
 FT STRAND 121 123
 FT TURN 131 132
 FT STRAND 135 135
 FT STRAND 138 146
 FT STRAND 151 158
 FT TURN 160 161
 FT TURN 165 167
 FT TURN 172 175
 FT TURN 176 177
 FT TURN 179 180
 FT TURN 182 197
 FT STRAND 203 203
 FT STRAND 205 207
 FT STRAND 210 210
 FT TURN 212 230
 FT TURN 231 231
 FT TURN 245 246
 FT TURN 248 249
 FT TURN 251 252
 FT TURN 255 260
 FT TURN 274 275
 SQ SEQUENCE 286 AA; 32184 MW; F29390260B60C8B2 CRC64;

 Query Match 61.8%; Score 34; DB 1; Length 286;
 Best Local Similarity 83.3%; Pred. No. 16;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

 QY 3 HNYGSF 8
 Db 91 HNYGAF 96
 |||||

 RESULT 13
 ABP2_SCHPO STANDARD; PRT; 527 AA.
 ID ABP2_SCHPO
 AC Q9USY4; P78967;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE ARS-binding protein 2.
 GN ABP2 OR SPBC1861.02.
 OS Schizosaccharomyces pombe (fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;

 Schizosaccharomycetes.
 NCBI_TaxID=4896;
 [1]
 RP SEQUENCE FROM N.A., SEQUENCE OF 154-171; 302-308; 312-328; 377-384
 AND 419-431, FUNCTION, SUBCELLULAR LOCATION, AND MUTAGENESIS OF
 ARG-331; GLY-332 AND ARG-333.
 RP STRAIN=972;
 RC MEDLINE=98147808; PubMed=9488484;
 RX Sanchez J.P., Murakami Y., Huberman J.A., Hurwitz J.;
 RA "Isolation, characterization, and molecular cloning of a protein
 (Abp2) that binds to a Schizosaccharomycetes pombe origin of replication
 (ars3002).";
 RL Mol. Cell. Biol. 18:1670-1681(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=21848401; PubMed=11859360;
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Sgouros J., Peat N., Hayes J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Feltwell J., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holroyd S., Hornsby T., Howarth S., Huckie E.J., Hunt S., Jagels K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
 RA Weltjens I., Vansstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Reinhardt R., Pohl T.M.,
 RA Borzym K., Langer I., Beck A., Leirach H., Wambutt R., Purnelle B.,
 RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsberg S.L.,
 RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
 RL "The genome sequence of Schizosaccharomycetes pombe.";
 Nature 415:871-880(2002).
 CC -1- FUNCTION: BINDS, PREFERENTIALLY, TO THE MAUNDRELL ARS CONSENSUS
 SEQUENCE WITHIN ARS3002.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -----
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 CC -----
 CC EMBL; U73044; AAC49930.1; -
 DR EMBL; AL109834; CAB52738.1; -
 KW Nuclear protein; DNA-binding.
 FT MUTAGEN 331 331 R->A: 40-FOLD DECREASE IN DNA-BINDING.
 FT MUTAGEN 332 332 G->A: LOSS OF DNA-BINDING.
 FT MUTAGEN 333 333 R->A: LOSS OF DNA-BINDING.
 FT CONFLICT 260 260 A -> P (IN REF. 1).
 SQ SEQUENCE 527 AA; 59629 MW; 2860A5683999B9F4 CRC64;

 Query Match 61.8%; Score 34; DB 1; Length 527;
 Best Local Similarity 75.0%; Pred. No. 31;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

 QY 3 HNYGSFAT 10
 Db 192 HNLGSFVT 199
 |||||

RESULT 14

CCSA_PEA STANDARD; PRT; 65 AA.
 ID CCSA_PEA
 AC P31172;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Cytochrome c biogenesis protein ccsa (Fragment).
 GN CCSA.
 OS Pisum sativum (Garden pea).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
 OX NCBI_TaxID=3888;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Alaska;
 RX MEDLINE=91355950; PubMed=1884007;
 RA Nagano Y., Ishikawa H., Matsuno R., Sasaki Y.;
 RT "Nucleotide sequence and expression of the ribosomal protein L2 gene
 in pea chloroplasts";
 RL Plant Mol. Biol. 17:541-545(1991).
 CC -!- FUNCTION: REQUIRED DURING CYTOCHROME BIOGENESIS AT THE STEP OF
 HEME ATTACHMENT (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE CCMF/CYCK/CCL1/NRFE/CCSA FAMILY.
 CC -----
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 CC -----
 DR EMBL; X59015; CAA41754.1; -;
 DR PIR; S17441; S17441.
 DR InterPro; IPR002541; CytC_asm.
 DR Pfam; PF01578; CytC_asm; 1.
 KW Cytochrome c-type biogenesis; Chloroplast.
 NON_TER 1
 SQ SEQUENCE 65 AA; 7396 MW; 9E523E0C70B102AA CRC64;

Query Match 60.0%; Score 33; DB 1; Length 65;
 Best Local Similarity 62.5%; Pred. No. 5.3;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFAT 10
 I:||||:
 Db 57 HSYGSFTS 64

RESULT 15

CCSA_ARATH STANDARD; PRT; 328 AA.
 ID CCSA_ARATH
 AC P56770;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Cytochrome c biogenesis protein ccsa.
 GN CCSA.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=20039611; PubMed=10574454;
 RA Sato S., Nakamura Y., Kaneko T., Asamizu E., Tabata S.;
 RT "Complete structure of the chloroplast genome of Arabidopsis

thaliana.";
 RL DNA Res. 6:283-290(1999).
 CC -!- FUNCTION: REQUIRED DURING CYTOCHROME BIOGENESIS AT THE STEP OF
 HEME ATTACHMENT (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE CCMF/CYCK/CCL1/NRFE/CCSA FAMILY.
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 CC -----
 DR EMBL; AP000423; BAA84436.1; -;
 DR InterPro; IPR002541; CytC_asm.
 DR Pfam; PF01578; CytC_asm; 1.
 KW Cytochrome c-type biogenesis; Chloroplast.
 SQ SEQUENCE 328 AA; 37732 MW; C88D1508B2924D6F CRC64;
 Query Match 60.0%; Score 33; DB 1; Length 328;
 Best Local Similarity 62.5%; Pred. No. 29;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 3 HNYGSFAT 10
 I:||||:
 Db 320 HSYGSFTS 327

Search completed: November 18, 2002, 17:33:27
 Job time : 3.45098 secs

GenCore version 5.1.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:01 ; Search time 10.4412 Seconds
(without alignments)
197.341 Million cell updates/sec

Title: US-09-016-061-70
Perfect score: 55
Sequence: 1 ARHNYGSPAT 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertibrate:*
14: sp_unclassified:*
15: sp_rvrius:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	43	78.2	839	10 Q9LIE5	Q9LIE5 arabidopsis
2	40	72.7	276	7 Q9GJN0	Q9GJN0 calman croc
3	39	70.9	446	5 O62086	O62086 caenorhabdl
4	38	69.1	89	7 O19495	O19495 gallus gall
5	37	67.3	5317	5 Q8TA74	Q8TA74 hemiscentrot
6	36	65.5	39	7 P79474	P79474 cervus elap
7	36	65.5	39	7 P79477	P79477 cervus elap
8	36	65.5	39	7 P79478	P79478 cervus elap
9	36	65.5	39	7 P79479	P79479 cervus elap
10	36	65.5	67	7 Q8SP02	Q8SP02 hapalenur g
11	36	65.5	74	6 Q9PTM4	Q9PTM4 bos taurus
12	36	65.5	75	7 Q9GJ15	Q9GJ15 bos taurus
13	36	65.5	76	7 Q9TPC2	Q9TPC2 macaca mula
14	36	65.5	77	7 Q9GJ91	Q9GJ91 ovis aries
15	36	65.5	77	7 Q9GJ90	Q9GJ90 ovis aries
16	36	65.5	77	7 Q9GJ82	Q9GJ82 ovis aries

17	36	65.5	78	6 O97968	O97968 ovis aries
18	36	65.5	78	6 O97835	O97835 ovis aries
19	36	65.5	78	6 O97839	O97839 ovis aries
20	36	65.5	78	6 O97844	O97844 ovis aries
21	36	65.5	78	7 O9MMT6	O9MMT6 leopardus p
22	36	65.5	78	7 O9MMT5	O9MMT5 leopardus p
23	36	65.5	78	7 O9MMT4	O9MMT4 leopardus p
24	36	65.5	78	7 O95HD1	O95HD1 ovis aries
25	36	65.5	78	7 O95HC6	O95HC6 ovis aries
26	36	65.5	79	7 O9MX19	O9MX19 leopardus p
27	36	65.5	79	7 O9MX13	O9MX13 leopardus p
28	36	65.5	79	7 O9MX03	O9MX03 leopardus p
29	36	65.5	79	7 O9MX00	O9MX00 leopardus p
30	36	65.5	79	7 O9MW29	O9MW29 leopardus p
31	36	65.5	79	7 O9MW28	O9MW28 leopardus p
32	36	65.5	79	7 O9MW27	O9MW27 leopardus p
33	36	65.5	79	7 O9MWY9	O9MWY9 leopardus p
34	36	65.5	79	7 O9MWY8	O9MWY8 leopardus p
35	36	65.5	79	7 O9MWY6	O9MWY6 leopardus p
36	36	65.5	79	7 O9MWY5	O9MWY5 leopardus p
37	36	65.5	79	7 O9MWY4	O9MWY4 leopardus p
38	36	65.5	79	7 O9MWY3	O9MWY3 leopardus p
39	36	65.5	79	7 O9MWX6	O9MWX6 leopardus p
40	36	65.5	79	7 O9MWX5	O9MWX5 leopardus p
41	36	65.5	79	7 O9MWX4	O9MWX4 leopardus p
42	36	65.5	79	7 O9MWX1	O9MWX1 leopardus p
43	36	65.5	79	7 O9MWX0	O9MWX0 leopardus p
44	36	65.5	79	7 O9MMW9	O9MMW9 leopardus p
45	36	65.5	79	7 O9MMW7	O9MMW7 leopardus p

ALIGNMENTS

RESULT 1

Q9LIE5 ID Q9LIE5 PRELIMINARY; PRT; 839 AA.
AC Q9LIE5; Q9LIE5, 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Far-red impaired response protein, mutator-like transposase-like
DE protein, phytochrome A signaling protein-like.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=20363099; PubMed=10907853;
RA Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.
RT Sequence features of the regions of 4,251,695 bp covered by ninety p1,
RT TAC and BAC clones.";
RL DNA Res. 7:217-221(2000).
DR EMBL; AP001306; BAB03065.1; -.
DR InterPro; IPR004330; FARI.
DR InterPro; IPR001000; Glyco_hydro_10.
DR Pfam; PF03101; FARI; 1.
DR PROSITE; PS00591; GLYCOSYL-HYDROL_F10; UNKNOWN_1.
SQ SEQUENCE 839 AA; 95996 MW; CBBF60DF8B6797F8 CRC64;

Query Match 78.2% Score 43; DB 10; Length 839;
Best Local Similarity 87.5%; Pred. No. 5.1;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 ARHNYGSF 8
Db 274 SRHNYGSF 281

RESULT 2
Q9GJNO Q9GJNO PRELIMINARY; PRT; 276 AA.
AC Q9GJNO;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II beta chain.
GN HClIBETA.
OS Caiman crocodilus (Spectacled caiman) (Caiman sclerops).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Crocodylidae; Alligatorinae; Caiman.
OX NCBI_TaxID=8499;
RN [1]
RP SEQUENCE FROM N.A.
RA Voldby J., Vitved L., Due M., Gronlund J., Holmskov U., Teisner B.,
RA Salomonsen J., Brugaard K., Skjodt K.;
RT "Cloning, sequence and genomic structure of MHC class II antigens from
RT the spectacled caiman, Caiman crocodilus.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF256651; AAF99283.1; -.
DR HSSP; P13760; 2SEB.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR000353; MHC_II_beta.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00969; MHC_II_beta; 1.
DR ProDom; PD000328; MHC_II_beta; 1.
DR SMART; SM00407; IGL; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Glycoprotein; MHC II; Transmembrane.
SQ SEQUENCE 276 AA; 30366 MW; EA8A4684986A6A6A CRC64;

Query Match 72.7%; Score 40; DB 7; Length 276;
Best Local Similarity 87.5%; Pred. No. 5.7; Mismatches 1; Indels 0; Gaps 0;
Matches 7; Conservative 0;

Qy 2 RHNYSGSA 9
Db 108 RHNYSGSA 115

RESULT 3
O62086 O62086 PRELIMINARY; PRT; 446 AA.
AC O62086;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE C31H5.6 protein.
GN C31H5.6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Kershaw J.K.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE-99069613; PubMed=9851916;
RT none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology.";
RT Science 282:2012-2018(1998).
DR EMBL; Z93778; CAB07846.1; -.
DR InterPro; IPR000379; Ser_estrs_site.

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SQ SEQUENCE 446 AA; 50763 MW; 82AD969CDAD753DE CRC64;

Query Match 70.9%; Score 39; DB 5; Length 446;
Best Local Similarity 87.5%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYSGSA 9
Db 51 RHNYSGSA 58

RESULT 4
O19495 O19495 PRELIMINARY; PRT; 89 AA.
AC O19495;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II beta 1 domain (fragment).
GN B-LBI.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=15.151-5; TISSUE=BURSA;
RC MEDLINE-98179131; PubMed=9510552;
RA Pharr G.T., Dodgson J.B., Hunt H.D., Bacon L.D.;
RT "Class II MHC cDNAs in 1515 B-congenic chickens.";
RL Immunogenetics 47:350-354(1998).
DR EMBL; U91532; AAC15813.1; -.
DR InterPro; IPR000353; MHC_II_beta.
DR Pfam; PF00969; MHC_II_beta; 1.
DR ProDom; PD000328; MHC_II_beta; 1.
KW Glycoprotein; MHC II; Transmembrane.
FT NON_TER 1
FT NON_TER 89
SQ SEQUENCE 89 AA; 10724 MW; BC7D558B6AEB1379 CRC64;

Query Match 69.1%; Score 38; DB 7; Length 89;
Best Local Similarity 85.7%; Pred. No. 3.9;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYSGF 8
Db 75 RHNYSGF 81

RESULT 5
Q8TA74 Q8TA74 PRELIMINARY; PRT; 5317 AA.
AC Q8TA74;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Ryanodine receptor.
OS Hemiacetrotus pulcherrimus (Sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Echinacea; Echinozoa; Strongylocentrotidae;
OC Hemiacetrotus.
OX NCBI_TaxID=7650;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-21821894; PubMed=11832393;
RA Shiwa M., Murayama T., Ogawa Y.;
RT "Molecular cloning and characterization of ryanodine receptor from
RT unfertilized sea urchin eggs.";
RT Am. J. Physiol. Regul. Integr. Comp. Physiol. 282:R727-R737(2002).
DR EMBL; AB051576; BAB84714.1; -.
KW Receptor.
SQ SEQUENCE 5317 AA; 597209 MW; 2FA8A1D8CBE28A78 CRC64;

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Query Match          67.3%; Score 37; DB 5; Length 5317;
Best Local Similarity 85.7%; Pred. No. 6.9e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGS 7
Db 3329 ARHNYGA 3335

RESULT 6
P79474
ID P79474 PRELIMINARY; PRT; 39 AA.
AC P79474;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MHC class II DRB (Fragment).
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervioidea;
OC Cervidae; Cervinae; Cervus.
OX NCBI_TaxID=9860;
RN [1]
RP SEQUENCE FROM N.A.
RA Swarbrick P.A., Crawford A.M.;
RT "The MHC class II DRB intron 2 microsatellite of red deer.";
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U63077; AAB3777.1; -.
DR InterPro; IPR000353; MHC_II_beta.
DR Pfam; PF00969; MHC_II_beta; 1.
DR ProDom; PD000328; MHC_II_beta; 1.
KW Glycoprotein; MHC II; Transmembrane.
FT NON_TER 1
FT NON_TER 39
SQ SEQUENCE 39 AA; 4767 MW; CAF3680999733DID CRC64;

Query Match          65.5%; Score 36; DB 7; Length 39;
Best Local Similarity 85.7%; Pred. No. 3.9;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 25 RHNYGVF 31

RESULT 7
P79477
ID P79477 PRELIMINARY; PRT; 39 AA.
AC P79477;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MHC class II DRB (Fragment).
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervioidea;
OC Cervidae; Cervinae; Cervus.
OX NCBI_TaxID=9860;
RN [1]
RP SEQUENCE FROM N.A.
RA Swarbrick P.A., Crawford A.M.;
RT "The MHC class II DRB intron 2 microsatellite of red deer.";
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U63080; AAB37780.1; -.
DR InterPro; IPR000353; MHC_II_beta.
DR Pfam; PF00969; MHC_II_beta; 1.
DR ProDom; PD000328; MHC_II_beta; 1.
KW Glycoprotein; MHC II; Transmembrane.
FT NON_TER 1
FT NON_TER 39
SQ SEQUENCE 39 AA; 4806 MW; C2188A16752A3C1D CRC64;

Query Match          65.5%; Score 36; DB 7; Length 39;
Best Local Similarity 85.7%; Pred. No. 3.9;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 25 RHNYGVF 31

RESULT 8
P79478
ID P79478 PRELIMINARY; PRT; 39 AA.
AC P79478;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MHC class II DRB (Fragment).
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervioidea;
OC Cervidae; Cervinae; Cervus.
OX NCBI_TaxID=9860;
RN [1]
RP SEQUENCE FROM N.A.
RA Swarbrick P.A., Crawford A.M.;
RT "The MHC class II DRB intron 2 microsatellite of red deer.";
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U63081; AAB37781.1; -.
DR InterPro; IPR000353; MHC_II_beta.
DR Pfam; PF00969; MHC_II_beta; 1.
DR ProDom; PD000328; MHC_II_beta; 1.
KW Glycoprotein; MHC II; Transmembrane.
FT NON_TER 1
FT NON_TER 39
SQ SEQUENCE 39 AA; 4806 MW; C2188A16752A3C1D CRC64;

Query Match          65.5%; Score 36; DB 7; Length 39;
Best Local Similarity 85.7%; Pred. No. 3.9;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 25 RHNYGVF 31

RESULT 9
P79479
ID P79479 PRELIMINARY; PRT; 39 AA.
AC P79479;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MHC class II DRB (Fragment).
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervioidea;
OC Cervidae; Cervinae; Cervus.
OX NCBI_TaxID=9860;
RN [1]
RP SEQUENCE FROM N.A.
RA Swarbrick P.A., Crawford A.M.;
RT "The MHC class II DRB intron 2 microsatellite of red deer.";
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U63082; AAB37782.1; -.
DR InterPro; IPR000353; MHC_II_beta.
DR Pfam; PF00969; MHC_II_beta; 1.
DR ProDom; PD000328; MHC_II_beta; 1.
KW Glycoprotein; MHC II; Transmembrane.
FT NON_TER 1
FT NON_TER 39
SQ SEQUENCE 39 AA; 4806 MW; C2188A16752A3C1D CRC64;

Query Match          65.5%; Score 36; DB 7; Length 39;
Best Local Similarity 85.7%; Pred. No. 3.9;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 25 RHNYGVF 31
```

Best Local Similarity 85.7%; Pred. No. 3.9;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
|||||
Db 25 RHNYGVF 31

RESULT 10

Q8SP02 PRELIMINARY; PRT; 67 AA.
AC Q8SP02; (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DE MHC class II antigen (Fragment).
GN HGG-DRB.
OS Hapalemur griseus griseus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Strepsirrhini; Lemnidae; Hapalemur.
OX NCBI_TaxID=122219;
RN [1]
RP SEQUENCE FROM N.A.
RA Go Y., Satta Y., Kawamoto Y., Rakotoarisoa G., Randrianja A.,
RA Koyama N., Hirai H.;
RT "Mhc-DRB genes evolution in lemurs.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB078220; BAB88434.1; -;
FT NON_TER 1
FT NON_TER 67
SQ SEQUENCE 67 AA; 8083 MW; 559300839F0EFA52 CRC64;

Query Match 65.5%; Score 36; DB 7; Length 67;
Best Local Similarity 85.7%; Pred. No. 7.2;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
|||||
Db 59 RHNYGVF 65

RESULT 11

Q9TTM4 PRELIMINARY; PRT; 74 AA.
AC Q9TTM4;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE MHC(BOLA) class II DR-beta chain (Fragment).
GN BOLA-DRB3.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-JAPANESE BLACK;
RA Takeshima S., Ikegami M., Morita M., Nakai Y., Aida Y.;
RT "Identification of BOLA-DRB3 exon 2 of Japanese black cattle.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB033388; BAA85470.1; -;
DR InterPro; IPR000353; MHC_II_beta.
DR Pfam; PF00969; MHC_II_beta; 1.
DR ProDom; PD000328; MHC_II_beta; 1.
KW Glycoprotein; MHC II; Transmembrane.
FT NON_TER 1
FT NON_TER 74
SQ SEQUENCE 74 AA; 9132 MW; C5834842F0E38BA6 CRC64;

Query Match 65.5%; Score 36; DB 6; Length 74;
Best Local Similarity 85.7%; Pred. No. 8.1;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
|||||
Db 68 RHNYGVF 74

RESULT 12

Q9GIJ5 PRELIMINARY; PRT; 75 AA.
AC Q9GIJ5;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MHC(BOLA) class II DR-beta chain (Fragment).
GN BOLA-DRB3.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-JAPANESE BLACK; TISSUE-PERIPHERAL BLOOD LYMPHOCYTE;
RA Takeshima S., Ikegami M., Saitou N., Morita M., Inoko T., Aida Y.;
RT "Nature and origin of polymorphism in BOLA-DRB3 gene.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB053167; BAB20423.1; -;
DR InterPro; IPR000353; MHC_II_beta.
DR Pfam; PF00969; MHC_II_beta; 1.
DR ProDom; PD000328; MHC_II_beta; 1.
KW Glycoprotein; MHC II; Transmembrane.
FT NON_TER 1
FT NON_TER 75
SQ SEQUENCE 75 AA; 9260 MW; C58310BD57BB7401 CRC64;

Query Match 65.5%; Score 36; DB 7; Length 75;
Best Local Similarity 85.7%; Pred. No. 8.2;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
|||||
Db 69 RHNYGVF 75

RESULT 13

Q9TPC2 PRELIMINARY; PRT; 76 AA.
AC Q9TPC2;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MHC class II antigen (Fragment).
GN MAMU-DRB1.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Saueremann U., Khazand M., Nagy M., Peiberg C.;
RT "Mhc-DQ-DRB-haplotype analysis in the rhesus macaque; evidence for a
RT number of different haplotypes displaying a low allelic
RT polymorphism.";
RL Tissue Antigens 0:0-0(1999).
DR EMBL; AF175315; AAF07040.1; -;
DR HSSP; P13758; 1DLH.
DR InterPro; IPR000353; MHC_II_beta.
DR Pfam; PF00969; MHC_II_beta; 1.
DR ProDom; PD000328; MHC_II_beta; 1.
KW Glycoprotein; MHC II; Transmembrane.
FT NON_TER 1
FT NON_TER 76

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SQ SEQUENCE 76 AA; 9315 MW; 1DC073E1B87A94D0 CRC64;
  Query Match 65.5%; Score 36; DB 7; Length 76;
  Best Local Similarity 85.7%; Pred. No. 8.3;
  Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 67 RHNYGVF 73

RESULT 14
Q9GJ91 PRELIMINARY; PRT; 77 AA.
AC Q9GJ91;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II DR beta chain (Fragment).
GN DRB1.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BREED LATXA;
RX MEDLINE=20456715; PubMed=11003382;
RA Jugo B.M., Vicario A.;
RT "Single-strand conformational polymorphism and sequence polymorphism
of Mhc-DRB in Latxa and Karrantzar sheep: implications for Caprinae
phylogeny.";
RL Immunogenetics 51:887-897(2000).
DR EMBL; AF126432; AAF36441.1; -.
DR InterPro; IPR000353; MHC_II_beta.
DR Pfam; PF00969; MHC_II_beta.1.
DR ProDom; PD000328; MHC_II_beta; 1.
KW Glycoprotein; MHC II; Transmembrane.
FT NON_TER 1
FT NON_TER 77
SQ SEQUENCE 77 AA; 9301 MW; DF90D137E31E2C23 CRC64;

  Query Match 65.5%; Score 36; DB 7; Length 77;
  Best Local Similarity 85.7%; Pred. No. 8.4;
  Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 71 RHNYGVF 77

RESULT 15
Q9GJ90 PRELIMINARY; PRT; 77 AA.
AC Q9GJ90;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II DR beta chain (Fragment).
GN DRB1.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BREED LATXA;
RX MEDLINE=20456715; PubMed=11003382;
RA Jugo B.M., Vicario A.;
RT "Single-strand conformational polymorphism and sequence polymorphism
of Mhc-DRB in Latxa and Karrantzar sheep: implications for Caprinae

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RT phylogeny.";
RL Immunogenetics 51:887-897(2000).
DR EMBL; AF126433; AAF36442.1; -.
DR InterPro; IPR000353; MHC_II_beta.
DR Pfam; PF00969; MHC_II_beta; 1.
DR ProDom; PD000328; MHC_II_beta; 1.
KW Glycoprotein; MHC II; Transmembrane.
FT NON_TER 1
FT NON_TER 77
SQ SEQUENCE 77 AA; 9561 MW; 6AFF8613DC9B4902 CRC64;

  Query Match 65.5%; Score 36; DB 7; Length 77;
  Best Local Similarity 85.7%; Pred. No. 8.4;
  Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 71 RHNYGVF 77

Search completed: November 18, 2002, 17:40:47
Job time : 11.4912 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:21:57 ; Search time 13.8235 Seconds
(without alignments)
96.394 Million cell updates/sec

Title: US-09-016-061-70
Perfect score: 55
Sequence: 1 ARHNYGSFAT 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	55	100.0	10	AAW76025	LM609 grafted anti
2	55	100.0	10	AAW76025	Mutant VH CDR3 pep
3	51	92.7	10	AAW76024	LM609 grafted anti
4	51	92.7	10	AAW76024	Mutant VH CDR3 pep
5	50	90.9	10	AAW76026	LM609 grafted anti
6	50	90.9	10	AAW76027	LM609 grafted anti
7	50	90.9	10	AAW76028	LM609 grafted anti
8	50	90.9	10	AAW76029	LM609 grafted anti
9	50	90.9	10	AAW76030	LM609 grafted anti
10	50	90.9	10	AAW76010	LM609 grafted anti

11	50	90.9	10	22	AAW76025	LM609 grafted anti
12	50	90.9	10	22	AAW76025	Mutant VH CDR3 pep
13	50	90.9	10	22	AAW76025	Mutant VH CDR3 pep
14	50	90.9	10	22	AAW76025	Mutant VH CDR3 pep
15	50	90.9	10	22	AAW76025	Mutant VH CDR3 pep
16	50	90.9	10	22	AAW76025	Mutant VH CDR3 pep
17	50	90.9	117	19	AAW76003	Vitaxin antibody h
18	50	90.9	117	19	AAW76003	LM609 antibody hea
19	50	90.9	117	20	AAW76003	Murine monoclonal
20	50	90.9	117	20	AAW76003	Humanised LM609 an
21	50	90.9	117	22	AAW76003	A heavy chain vari
22	50	90.9	117	22	AAW76003	A heavy chain vari
23	50	90.9	117	22	AAW76003	Vitaxin heavy chai
24	50	90.9	117	22	AAW76003	Antibody LM609 hea
25	50	90.9	118	20	AAW76003	Humanised LM609 an
26	50	90.9	118	20	AAW76003	Humanised LM609 an
27	50	90.9	118	20	AAW76003	Humanised LM609 an
28	50	90.9	118	20	AAW76003	Humanised LM609 an
29	50	90.9	130	20	AAW76003	Murine monoclonal
30	47	85.5	10	19	AAW76021	LM609 grafted anti
31	47	85.5	10	22	AAW76021	Mutant VH CDR3 pep
32	46	83.6	10	19	AAW76037	LM609 grafted anti
33	46	83.6	10	19	AAW76039	LM609 grafted anti
34	46	83.6	10	19	AAW76040	LM609 grafted anti
35	46	83.6	10	19	AAW76022	LM609 grafted anti
36	46	83.6	10	19	AAW76023	LM609 grafted anti
37	46	83.6	10	22	AAW76023	Mutant VH CDR3 pep
38	46	83.6	10	22	AAW76023	Mutant VH CDR3 pep
39	46	83.6	10	22	AAW76023	Multiple mutant VH
40	46	83.6	10	22	AAW76023	Multiple mutant VH
41	46	83.6	10	22	AAW76023	Multiple mutant VH
42	45	81.8	10	19	AAW76020	LM609 grafted anti
43	45	81.8	10	22	AAW76020	Mutant VH CDR3 pep
44	42	76.4	110	20	AAW84099	Vitronectin alpha-
45	42	76.4	117	20	AAW84093	Murine vitronectin

ALIGNMENTS

RESULT 1
AAW76025
ID AAW76025 standard; Protein; 10 AA.
XX
AC AAW76025;
XX
DT 02-NOV-1998 (first entry)
XX
DE LM609 grafted antibody V-H region CDR3 protein fragment #7.
XX
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
XX
OS Mus sp.
XX
PN WO9833919-A2.
XX
PD 06-AUG-1998.
XX
PF 30-JAN-1998; 98WO-US01826.
XX
PR 30-JAN-1997; 97US-0791391.
XX
PA (IXSY-) IXSYS INC.
XX
PI Glaser SM. Huse WD;
XX
DR WPI; 1998-437472/37.
DR N-PSDB; AAW49862.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
PS Claim 62; Page 41; 129pp; English.
XX
CC AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
CC antibodies contain non-murine framework regions so are suitable for use
CC in humans. Enhanced types of LM609 have affinity more than 90 times
CC greater than that of parent the parent antibody.
XX
SQ Sequence 10 AA;
Query Match 100.0%; Score 55; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. NO. 0.0037;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ARHNYGSFAT 10
Db 1 ARHNYGSFAT 10
|||||
RESULT 2
AAB61383
ID AAB61383 standard; peptide; 10 AA.
XX
AC AAB61383;
XX
DT 03-APR-2001 (first entry)
XX
DE Mutant VH CDR3 peptide #6.
XX
XX LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
KW inflammatory; cancer; retina; restenosis; osteoporosis.
XX
XX Unidentified.
OS
XX WO200078815-A1.
PN
XX
PD 28-DEC-2000.
XX
XX 23-JUN-2000; 2000WO-US17454.
XX
XX 24-JUN-1999; 99US-0339922.
PR
XX (MOLE-) APPLIED MOLECULAR EVOLUTION.
PA
XX
PI Huse WD, Wu H;
XX
XX WPI; 2001-050110/06.
DR
XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
XX to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
PT osteoporosis -
XX
PS Disclosure; Page 41; 132pp; English.
XX
XX The present invention relates to enhanced LM609 grafted antibodies
CC exhibiting selective binding affinity to alphavbeta_3 integrin or
CC their functional fragments. The antibodies or their functional
CC fragments can be used in the diagnosis and treatment of
CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory

CC diseases (such as psoriasis and chronic articular rheumatism),
CC disorders associated with inappropriate or inopportune invasion of
CC vessels (such as diabetic retinopathy, neovascular glaucoma and
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
CC diseases (such as macular degeneration), restenosis and
CC osteoporosis.
XX
SQ Sequence 10 AA;
Query Match 100.0%; Score 55; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. NO. 0.0037;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ARHNYGSFAT 10
Db 1 ARHNYGSFAT 10
|||||
RESULT 3
AAW76024
ID AAW76024 standard; Protein; 10 AA.
XX
AC AAW76024;
XX
DT 02-NOV-1998 (first entry)
XX
XX LM609 grafted antibody V-H region CDR3 protein fragment #6.
DE
XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
XX
XX Mus sp.
XX WO9833919-A2.
XX
PD 06-AUG-1998.
XX
PF 30-JAN-1998; 98WO-US01826.
XX
PR 30-JAN-1997; 97US-0791391.
XX
XX (IXSY-) IXSYS INC.
XX
XX Glaser SM, Huse WD;
PI
XX WPI; 1998-437472/37.
DR
XX N-PSDB; AAV49861.
XX
XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
XX
PS Claim 62; Page 41; 129pp; English.
XX
XX AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
CC antibodies contain non-murine framework regions so are suitable for use
CC in humans. Enhanced types of LM609 have affinity more than 90 times
CC greater than that of parent the parent antibody.
XX
SQ Sequence 10 AA;

```

Query Match      92.7%; Score 51; DB 19; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.018;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFAT 10
DB 1 ARHNYGSFAS 10
      |||||
RESULT 4
ID AAB61382 standard; peptide; 10 AA.
XX
AC AAB61382;
XX
DT 03-APR-2001 (first entry)
XX
DE Mutant VH CDR3 peptide #5.
XX
KW LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
KW inflammatory; cancer; retina; restenosis; osteoporosis.
XX
OS Unidentified.
XX
PN WO200078815-A1.
XX
PD 28-DEC-2000.
XX
PF 23-JUN-2000; 2000WO-US17454.
XX
PR 24-JUN-1999; 99US-0339922.
XX
PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX
PI Huse WD, Wu H;
XX
DR WPI; 2001-050110/06.
XX
PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity
PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
PT osteoporosis.
XX
PS Disclosure; Page 41; 132pp; English.
XX
CC The present invention relates to enhanced LM609 grafted antibodies
CC exhibiting selective binding affinity to alphavbeta_3 integrin or
CC their functional fragments. The antibodies or their functional
CC fragments can be used in the diagnosis and treatment of
CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
CC diseases (such as psoriasis and chronic articular rheumatism),
CC disorders associated with inappropriate or inopportune invasion of
CC vessels (such as diabetic retinopathy, neovascular glaucoma and
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
CC diseases (such as macular degeneration), restenosis and
CC osteoporosis.
XX
SQ Sequence 10 AA;

Query Match      92.7%; Score 51; DB 22; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.018;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFAT 10
DB 1 ARHNYGSFAS 10
      |||||
RESULT 5
ID AAW76026 standard; Protein; 10 AA.
XX
AC AAW76026;
XX
DT 02-NOV-1998 (first entry)
XX
DE LM609 grafted antibody V-H region CDR3 protein fragment #8.
XX
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
XX
OS Mus SP.
XX
PN WO9833919-A2.
XX
PD 06-AUG-1998.
XX
PF 30-JAN-1998; 98WO-US01826.
XX
PR 30-JAN-1997; 97US-0791391.
XX
PA (IXSY-) IXSYS INC.
XX
PI Glaser SM, Huse WD;
XX
DR WPI; 1998-437472/37.
XX
DR N-PSDB; AAV49863.
XX
PT Humanised antibody, vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
PS Claim 62; Page 41; 129pp; English.
XX
CC AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
CC antibodies contain non-murine framework regions so are suitable for use
CC in humans. Enhanced types of LM609 have affinity more than 90 times
CC greater than that of parent the parent antibody.
XX
SQ Sequence 10 AA;

Query Match      90.9%; Score 50; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
DB 1 ARHNYGSFA 9
      |||||
RESULT 6
ID AAW76027 standard; Protein; 10 AA.
XX
AC AAW76027;
XX
DT 02-NOV-1998 (first entry)
XX
DE LM609 grafted antibody V-H region CDR3 protein fragment #9.
XX
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;

```

KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.

XX Mus sp.

XX WO9833919-A2.

XX 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

XX (IXSV-) IXSYS INC.

XX Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

XX N-PSDB; AAV49864.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

PS Claim 62; Page 41; 129pp; English.

XX AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
 CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
 CC antibodies contain non-murine framework regions so are suitable for use
 CC in humans. Enhanced types of LM609 have affinity more than 90 times
 CC greater than that of parent the parent antibody.

XX Sequence 10 AA;

Query Match 90.9%; Score 50; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.027;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9

DB 1 ARHNYGSFA 9

RESULT 7

AAW76028

ID AAW76028 standard; Protein; 10 AA.

XX AAW76028;

XX 02-NOV-1998 (first entry)

XX LM609 grafted antibody V-H region CDR3 protein fragment #10.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.

XX Mus sp.

XX WO9833919-A2.

XX 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

XX Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

XX N-PSDB; AAV49865.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

XX Claim 62; Page 41; 129pp; English.

XX AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
 CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
 CC antibodies contain non-murine framework regions so are suitable for use
 CC in humans. Enhanced types of LM609 have affinity more than 90 times
 CC greater than that of parent the parent antibody.

XX Sequence 10 AA;

Query Match 90.9%; Score 50; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.027;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9

DB 1 ARHNYGSFA 9

RESULT 8

AAW76029

ID AAW76029 standard; Protein; 10 AA.

XX AAW76029;

XX 02-NOV-1998 (first entry)

XX LM609 grafted antibody V-H region CDR3 protein fragment #11.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.

XX Mus sp.

XX WO9833919-A2.

XX 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

XX Glaser SM, Huse WD;
 XX WPI; 1998-437472/37.
 DR N-PSDB; AAV49866.
 XX
 XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 XX Claim 62; Page 41; 129pp; English.
 XX
 XX AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
 CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
 CC antibodies contain non-murine framework regions so are suitable for use
 CC in humans. Enhanced types of LM609 have affinity more than 90 times
 CC greater than that of parent the parent antibody.
 XX
 XX Sequence 10 AA;
 SQ
 Query Match 90.9%; Score 50; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.027;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ARHNYGSEA 9
 Db | | | | | | | |
 1 ARHNYGSEA 9
 RESULT 9
 AAW76030
 ID AAW76030 standard; Protein; 10 AA.
 AC AAW76030;
 DT 02-NOV-1998 (first entry)
 XX LM609 grafted antibody V-H region CDR3 protein fragment #12.
 DE
 XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 XX
 OS Mus sp.
 XX
 XX WO9833919-A2.
 XX
 XX 06-AUG-1998.
 XX
 XX 30-JAN-1998; 98WO-US01826.
 XX
 XX 30-JAN-1997; 97US-0791391.
 XX
 XX (IXSY-) IXSYS INC.
 XX
 XX Glaser SM, Huse WD;
 XX WPI; 1998-437472/37.
 DR N-PSDB; AAV49867.
 XX
 XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal

PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 XX Claim 62; Page 41; 129pp; English.
 XX
 XX AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
 CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
 CC antibodies contain non-murine framework regions so are suitable for use
 CC in humans. Enhanced types of LM609 have affinity more than 90 times
 CC greater than that of parent the parent antibody.
 XX
 XX Sequence 10 AA;
 SQ
 Query Match 90.9%; Score 50; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.027;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ARHNYGSEA 9
 Db | | | | | | | |
 1 ARHNYGSEA 9
 RESULT 10
 AAW76010
 ID AAW76010 standard; Protein; 10 AA.
 AC AAW76010;
 DT 02-NOV-1998 (first entry)
 XX LM609 grafted antibody V-H region CDR3 protein fragment #1.
 DE
 XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 XX
 OS Mus sp.
 XX
 XX WO9833919-A2.
 XX
 XX 06-AUG-1998.
 XX
 XX 30-JAN-1998; 98WO-US01826.
 XX
 XX 30-JAN-1997; 97US-0791391.
 XX
 XX (IXSY-) IXSYS INC.
 XX
 XX Glaser SM, Huse WD;
 XX WPI; 1998-437472/37.
 DR N-PSDB; AAV49847.
 XX
 XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 XX Disclosure; Page 40; 129pp; English.
 XX
 XX AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to

CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
 CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
 CC antibodies contain non-murine framework regions so are suitable for use
 CC in humans. Enhanced types of LM609 have affinity more than 90 times
 CC greater than that of parent the parent antibody.

XX Sequence 10 AA;

Query Match 90.9%; Score 50; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.027;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
 DB 1 ARHNYGSFA 9

RESULT 11

AAB61368
 ID AAB61368 standard; peptide; 10 AA.

XX

AC AAB61368;

DT 03-APR-2001 (first entry)

DE LM609 VH CDR3 peptide.

XX LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis.

XX Unidentified.

XX WO200078815-A1.

XX 28-DEC-2000.

XX 23-JUN-2000; 2000WO-US17454.

XX 24-JUN-1999; 99US-0339922.

XX (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX Huse WD, Wu H;

XX WPI; 2001-050110/06.

XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis.

XX Disclosure: Page 39; 132pp; English.

XX The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphavbeta_3 integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.

XX Sequence 10 AA;

Query Match 90.9%; Score 50; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.027;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
 DB 1 ARHNYGSFA 9

RESULT 12

AAB61384
 ID AAB61384 standard; peptide; 10 AA.

XX

AC AAB61384;

DT 03-APR-2001 (first entry)

DE Mutant VH CDR3 peptide #7.

XX LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis.

XX Unidentified.

XX WO200078815-A1.

XX 28-DEC-2000.

XX 23-JUN-2000; 2000WO-US17454.

XX 24-JUN-1999; 99US-0339922.

XX (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX Huse WD, Wu H;

XX WPI; 2001-050110/06.

XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis.

XX Disclosure: Page 41; 132pp; English.

XX The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphavbeta_3 integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.

XX Sequence 10 AA;

Query Match 90.9%; Score 50; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.027;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
 DB 1 ARHNYGSFA 9

RESULT 13

AAB61385
 ID AAB61385 standard; peptide; 10 AA.

XX

AC AAB61385;

DT 03-APR-2001 (first entry)

XX DE Mutant VH CDR3 peptide #8.
 XX LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis.
 XX Unidentified.
 XX WO200078815-A1.
 XX 28-DEC-2000.
 XX 23-JUN-2000; 2000WO-US17454.
 XX 24-JUN-1999; 99US-0339922.
 XX (MOLE-) APPLIED MOLECULAR EVOLUTION.
 XX Huse WD, Wu H;
 XX WPI; 2001-050110/06.
 XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -
 XX Disclosure; Page 41; 132pp; English.
 XX The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphavbeta_3 integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis -
 XX Sequence 10 AA;
 PS Query Match 90.9%; Score 50; DB 22; Length 10;
 XX Best Local Similarity 100.0%; Pred. No. 0.027;
 XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ARHNYGSFA 9
 Db | | | | | | | | | |
 Db 1 ARHNYGSFA 9
 RESULT 14
 AAB61386
 ID AAB61386 standard; peptide; 10 AA.
 XX AC AAB61386;
 XX 03-APR-2001 (first entry)
 XX Mutant VH CDR3 peptide #9.
 DE LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
 XX inflammatory; cancer; retina; restenosis; osteoporosis.
 XX Unidentified.
 XX WO200078815-A1.
 XX 28-DEC-2000.
 XX 23-JUN-2000; 2000WO-US17454.

XX 24-JUN-1999; 99US-0339922.
 XX (MOLE-) APPLIED MOLECULAR EVOLUTION.
 XX Huse WD, Wu H;
 XX WPI; 2001-050110/06.
 XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -
 XX Disclosure; Page 41; 132pp; English.
 XX The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphavbeta_3 integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis -
 XX Sequence 10 AA;
 PS Query Match 90.9%; Score 50; DB 22; Length 10;
 XX Best Local Similarity 100.0%; Pred. No. 0.027;
 XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ARHNYGSFA 9
 Db | | | | | | | | | |
 Db 1 ARHNYGSFA 9
 RESULT 15
 AAB61387
 ID AAB61387 standard; peptide; 10 AA.
 XX AC AAB61387;
 XX 03-APR-2001 (first entry)
 XX Mutant VH CDR3 peptide #10.
 DE LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis.
 XX Unidentified.
 XX WO200078815-A1.
 XX 28-DEC-2000.
 XX 23-JUN-2000; 2000WO-US17454.
 XX 24-JUN-1999; 99US-0339922.
 XX (MOLE-) APPLIED MOLECULAR EVOLUTION.
 XX Huse WD, Wu H;
 XX WPI; 2001-050110/06.
 XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -
 XX Disclosure; Page 41; 132pp; English.
 PS

XX The present invention relates to enhanced LM609 grafted antibodies
CC exhibiting selective binding affinity to alphaVbeta₃ integrin or
CC their functional fragments. The antibodies or their functional
CC fragments can be used in the diagnosis and treatment of
CC alphaVbeta₃-mediated diseases such as angiogenesis, inflammatory
CC diseases (such as psoriasis and chronic articular rheumatism),
CC disorders associated with inappropriate or inopportune invasion of
CC vessels (such as diabetic retinopathy, neovascular glaucoma and
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
CC diseases (such as macular degeneration), restenosis and
CC osteoporosis.

XX
SQ Sequence 10 AA;

Query Match 90.9%; Score 50; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
| | | | | | | | | |
Db 1 ARHNYGSFA 9

Search completed: November 18, 2002, 17:31:38
Job time : 14.8235 secs

GenCore version 5.1.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:54:45 ; Search time 1.96078 Seconds
(without alignments)
76.811 Million cell updates/sec

Title: US-09-016-061-70

Perfect score: 55

Sequence: 1 ARHNGVSFAT 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 97044 seqs, 15060890 residues

Total number of hits satisfying chosen parameters: 97044

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

- 1: /cgn2_6/ptodata/1/pubpaa/us08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/us06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/us06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/us07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/us07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/us08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/us09_NEW_PUB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/us09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/us10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/us10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/us60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/us60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	50	90.9	117	8	US-08-790-540A-2
2	50	90.9	117	8	US-08-790-540A-6
3	50	90.9	117	8	US-08-791-391A-2
4	50	90.9	117	8	US-08-791-391A-6
5	36	65.5	14	1	US-08-677-599B-22
6	36	65.5	101	10	US-09-764-853-432
7	34	61.8	30	10	US-09-839-884-40
8	34	61.8	287	10	US-09-415-540-5
9	34	61.8	505	10	US-09-888-243-5
10	33	60.0	14	1	US-08-677-599B-21
11	33	60.0	512	10	US-09-815-242-11232
12	32	58.2	14	1	US-08-677-599B-11
13	32	58.2	14	1	US-08-677-599B-12
14	32	58.2	14	1	US-08-677-599B-13
15	32	58.2	14	1	US-08-677-599B-14
16	32	58.2	14	1	US-08-677-599B-15
17	32	58.2	14	1	US-08-677-599B-16
18	32	58.2	14	1	US-08-677-599B-17
19	32	58.2	14	1	US-08-677-599B-18

20	32	58.2	14	1	US-08-677-599B-19
21	32	58.2	14	1	US-08-677-599B-20
22	32	58.2	14	1	US-08-677-599B-23
23	32	58.2	15	10	US-09-756-998B-11
24	32	58.2	25	1	US-08-677-599B-8
25	32	58.2	93	12	US-10-081-281-121
26	32	58.2	94	10	US-09-766-378A-37
27	32	58.2	181	10	US-09-815-837-103
28	32	58.2	183	10	US-09-815-837-16
29	32	58.2	184	10	US-09-815-837-15
30	32	58.2	185	10	US-09-815-837-13
31	32	58.2	185	10	US-09-815-837-14
32	32	58.2	186	10	US-09-815-837-17
33	32	58.2	186	10	US-09-815-837-19
34	32	58.2	186	10	US-09-815-837-20
35	32	58.2	187	10	US-09-815-837-18
36	32	58.2	189	10	US-09-815-837-21
37	32	58.2	189	10	US-09-815-837-22
38	32	58.2	193	10	US-09-815-837-23
39	32	58.2	193	10	US-09-815-837-24
40	32	58.2	196	10	US-09-741-669-368
41	32	58.2	196	10	US-09-912-020-376
42	32	58.2	199	10	US-09-815-837-56
43	32	58.2	199	10	US-09-815-837-60
44	32	58.2	207	12	US-10-081-281-93
45	32	58.2	208	10	US-09-815-837-102

ALIGNMENTS

RESULT 1

US-08-790-540A-2
; Sequence 2, Application US/08790540A
; Patent No. US20010011125A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08790, 540A
; APPLICATION NUMBER: US/08790, 540A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-790-540A-2

Query Match 90.9%; Score 50; DB 8; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.0071;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
|||||

Db 97 ARHNYGSFA 105

RESULT 2
US-08-790-540A-6
; Sequence 6, Application US/08790540A
; Patent No. US2001001125A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TELEPHONE: (619) 535-9001
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,540A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-790-540A-6

Query Match 90.9%; Score 50; DB 8; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.0071;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
|||||

Db 97 ARHNYGSFA 105

RESULT 3
US-08-791-391A-2
; Sequence 2, Application US/08791391A
; Patent No. US20010016645A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TELEPHONE: (619) 535-9001
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,391A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-391A-2

Query Match 90.9%; Score 50; DB 8; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.0071;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
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Db 97 ARHNYGSFA 105

RESULT 4
US-08-791-391A-6
; Sequence 6, Application US/08791391A
; Patent No. US20010016645A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TELEPHONE: (619) 535-9001
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,391A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-391A-6

Query Match 90.9%; Score 50; DB 8; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.0071;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSA 9
Db 97 ARHNYGSA 105
|||||

RESULT 5

US-08-677-599B-22
; Sequence 22, Application US/08677599B
; Patent No. US20020155117A1
; GENERAL INFORMATION:
; APPLICANT: Sucia-Foca, Nicole
; TITLE OF INVENTION: METHODS FOR DETECTING ORGAN ALLOGRAFT
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/677,599B
; FILING DATE: 08-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq., John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 50161-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212/278/0400
; TELEFAX: 212/391/0525
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-677-599B-22

Query Match 65.5%; Score 36; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYG 6
Db 9 ARHNYG 14
|||||

RESULT 6

US-09-764-853-432
; Sequence 432, Application US/09764853
; Patent No. US20020090672A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJ206
; CURRENT APPLICATION NUMBER: US/09/764,853
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 939
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 432
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-853-432

Query Match 65.5%; Score 36; DB 10; Length 101;
Best Local Similarity 85.7%; Pred. No. 2.7;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYSF 8
Db 64 RHNYSF 70
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RESULT 7

US-09-839-884-40
; Sequence 40, Application US/09839884
; Patent No. US20020076739A1
; GENERAL INFORMATION:
; APPLICANT: Aebersold, Rudolf H.
; APPLICANT: Gelb, Michael H.
; APPLICANT: Gygi, Steven
; APPLICANT: Scott, C R
; APPLICANT: Turecek, Frantisek
; APPLICANT: Gerber, Scott A
; APPLICANT: Rist, Beate
; TITLE OF INVENTION: Rapid Quantitative Analysis of Proteins or Protein
; FILE REFERENCE: 64-98A
; CURRENT APPLICATION NUMBER: US/09/839,884
; CURRENT FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: 09/383,062
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 60/097,788
; PRIOR FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40
; LENGTH: 30
; TYPE: PRT
; ORGANISM: yeast
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (2)
; OTHER INFORMATION: C at position 2 is ICAT-labeled cysteinyl residue.
US-09-839-884-40

Query Match 61.8%; Score 34; DB 10; Length 30;
Best Local Similarity 83.3%; Pred. No. 1.8;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
Db 10 HNYGAF 15
|||||

RESULT 8

US-09-415-540-5
; Sequence 5, Application US/09415540
; Patent No. US20010010911A1
; GENERAL INFORMATION:
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: A NOVEL HUMAN PYROPHOSPHATASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/415,540
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/741,437
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0148 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 855-0555
TELEFAX: (415) 845-4166
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 287 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 4199
US-09-415-540-5

Query Match 61.8%; Score 34; DB 10; Length 287;
Best Local Similarity 83.3%; Pred. No. 19;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSP 8
DB 92 HNYGAF 97

RESULT 9
US-09-888-243-5
Sequence 5, Application US/09888243
Patent No. US20020136714A1
GENERAL INFORMATION:
APPLICANT: Yuan, Junying
APPLICANT: Shaham, Shai
TITLE OF INVENTION: Relatedness of Human Interleukin-1beta
TITLE OF INVENTION: Convertase Gene to a C. Elegans Cell Death Gene, Inhibitory
TITLE OF INVENTION: Portions of these Genes and Uses Therefor
FILE REFERENCE: 01997/211003
CURRENT APPLICATION NUMBER: US/09/888,243
CURRENT FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: US 09/083,662
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: US 08/394,189
PRIOR FILING DATE: 1995-02-24
PRIOR APPLICATION NUMBER: US 08/282,211
PRIOR FILING DATE: 1994-07-11
PRIOR APPLICATION NUMBER: US 07/984,182
PRIOR FILING DATE: 1992-11-20
PRIOR APPLICATION NUMBER: US 07/897,788
PRIOR FILING DATE: 1992-06-12
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 505
TYPE: PRT
ORGANISM: Caenorhabditis briggsae
FEATURES:
NAME/KEY: VARIANT
LOCATION: 94, 95, 96, 120, 179, 318
OTHER INFORMATION: Xaa = Any Amino Acid

US-09-888-243-5

Query Match 61.8%; Score 34; DB 10; Length 505;
Best Local Similarity 77.8%; Pred. No. 34;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSPAT 10
DB 164 RHNYMSAAT 172

RESULT 10
US-08-677-599B-21
Sequence 21, Application US/08677599B
Patent No. US20020155117A1
GENERAL INFORMATION:
APPLICANT: Sucia-Poca, Nicole
TITLE OF INVENTION: METHODS FOR DETECTING ORGAN ALLOGRAFT
TITLE OF INVENTION: REJECTION AND USES THEREOF
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/677,599B
FILING DATE: 08-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White Esq., John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 50161-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212/278/0400
TELEFAX: 212/391/0525
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-677-599B-21

Query Match 60.0%; Score 33; DB 1; Length 14;
Best Local Similarity 83.3%; Pred. No. 1.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYG 6
DB 9 SRHNYG 14

RESULT 11
US-09-815-242-11232
Sequence 11232, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.

APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 1410
SOFTWARE: FASCSQ for Windows Version 4.0
SEQ ID NO 11232
LENGTH: 512
TYPE: PRT
ORGANISM: Haemophilus influenzae
US-09-815-242-11232

Query Match 60.0%; Score 33; DB 10; Length 512;
Best Local Similarity 60.0%; Pred. No. 53;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARNYGSFAT 10
| | | | |
DB 145 AAHEFGSFFT 154

RESULT 12
US-08-677-599B-11
Sequence 11, Application US/08677599B
Patent No. US20020155117A1
GENERAL INFORMATION:
APPLICANT: Sucia-Foca, Nicole
TITLE OF INVENTION: METHODS FOR DETECTING ORGAN ALLOGRAFT
FILE OF INVENTION: REJECTION AND USES THEREOF
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/677,599B
FILING DATE: 08-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White Esq., John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 50161-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212/278/0400
TELEFAX: 212/391/0525
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-677-599B-11

Query Match 58.2%; Score 32; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHYNG 6
| | | | |
DB 10 RHYNG 14

RESULT 13
US-08-677-599B-12
Sequence 12, Application US/08677599B
Patent No. US20020155117A1
GENERAL INFORMATION:
APPLICANT: Sucia-Foca, Nicole
TITLE OF INVENTION: METHODS FOR DETECTING ORGAN ALLOGRAFT
FILE OF INVENTION: REJECTION AND USES THEREOF
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/677,599B
FILING DATE: 08-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White Esq., John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 50161-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212/278/0400
TELEFAX: 212/391/0525
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-677-599B-12

Query Match 58.2%; Score 32; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHYNG 6
| | | | |
DB 10 RHYNG 14

RESULT 14
US-08-677-599B-13
Sequence 13, Application US/08677599B
Patent No. US20020155117A1
GENERAL INFORMATION:
APPLICANT: Sucia-Foca, Nicole
TITLE OF INVENTION: METHODS FOR DETECTING ORGAN ALLOGRAFT
FILE OF INVENTION: REJECTION AND USES THEREOF
NUMBER OF SEQUENCES: 23

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/677,599B
; FILING DATE: 08-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq., John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 50161-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212/278/0400
; TELEFAX: 212/391/0525
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-677-599B-13

Query Match 58.2%; Score 32; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHNYG 6
Db 10 RHNYG 14

RESULT 15
US-08-677-599B-14
; Sequence 14, Application US/08677599B
; Patent No. US2002015117A1
; GENERAL INFORMATION:
; APPLICANT: Sucia-Foca, Nicole
; TITLE OF INVENTION: METHODS FOR DETECTING ORGAN ALLOGRAFT
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/677,599B
; FILING DATE: 08-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq., John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 50161-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212/278/0400
; TELEFAX: 212/391/0525

; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-677-599B-14

Query Match 58.2%; Score 32; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHNYG 6
Db 10 RHNYG 14

Search completed: November 18, 2002, 18:45:16
Job time : 1.96078 secs

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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:01 ; Search time 4.2402 seconds
(without alignments)
69.390 Million cell updates/sec

Title: US-09-016-061-70

Perfect score: 55

Sequence: 1 ARHNYGSPAT 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents.AA.*

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2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep.*
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4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	65.5	94	3 US-09-147-550-14	Sequence 14, Appl
2	36	65.5	94	3 US-09-147-550-45	Sequence 45, Appl
3	36	65.5	94	3 US-09-147-550-48	Sequence 48, Appl
4	36	65.5	94	3 US-09-147-550-77	Sequence 77, Appl
5	36	65.5	94	3 US-09-147-550-84	Sequence 84, Appl
6	36	65.5	94	3 US-09-147-550-90	Sequence 90, Appl
7	36	65.5	94	3 US-09-147-550-101	Sequence 101, Appl
8	36	65.5	94	4 US-09-557-917-14	Sequence 14, Appl
9	36	65.5	94	4 US-09-557-917-45	Sequence 45, Appl
10	36	65.5	94	4 US-09-557-917-48	Sequence 48, Appl
11	36	65.5	94	4 US-09-557-917-77	Sequence 77, Appl
12	36	65.5	94	4 US-09-557-917-84	Sequence 84, Appl
13	36	65.5	94	4 US-09-557-917-90	Sequence 90, Appl
14	36	65.5	94	4 US-09-557-917-101	Sequence 101, Appl
15	36	65.5	119	3 US-08-767-128-6	Sequence 6, Appl
16	34	61.8	191	4 US-09-443-041A-20	Sequence 24, Appl
17	34	61.8	236	4 US-09-443-041A-30	Sequence 30, Appl
18	34	61.8	260	4 US-09-443-041A-10	Sequence 10, Appl
19	34	61.8	261	4 US-09-443-041A-26	Sequence 26, Appl
20	34	61.8	269	4 US-09-443-041A-28	Sequence 28, Appl
21	34	61.8	271	4 US-09-443-041A-32	Sequence 32, Appl
22	34	61.8	271	4 US-09-443-041A-33	Sequence 33, Appl
23	34	61.8	286	2 US-08-809-267-3	Sequence 3, Appl
24	34	61.8	286	5 PCT-US95-13662A-3	Sequence 3, Appl
25	34	61.8	287	2 US-08-741-437-5	Sequence 5, Appl
26	34	61.8	287	2 US-09-134-593-5	Sequence 5, Appl
27	34	61.8	503	3 US-08-258-287B-36	Sequence 36, Appl

Sequence 36, Appl
Sequence 5, Appl
Sequence 20, Appl
Sequence 5, Appl
Sequence 7, Appl
Sequence 2, Appl
Sequence 44, Appl
Sequence 44, Appl
Sequence 44, Appl
Sequence 84, Appl
Sequence 84, Appl
Sequence 84, Appl
Sequence 84, Appl
Sequence 84, Appl
Sequence 281, App
Sequence 129, App
Sequence 84, Appl

ALIGNMENTS

RESULT 1

US-09-147-550-14
; Sequence 14, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-777979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-14

Query Match 65.5%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 80 RHNYGVF 86

RESULT 2

US-09-147-550-45
; Sequence 45, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-777979

; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-45

Query Match 65.5%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
|||||
DB 80 RHNYGVF 86

RESULT 3

; Sequence 48, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-48

Query Match 65.5%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
|||||
DB 80 RHNYGVF 86

RESULT 4

; Sequence 77, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 77
; LENGTH: 94

; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-77

Query Match 65.5%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
|||||
DB 80 RHNYGVF 86

RESULT 5

; Sequence 84, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-84

Query Match 65.5%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
|||||
DB 80 RHNYGVF 86

RESULT 6

; Sequence 90, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 90
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-90

Query Match 65.5%; Score 36; DB 3; Length 94;

Best Local Similarity 85.7%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 80 RHNYGVF 86

RESULT 7

US-09-147-550-101
; Sequence 101, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 101
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-101

Query Match 65.5%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 80 RHNYGVF 86

RESULT 8

US-09-557-917-14
; Sequence 14, Application US/09557917
; Patent No. 6284457
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 14
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-14

Query Match 65.5%; Score 36; DB 4; Length 94;
Best Local Similarity 85.7%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8

QY 2 RHNYGSF 8
Db 80 RHNYGVF 86

RESULT 9

US-09-557-917-45
; Sequence 45, Application US/09557917
; Patent No. 6284457
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 45
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-45

Query Match 65.5%; Score 36; DB 4; Length 94;
Best Local Similarity 85.7%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 80 RHNYGVF 86

RESULT 10

US-09-557-917-48
; Sequence 48, Application US/09557917
; Patent No. 6284457
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 48
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-48

Query Match 65.5%; Score 36; DB 4; Length 94;
Best Local Similarity 85.7%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8


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Db      80 RHNYGVF 86
||||| I
RESULT 11
US-09-557-917-77
; Sequence 77, Application US/09557917
; Patent No. 6284457
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 77
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-77
Query Match      65.5%; Score 36; DB 4; Length 94;
Best Local Similarity 85.7%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

QY      2 RHNYGSF 8
||||| I
Db      80 RHNYGVF 86

RESULT 12
US-09-557-917-84
; Sequence 84, Application US/09557917
; Patent No. 6284457
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-84
Query Match      65.5%; Score 36; DB 4; Length 94;
Best Local Similarity 85.7%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

QY      2 RHNYGSF 8
||||| I
Db      80 RHNYGVF 86

RESULT 13
US-09-557-917-90
; Sequence 90, Application US/09557917
; Patent No. 6284457
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 90
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-90
Query Match      65.5%; Score 36; DB 4; Length 94;
Best Local Similarity 85.7%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 RHNYGSF 8
||||| I
Db      80 RHNYGVF 86

RESULT 14
US-09-557-917-101
; Sequence 101, Application US/09557917
; Patent No. 6284457
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-101
Query Match      65.5%; Score 36; DB 4; Length 94;
Best Local Similarity 85.7%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 RHNYGSF 8
||||| I
Db      80 RHNYGVF 86
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Search completed: November 18, 2002, 17:43:37
Job time : 4.2402 secs

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RESULT 15
US-08-767-128-6
; Sequence 6, Application US/08767128
; Patent No. 6111079
; GENERAL INFORMATION:
; APPLICANT: WYLIE, DWANE E.
; APPLICANT: LOPEZ, OSVALDO
; APPLICANT: MURRAY, PETER JOSEPH
; APPLICANT: GOEBEL, PETER
; TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
; TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
; STREET: 3100 No. 6111079 West Center, 90 South Seventh St
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/767,128
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE: 05-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/09258
; FILING DATE: 08/541,373
; APPLICATION NUMBER: 08/541,373
; FILING DATE: 10-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/462,798
; FILING DATE: 05-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G.
; REGISTRATION NUMBER: 35,093
; REFERENCE/DOCKET NUMBER: 8648.49USF1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/371-5278
; TELEFAX: 612/332-9081
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; US-08-767-128-6
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Query Match 65.5%; Score 36; DB 3; Length 119;
Best Local Similarity 66.7%; Pred. No. 19;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSEA 9
Db 97 ARHHGYGA 105
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:01 : Search time 4.90196 Seconds
(without alignments)
196.114 Million cell updates/sec

Title: US-09-016-061-72

Perfect score: 56

Sequence: 1 ARHNYGSEFAD 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR:73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	40	71.4	210	1 B69265	conserved hypother
2	39	69.6	446	2 T19625	hypothetical prote
3	38	67.9	464	2 B70828	hypothetical prote
4	37	66.1	275	2 T04480	acyl-CoA oxidase h
5	36	64.3	82	2 I51106	Major Histocompati
6	36	64.3	89	2 S38688	MHC class II histo
7	36	64.3	89	2 S38683	MHC class II histo
8	36	64.3	89	2 S38684	MHC class II histo
9	36	64.3	225	2 I47095	MHC class II OVAR-
10	36	64.3	581	1 A37913	serine/threonine-s
11	36	64.3	645	2 AE2655	conserved hypother
12	36	64.3	672	2 A97437	hypothetical 71.3K
13	36	64.3	684	2 G84730	Mutator-like trans
14	36	64.3	723	2 F83173	outer membrane pro
15	36	64.3	731	1 JC2464	probable copper-tr
16	35	62.5	195	2 G86742	conserved hypother
17	35	62.5	232	2 G69080	conserved hypother
18	35	62.5	243	2 D72098	serine esterase, p
19	35	62.5	243	2 G86524	lysophospholipase
20	35	62.5	275	2 G75130	translation initia
21	35	62.5	275	2 D71087	probable translati
22	35	62.5	347	2 A34771	phosphatidylcholin
23	35	62.5	374	2 A83761	hypothetical prote
24	35	62.5	520	2 S78502	paired box transcr
25	35	62.5	538	2 T28874	hypothetical prote
26	35	62.5	682	2 JQ0420	beta-1,3-glucanase
27	35	62.5	743	2 T15062	hypothetical prote
28	34	60.7	108	2 S26316	Ig heavy chain v r
29	34	60.7	110	2 S26317	Ig heavy chain v r

30	34	60.7	218	2 E97915	choline binding pr
31	34	60.7	285	2 C95045	choline binding pr
32	34	60.7	287	1 PWB1	inorganic diphosph
33	34	60.7	287	1 PWB1	inorganic diphosph
34	34	60.7	309	2 AD0502	homoserine kinase
35	34	60.7	309	2 T41494	zinc finger, ADP-r
36	34	60.7	372	2 T51082	hypothetical prote
37	34	60.7	407	2 H71857	pyruvate ferredoxi
38	34	60.7	407	2 F64658	pyruvate synthase
39	34	60.7	442	2 G69264	conserved hypother
40	34	60.7	453	2 A05139	serum albumin - mo
41	34	60.7	514	2 T10559	hypothetical prote
42	34	60.7	654	2 AG3522	iron-regulated out
43	34	60.7	753	2 AH0097	probable biotin su
44	34	60.7	1052	2 AF2959	conserved hypother
45	34	60.7	1263	2 T00649	hypothetical prote

ALIGNMENTS

RESULT 1

B69265
conserved hypothetical protein AF0122 - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C:Accession: B69265
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes,
Smith, H.O.; Woese, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch
A:Reference number: A69250; MUID:98049343; PMID:9389475
A:Accession: B69265
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-210 <KLE>
A:Cross-references: GB:AE001098; GB:AE000782; NID:g2689421; PIDN:AAB91117.1; PID:g265
C:Superfamily: conserved hypothetical protein AF0119

Query Match 71.4%; Score 40; DB 1; Length 210;
Best Local Similarity 77.8%; Pred. No. 4;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RHNYGSEAD 10
||| ||| |
Db 128 RHAYGSFVD 136

RESULT 2

T19625

hypothetical protein C31H5.6 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000

C:Accession: T19625

R:Kershaw, J.

submitted to the EMBL Data Library, April 1997

A:Reference number: Z19153

A:Accession: T19625

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-446 <WIL>

A:Cross-references: EMBL:Z93778; PIDN:CAB07846.1; GSPDB:GN00019; CESP:C31H5.6

A:Experimental source: clone C31H5

C:Genetics:

A:Gene: CESP-C31H5.6

A:Map position: 1

A:Introns: 49/2; 85/1; 120/2; 183/3; 218/3; 255/3; 285/2; 331/3; 360/3

C:Superfamily: Caenorhabditis elegans hypothetical protein W03D8.8

Query Match 69.6%; Score 39; DB 2; Length 446;

Best Local Similarity 87.5%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSFA 9
|||||
Db 51 RHNYGSHA 58

RESULT 3
B70828
hypothetical protein RV0462 - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 03-Nov-2000
C:Accession: B70828
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: B70828
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-464 <COL>
A:Cross-references: GB:AL021933; GB:AL123456; NID:g3261529; PIDN:CAA17417.1; PID:g290953
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: Rv0462
C:Superfamily: dihydrolipoamide dehydrogenase; dihydrolipoamide dehydrogenase homology
C:Keywords: redox-active disulfide
F:7-450/Domain: dihydrolipoamide dehydrogenase homology <DLD>
F:41-46/Disulfide bonds: redox-active #status predicted

Query Match 67.9%; Score 38; DB 2; Length 464;
Best Local Similarity 75.0%; Pred. No. 21;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 HNYGSFAD 10
|||
Db 110 HGCGTFAD 117

RESULT 4
T04480
acyl-CoA oxidase homolog - barley (fragment)
C:Species: Hordeum vulgare (barley)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 08-Oct-1999
C:Accession: T04480
R:Grossi, M.; Gullii, M.; Stanca, A.M.; Cattivelli, L. Plant Sci. 105, 71-80, 1995
A:Title: Characterization of two barley genes that respond rapidly to dehydration stress
A:Reference number: Z15371
A:Accession: T04480
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-275 <GRO>
A:Cross-references: EMBL:X84055; NID:g642243; PIDN:CAA58874.1; PID:g642244
A:Experimental source: cv. Arda, leaf
C:Genetics:
A:Gene: cdr29

Query Match 66.1%; Score 37; DB 2; Length 275;
Best Local Similarity 70.0%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ARHNYGSFAD 10
|||
Db 1 ANHNSGSFLD 10

RESULT 5
151106

Major Histocompatibility Complex class IIB - ring-necked pheasant (fragment)
C:Species: Phasianus colchicus (ring-necked pheasant)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 23-Jul-1999
C:Accession: I51106
R:Witzell, H.; von Schantz, T.; Zoorob, R.; Auffray, C. Immunogenetics 39, 395-403, 1994
A:Title: Molecular characterization of three Mhc class II B haplotypes in the ring-necked pheasant
A:Reference number: I51103; MUID:94245280; PMID:7910588
A:Accession: I51106
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-82 <WIT>
A:Cross-references: EMBL:X75406; NID:g496926; PIDN:CAA53160.1; PID:g496927
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 64.3%; Score 36; DB 2; Length 82;
Best Local Similarity 85.7%; Pred. No. 9.1;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
|||||
Db 75 RHNYGVF 81

RESULT 6
S38688
MHC class II histocompatibility antigen HLA-DR-08 beta chain - northern lesser bushba
C:Species: Galago senegalensis (northern lesser bushbaby)
C:Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 19-May-2000
C:Accession: S38688
R:Figuerola, F.; O'Huigin, C.; Tichy, H.; Klein, J. submitted to the EMBL Data Library, November 1993
A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduce
A:Reference number: S38676
A:Accession: S38688
A:Molecule type: DNA
A:Residues: 1-89 <FIG>
A:Cross-references: EMBL:Z27158
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 64.3%; Score 36; DB 2; Length 89;
Best Local Similarity 85.7%; Pred. No. 9.8;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
|||||
Db 75 RHNYGVF 81

RESULT 7
S38683
MHC class II histocompatibility antigen HLA-DR-03 beta chain - northern lesser bushba
C:Species: Galago senegalensis (northern lesser bushbaby)
C:Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 19-May-2000
C:Accession: S38683
R:Figuerola, F.; O'Huigin, C.; Tichy, H.; Klein, J. submitted to the EMBL Data Library, November 1993
A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduce
A:Reference number: S38676
A:Accession: S38683
A:Molecule type: DNA
A:Residues: 1-89 <FIG>
A:Cross-references: EMBL:Z27153
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 64.3%; Score 36; DB 2; Length 89;
Best Local Similarity 85.7%; Pred. No. 9.8;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
|||||
Db 75 RHNYGVF 81

```
RESULT 8
S38684
MHC class II histocompatibility antigen HLA-DR-04 beta chain - northern lesser bushbaby
C:Species: Galago senegalensis (northern lesser bushbaby)
C:Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 19-May-2000
C:Accession: S38684
R:Figueroa, F.; O'Huigin, C.; Tichy, H.; Klein, J.
submitted to the EMBL Data Library, November 1993
A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduced f
A:Reference number: S38676
A:Accession: S38684
A:Molecule type: DNA
A:Residues: 1-89 <FIG>
A:Cross-references: EMBL:227154
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 64.3%; Score 36; DB 2; Length 89;
Best Local Similarity 85.7%; Pred. No. 9.8;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
DB 75 RHNYGVF 81

RESULT 9
I47095
MHC class II OVAR-DR-beta-3 - sheep (fragment)
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 15-Oct-1996 #sequence_revision 15-Oct-1996 #text_change 21-Jan-2000
C:Accession: I47095
R:Fabb, S.A.; Maddox, J.F.; Gogolin-Ewens, K.J.; Baker, L.; Wu, M.J.; Brandon, M.R.
Anim. Genet. 24, 249-255, 1993
A:Title: Isolation, characterization and evolution of ovine major histocompatibility com
A:Reference number: I47075; MUID:94057592; PMID:7902039
A:Accession: I47095
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-225 <FAB>
A:Cross-references: GB:L04790; NID:9458880; PIDN:AAA16562.1; PID:9458881
C:Genetics:
A:Gene: OVAR-DRB3
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology
F:98-163/Domain: immunoglobulin homology <IMM>

Query Match 64.3%; Score 36; DB 2; Length 225;
Best Local Similarity 85.7%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
DB 68 RHNYGVF 74

RESULT 10
A37913
serine/threonine-specific protein kinase (EC 2.7.1.-) mkl1 - fission yeast (Schizosaccha
N:Alternate names: mitosis inhibitor protein kinase
C:Species: Schizosaccharomyces pombe
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Dec-1999
C:Accession: A37913; T40626
R:Lundgren, K.; Walworth, N.; Boehr, R.; Dembski, M.; Kirschner, M.; Beach, D.
Cell 64, 1111-1122, 1991
A:Title: mkl1 and weel cooperate in the inhibitory tyrosine phosphorylation of cdc2.
A:Reference number: A37913; MUID:91168259; PMID:1706223
A:Accession: A37913
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-581 <LUN>
A:Cross-references: NID:M60834; NID:q173413; PIDN:AAA91278.1; PID:g1213637
R:Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Rieger, M.
submitted to the EMBL Data Library, December 1998
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A:Reference number: 221941
A:Accession: T40626
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-581 <LYN>
A:Cross-references: EMBL:AL034563; PIDN:CAA22534.1; GSPDB:GN00067; SPDB:SPBC660.14
C:Genetics:
A:Gene: SPBC660.14
A:Map position: 2
A:Introns: 403/3
C:Superfamily: fission yeast mkl1 protein; protein kinase homology
C:Keywords: Atp; phosphotransferase; serine/threonine-specific protein kinase
F:287-558/Domain: protein kinase homology <KIN>

Query Match 64.3%; Score 36; DB 1; Length 581;
Best Local Similarity 70.0%; Pred. No. 63;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARHNYGSFAD 10
DB 463 ASHNYGKPAD 472

RESULT 11
AE2655
conserved hypothetical protein Atu0643 [imported] - Agrobacterium tumefaciens (strain
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
C:Accession: AE2655
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McCl
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; PMID:11743193
A:Accession: AE2655
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-645 <KUR>
A:Cross-references: GB:AE008688; PIDN:AAI41659.1; PID:g17739001; GSPDB:GN00186
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: Atu0643
A:Map position: circular chromosome

Query Match 64.3%; Score 36; DB 2; Length 645;
Best Local Similarity 70.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARHNYGSFAD 10
DB 587 AGSNYGSFGD 596

RESULT 12
A97437
hypothetical 71.3K protein in trpL-btuR intergenic region (orf2/3) [imported] - Agrob
C:Species: Agrobacterium tumefaciens
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
C:Accession: A97437
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldm
; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz,
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium
A:Reference number: A97359; PMID:11743194
A:Accession: A97437
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-672 <KUR>
A:Cross-references: GB:AE007869; PIDN:AAK86450.1; PID:g15155592; GSPDB:GN00169
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C:Genetics:

A:Gene: AGR_C_1142

A:Map position: circular chromosome

Query Match 64.3%; Score 36; DB 2; Length 672;
 Best Local Similarity 70.0%; Pred. No. 73;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARHNYGSFAD 10
 | | | | | | |
 Db 614 AGSNGSFGD 623

RESULT 13

G84730

Mutator-like transposase [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cross)

C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

C:Accession: G84730

R.; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: G84730

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-684 <STO>

A:Cross-references: GB:AE002093; NID:g3831469; PIDN:AAC69951.1; GSPDB:GN00139

C:Genetics:

A:Gene: At2g32250

A:Map position: 2

Query Match 64.3%; Score 36; DB 2; Length 684;
 Best Local Similarity 60.0%; Pred. No. 75;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFAD 10
 | | | | | | |
 Db 209 AKHDYCSFSD 218

RESULT 14

F83173

outer membrane protein OprC PA3790 [imported] - Pseudomonas aeruginosa (strain PA01)

C:Species: Pseudomonas aeruginosa

C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C:Accession: F83173

R.; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Br
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
 .; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho

A:Reference number: A82950; MUID:20437337; PMID:10984043

A:Accession: F83173

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-723 <STO>

A:Cross-references: GB:AE004797; GB:AE004091; NID:g9949950; PIDN:AAG07177.1; GSPDB:GN001

A:Experimental source: strain PA01

C:Genetics:

A:Gene: OprC; PA3790

Query Match 64.3%; Score 36; DB 2; Length 723;
 Best Local Similarity 62.5%; Pred. No. 79;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFAD 10
 | | | | | | |
 Db 407 FAYGAFGE 414

RESULT 15

JC2464

probable copper-transporting ATPase (EC 3.6.1.1-) HRA-1 - Enterobacteriaceae spp.
 C:Species: Enterobacteriaceae spp.

C:Date: 16-Oct-1998 #sequence_revision 16-Oct-1998 #text_change 18-Jun-1999

C:Accession: JC2464

R.; Trenor III, C.; Lin, W.; Andrews, M.C.

Biochem. Biophys. Res. Commun. 205, 1644-1650, 1994

A:Title: Novel bacterial P-type ATPases with histidine-rich heavy-metal-associated se
 A:Reference number: JC2464; MUID:95110304; PMID:7811248

A:Accession: JC2464

A:Molecule type: mRNA

A:Residues: 1-731 <TRE>

A:Cross-references: GB:U16558; NID:g643612; PIDN:AAA62113.1; PID:g643613

A:Experimental source: human small intestine cDNA library

A:Note: the source species is uncertain; the cloned sequence did not hybridize with h

C:Superfamily: Enterococcus copper-transporting ATPase copB; ATPase nucleotide-bindin

C:Keywords: ATP; copper transport; hydrolase; ion transport; phosphoprotein; transmem

F;7-92/Region: His-rich

F;135-477/Domain: ATPase transduction domain homology <ATP>

F;544-685/Domain: ATPase nucleotide-binding domain homology <ATN>

F;287/Active site: Glu #status predicted

F;431/Active site: Asp (aspartylphosphate intermediate) #status predicted

Query Match 64.3%; Score 36; DB 1; Length 731;
 Best Local Similarity 60.0%; Pred. No. 80;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSFAD 10
 | | | | | | |
 Db 88 AHHHGSFKD 97

Search completed: November 18, 2002, 17:47:06

Job time : 4.90196 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:00 : Search time 2.45098 Seconds
(without alignments)
169.223 Million cell updates/sec

Title: US-09-016-061-72

Perfect score: 56

Sequence: 1 ARHNYGSFAD 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	38	67.9	464	1 DLDH_MYCTU	O53747 mycobacteri
2	37	66.1	323	1 CCSA_LOTJA	Q9bba4 lotus japon
3	36	64.3	581	1 MIK1_SCHPO	P30290 schizosacch
4	35	62.5	275	1 IF2A_PYRAB	Q9vba4 pyrococcus
5	35	62.5	275	1 IF2A_PYRHO	O58655 pyrococcus
6	35	62.5	520	1 PAX7_HUMAN	P23759 homo sapien
7	35	62.5	682	1 E13B_BACCI	P23903 bacillus ci
8	34	60.7	284	1 IPRV_PICPA	O13505 pichia past
9	34	60.7	286	1 IPRV_KIOLA	P13998 kluyveromyc
10	34	60.7	286	1 IPRV_YEAST	P00817 saccharomyc
11	34	60.7	309	1 KHSE_SALTY	Q8xqp5 salmonella
12	34	60.7	608	1 ALBU_MOUSE	P07724 mus musculu
13	33.5	59.8	587	1 COLA_VIBPA	Q56696 vibrio para
14	33	58.9	448	1 NCAP_CVHOC	P33469 human coron
15	33	58.9	470	1 SYE2_RICPR	Q9zct8 rickettsia
16	33	58.9	473	1 SYE_AQUAE	P02771 aquifex aeo
17	33	58.9	608	1 ALBU_RAT	P02770 rattus norv
18	33	58.9	682	1 VG50_BPML5	Q05262 mycobacteri
19	32	57.1	65	1 CCSA_OENBE	P31565 oenothera b
20	32	57.1	65	1 CCSA_PEA	P31172 pisum sativ
21	32	57.1	196	1 HB2J_ECOLI	P37750 escherichia
22	32	57.1	198	1 HB2G_HUMAN	P01911 homo sapien
23	32	57.1	227	1 PRRA_RAT	P09320 rattus norv
24	32	57.1	246	1 YAFK_ECOLI	Q47148 escherichia
25	32	57.1	255	1 CBPM_STRAL	P00733 streptomyce
26	32	57.1	266	1 HB2A_HUMAN	P01913 homo sapien
27	32	57.1	266	1 HB2B_HUMAN	P01912 homo sapien
28	32	57.1	266	1 HB2C_HUMAN	P01914 homo sapien
29	32	57.1	266	1 HB2D_CANFA	P18470 canis famil
30	32	57.1	266	1 HB2D_HUMAN	P13759 homo sapien
31	32	57.1	266	1 HB2E_HUMAN	P04229 homo sapien
32	32	57.1	266	1 HB2F_HUMAN	P13758 homo sapien
33	32	57.1	266	1 HB2H_HUMAN	P13760 homo sapien

ALIGNMENTS

RESULT 1

ID	DLDH_MYCTU	STANDARD	PRT	464 AA
AC	O53747			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Dihydropyrimidine dehydrogenase (EC 1.8.1.4) (E3 component of alpha keto acid dehydrogenase complexes).			
GN	LPD OR RV0462 OR MT0478 OR MTV038.06.			
OS	Mycobacterium tuberculosis.			
OC	Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;			
OC	Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.			
OX	NCBI_TaxID=1773;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=H37RV;			
RX	MEDLINE=98295987; PubMed=9634230;			
RA	Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekala F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajadream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;			
RT	"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."			
RL	Nature 393:537-544(1998).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=CDC 1551 / Oshkosh;			
RA	Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ernolaeva M.D., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A., Bishai W.;			
RT	"Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains."			
RL	Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.			
CC	-i- FUNCTION: LIPOAMIDE DEHYDROGENASE IS A COMPONENT OF THE ALPHA-KETOACID DEHYDROGENASE COMPLEXES (BY SIMILARITY).			
CC	-i- CATALYTIC ACTIVITY: Dihydropyrimidine + NAD(+) = liposamide + NADH.			
CC	-i- COFACTOR: FAD (BY SIMILARITY).			
CC	-i- SUBUNIT: HOMODIMER (BY SIMILARITY).			
CC	-i- SUBCELLULAR LOCATION: Cytoplasmic (Potential).			
CC	-i- MISCELLANEOUS: THE ACTIVE SITE IS A REDOX-ACTIVE DISULFIDE BOND.			
CC	-i- SIMILARITY: BELONGS TO THE PYRIDINE NUCLEOTIDE-DISULFIDE OXIDOREDUCTASES CLASS-I.			
CC	-----			
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CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AL021933; CAAL7417.1; -;
 DR EMBL: AE006950; AAK44702.1; -;
 DR HSSP: P11959; 1EBD.
 DR TIGR: MT0478; -;
 DR TubercuList: Rv0462; -;
 DR InterPro: IPR001327; FAD_pyr_redox.
 DR InterPro: IPR000205; NAD_Binding.
 DR InterPro: IPR001100; pyr_redox.
 DR InterPro: IPR004099; pyr_redox_dim.
 DR Pfam: PF007070; pyr_redox; 1.
 DR Pfam: PF02852; pyr_redox_dim; 1.
 DR PRINTS: PR00368; FADPNR.
 DR PRINTS: PR00411; PNDRTASEI.
 DR PRODom: PD000139; FAD_pyr_redox; 1.
 DR PROSITE: PS00076; PYRIDINE_REDOX 1; 1.
 KW Redox-active center; Glycolysis; Oxidoreductase; NAD; Flavoprotein;
 KW FAD; Complete proteome.
 FT NP_BIND 5 34 FAD (ADP PART) (PROBABLE).
 FT DISULFID 41 46 REDOX-ACTIVE (BY SIMILARITY).
 FT NP_BIND 299 309 FAD (FLAVIN PART) (BY SIMILARITY).
 FT ACT_SITE 443 443 BY SIMILARITY.
 SQ SEQUENCE 464 AA; 49239 MW; DD93D95DC6F76B22 CRC64;
 Query Match 67.9%; Score 38; DB 1; Length 464;
 Best Local Similarity 75.0%; Pred. No. 5.8;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 3 HNYGSPAD 10
 Db 110 HGYGTFFAD 117
 RESULT 2
 CCSA_LOTJA STANDARD; PRT; 323 AA.
 AC Q9BBP4;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Cytochrome c biogenesis protein ccsa.
 GS CCSA.
 OS Lotus Japonicus.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae; Lotus.
 OX NCBI_TaxID=34305;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Accession MG-20;
 RX MEDLINE=21082929; PubMed=11214967;
 RA Kato T., Kaneko T., Sato S., Nakamura Y., Tabata S.;
 RT "Complete structure of the chloroplast genome of a legume, Lotus japonicus".
 RL DNA Res. 7:323-330(2000).
 CC -1- FUNCTION: REQUIRED DURING CYTOCHROME BIOGENESIS AT THE STEP OF
 CC HEME ATTACHMENT (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CCMP/CYCK/UCLL/NRFE/CCSA FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AP002983; BAB33244.1; -;
 DR InterPro: IPR002541; CytC_asm.
 DR Pfam: PF01578; CytC_asm; 1.
 KW Cytochrome c-type biogenesis; Chloroplast.

SQ SEQUENCE 323 AA; 37185 MW; 5A034E3E2829FE35 CRC64;
 Query Match 66.1%; Score 37; DB 1; Length 323;
 Best Local Similarity 100.0%; Pred. No. 6.3;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 HNYGSF 8
 Db 315 HNYGSF 320
 RESULT 3
 MIK1_SCHPO STANDARD; PRT; 581 AA.
 ID MIK1_SCHPO
 AC P30290;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Mitosis inhibitor protein kinase mik1 (EC 2.7.1.-).
 GN MIK1 OR SPBC660.14.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91168259; PubMed=1706223;
 RA Lundgren K., Walworth N., Boohar R., Dembski M., Kirschner M.,
 RA Beach D.;
 RT "mik1 and weel cooperate in the inhibitory tyrosine phosphorylation
 RT of cdc2".
 RL Cell 64:1111-1122(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=21848401; PubMed=11859360;
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Soutos J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
 RA Gentles S., Gobie A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volckaert G., Aert R., Robben J., Grynoprez B.,
 RA Welljens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Leirach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas R., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Carrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shpakovski G.V., Ussery D., Barrall B.G., Nurse P.;
 RT "The genome sequence of Schizosaccharomyces pombe".
 RL Nature 415:871-880(2002)
 CC -1- FUNCTION: PROTEIN KINASE THAT ACTS BOTH ON SERINES AND ON
 CC TYROSINES. IT ACTS AS A NEGATIVE REGULATOR OF ENTRY INTO MITOSIS
 CC (G2 TO M TRANSITION). PHOSPHORYLATES AND INHIBITS CDC2.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC WEEL SUBFAMILY.
 CC -----
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EMBL; M60834; AAA91278.1; -.
 EMBL; AL034563; CAA22534.1; -.
 PIR; A37913; A37913.
 InterPro: IPR000719; Euk_pkinase.
 InterPro: IPR002290; Ser_thr_pkinase.
 Pfam: PF00069; pkinase; 1.
 ProDom: PD000001; Euk_pkinase; 1.
 PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
 PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 Mitosis; Transferase; Serine/threonine-protein kinase;
 Tyrosine-protein kinase; ATP-binding.
 DOMAIN 289 561 PROTEIN KINASE.
 BIND 295 303 ATP (BY SIMILARITY).
 BINDING 320 330 ATP (BY SIMILARITY).
 ACT_SITE 417 417 BY SIMILARITY.
 SEQUENCE 581 AA; 65933 MW; 371E0CEDB2CAICE3 CRC64;

Query Match 64.3%; Score 36; DB 1; Length 581;
 Best Local Similarity 70.0%; Pred. No. 18;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARHNGSFAD 10
 | ||| |
 DB 463 ASHNGKPAD 472

RESULT 4

ID IF2A_PYRAB STANDARD; PRT; 275 AA.
 AC Q9V0E4;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Probable translation initiation factor 2 alpha subunit (eif-2-alpha).
 GN EIF2A OR PAB0368.
 OS Pyrococcus abyssi.
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 OC Pyrococcus.
 OX NCBI_TaxID=29292;
 [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=GE5 / Orsay;
 RA Heilig R.;
 RT "Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure and evolution."
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: EIF-2 FUNCTIONS IN THE EARLY STEPS OF PROTEIN SYNTHESIS
 CC BY FORMING A TERNARY COMPLEX WITH GTP AND INITIATOR TRNA
 CC (BY SIMILARITY).
 CC -!- SUBUNIT: HETEROTRIMER COMPOSED OF AN ALPHA, A BETA, AND A GAMMA
 CC -!- SIMILARITY: BELONGS TO THE EIF-2-ALPHA FAMILY.
 CC -!- SIMILARITY: CONTAINS 1 S1 MOTIF DOMAIN.

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EMBL; AJ248285; CAB49760.1; -.
 HSSP; P05055; 1SRO.
 InterPro: IPR003029; S1.
 Pfam: PF00575; S1; 1.
 SMART; SM00316; S1; 1.
 PROSITE; PS50126; S1; 1.

KW Initiation factor; Protein biosynthesis; RNA-binding;
 KW Complete proteome.
 FT DOMAIN 12 83 S1 MOTIF.
 SQ SEQUENCE 275 AA; 31912 MW; B2659F3A49879B4F CRC64;

Query Match 62.5%; Score 35; DB 1; Length 275;
 Best Local Similarity 62.5%; Pred. No. 13;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFAD 10
 | ||| |
 DB 23 HNYGAFLE 30

RESULT 5

ID IF2A_PYRHO STANDARD; PRT; 275 AA.
 AC O58655;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Probable translation initiation factor 2 alpha subunit (eif-2-alpha).
 GN EIF2A OR PH0961.
 OS Pyrococcus horikoshii.
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 OC Pyrococcus.
 OX NCBI_TaxID=53953;
 [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=OT3;
 RX MEDLINE=98344137; PubMed=9679194;
 RA Kwarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y., Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y., Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y., Funahashi T., Tanaka T., Kudoh Y., Yamaoka J., Kishida N., Oguchi A., Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K., Masuchi Y., Shizuya H., Kikuchi H.;
 RT "Complete sequence and gene organization of the genome of a hyper-thermophilic archaeobacterium, Pyrococcus horikoshii OT3."
 RL DNA Res. 5:55-76(1998).
 CC -!- FUNCTION: EIF-2 FUNCTIONS IN THE EARLY STEPS OF PROTEIN SYNTHESIS
 CC BY FORMING A TERNARY COMPLEX WITH GTP AND INITIATOR TRNA
 CC (BY SIMILARITY).
 CC -!- SUBUNIT: HETEROTRIMER COMPOSED OF AN ALPHA, A BETA, AND A GAMMA
 CC CHAIN (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE EIF-2-ALPHA FAMILY.
 CC -!- SIMILARITY: CONTAINS 1 S1 MOTIF DOMAIN.

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EMBL; AP000004; BAA30058.1; -.
 HSSP; P05055; 1SRO.
 InterPro: IPR003029; S1.
 Pfam; PF00575; S1; 1.
 SMART; SM00316; S1; 1.
 PROSITE; PS50126; S1; 1.
 Initiation factor; Protein biosynthesis; RNA-binding;
 KW Complete proteome.
 FT DOMAIN 12 83 S1 MOTIF.
 SQ SEQUENCE 275 AA; 31980 MW; 6AAAD15F10FFB436 CRC64;

Query Match 62.5%; Score 35; DB 1; Length 275;
 Best Local Similarity 62.5%; Pred. No. 13;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFAD 10
 | ||| |

Db 23 HNYGAFLE 30

RESULT 6

PAX7_HUMAN STANDARD; PRT; 520 AA.

AC P23759; 01-NOV-1991 (Rel. 20, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Paired box protein Pax-7 (HUP1).

GN PAX7 OR HUP1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.

RX MEDLINE=97480728; PubMed=9339373;

RA Vorobyov E., Mertsalov I., Dockhorn-Dworniczak B., Dworniczak B.,

RT Horst J.,

RT "The genomic organization and full coding region of the human PAX7

RT gene";

RL Genomics 45:168-174(1997).

RN [2]

RP SEQUENCE FROM N.A. (LONG FORM).

RA Heath P.;

RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE OF 1-467 FROM N.A. (LONG FORM).

RX MEDLINE=95075634; PubMed=7527137;

RA Schaefer B.W., Czerny T., Bernasconi M., Genini M., Busslinger M.;

RT "Molecular cloning and characterization of a human PAX-7 CDNA

RT expressed in normal and neoplastic myocytes.";

RL Nucleic Acids Res. 22:4574-4582(1994).

RN [4]

RP SEQUENCE OF 30-195 FROM N.A. (SHORT FORM).

RX MEDLINE=89305521; PubMed=2501086;

RA Burri M., Tromvoukis Y., Bopp D., Frigerio G., Noll M.;

RT "Conservation of the paired domain in metazoans and its structure in

RT three isolated human genes.";

RL EMBO J. 8:1183-1190(1989).

CC -!- FUNCTION: PROBABLE TRANSCRIPTION FACTOR. IT MAY HAVE A ROLE IN

CC MYOGENESIS.

CC -!- SUBUNIT: CAN BIND AS A HETERODIMER WITH PAX3.

CC -!- SUBCELLULAR LOCATION: Nuclear.

CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A LONG FORM (SHOWN HERE) AND

CC A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.

CC -!- DISEASE: RHABDOMYOSARCOMA-2 (RMS2) IS CHARACTERIZED BY A

CC CHROMOSOMAL TRANSLOCATION T(1;13)(P36;Q14) WHICH INVOLVES PAX7 AND

CC FOXO1A. THE RESULTING PROTEIN IS A TRANSCRIPTIONAL ACTIVATOR.

CC -!- SIMILARITY: BELONGS TO THE PAIRED HOMEBOX FAMILY.

CC -!- SIMILARITY: CONTAINS 1 PAIRED BOX DOMAIN.

CC -!- SIMILARITY: CONTAINS 1 HOMEBOX DOMAIN.

CC -----

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CC or send an email to license@isb-sib.ch).

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DR EMBL; X97110; CAA65521.1; JOINED.

DR EMBL; X97111; CAA65521.1; JOINED.

DR EMBL; X97112; CAA65521.1; JOINED.

DR EMBL; X97113; CAA65521.1; JOINED.

DR EMBL; X97114; CAA65521.1; JOINED.

DR EMBL; X97115; CAA65521.1; JOINED.

DR EMBL; X97116; CAA65521.1; JOINED.

DR EMBL; X97117; CAA65521.1; JOINED.

DR EMBL; X97118; CAA65521.1; JOINED.

DR EMBL; X97119; CAA655

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DR EMBL; M34503; AAA22474.1; -.
 DR PIR; J00420; J00420.
 DR InterPro; IPR000757; Glyco_hydro_16.
 DR Pfam; PF00722; Glyco_hydro_16; 1.
 DR PROSITE; PS01034; GLYCOSYL-HYDROL_F16; 1.
 KW Cell wall; Hydrolase; Glycosidase; Signal.
 FT SIGNAL 1 38
 FT CHAIN 39 682 GLUCAN ENDO-1,3-BETA-GLUCOSIDASE A1.
 FT ACT_SITE 552 552 NUCLEOPHILE (BY SIMILARITY).
 FT ACT_SITE 557 557 PROTON DONOR (BY SIMILARITY).
 SQ SEQUENCE 682 AA; 75465 MW; 8C4F407E34D4ADD5 CRC64;

Query Match 62.5%; Score 35; DB 1; Length 682;
 Best Local Similarity 62.5%; Pred. No. 34;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 HNYGSFAD 10
 Db 227 HNFQGFDT 234

RESULT 8
 ID IPYR_PICPA STANDARD; PRT; 284 AA.
 AC O13505;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Inorganic pyrophosphatase (EC 3.6.1.1) (Pyrophosphate phospho-
 DE hydrolase) (ppase).
 GN IPPI.
 OS Pichia pastoris (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Pichia.
 OX NCBI_TaxID=4922;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL Y-11430;
 RX MEDLINE=99034033; PubMed=9818724;
 RA Cosano I.C., Alvarez P., Molina M., Nombela C.;
 RT "Cloning and sequence analysis of the Pichia pastoris TRP1 and
 RT HIS3 genes.";
 RL Yeast 14:861-867(1998).
 CC -!- CATALYTIC ACTIVITY: Diphosphate + H(2)O = 2 phosphate.
 CC -!- COFACTOR: REQUIRES THE PRESENCE OF DIVALENT METAL CATION.
 CC -!- MAGNESIUM CONFERS THE HIGHEST ACTIVITY.
 CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: BELONGS TO THE PPASE FAMILY.

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DR EMBL; AJ001000; CAA04453.1; -.
 DR HSSP; P00817; IWGI.
 DR InterPro; IPR001596; Pyrophosphatase.
 DR Pfam; PF00719; Pyrophosphatase; 1.
 DR PROSITE; PS00387; PPASE; 1.
 KW Hydrolase; Magnesium.
 FT INIT_MPT 0 0 BY SIMILARITY.
 FT ACT_SITE 56 56 PROBABLE.
 FT BINDING 78 78 INORGANIC PYROPHOSPHATE (BY SIMILARITY).

SQ SEQUENCE 284 AA; 31937 MW; 3DAD27970D7775D6 CRC64;

Query Match 60.7%; Score 34; DB 1; Length 284;
 Best Local Similarity 83.3%; Pred. No. 21;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
 Db 91 HNYGAF 96

RESULT 9
 ID IPYR_KLULA STANDARD; PRT; 286 AA.
 AC P13996;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 01-OCT-1994 (Rel. 30, Last annotation update)
 DE Inorganic pyrophosphatase (EC 3.6.1.1) (Pyrophosphate phospho-
 DE hydrolase) (ppase).
 GN IPPI OR IPP.
 OS Kluyveromyces lactis (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
 OX NCBI_TaxID=28985;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89189093; PubMed=2538971;
 RA Stark M.J.R., Milner J.S.;
 RT "Cloning and analysis of the Kluyveromyces lactis TRP1 gene: a
 RT chromosomal locus flanked by genes encoding inorganic pyrophosphatase
 RT and histone H3.";
 RL Yeast 5:35-50(1989).
 RN [2]
 RP SIMILARITY TO E. COLI AND YEAST PPASES.
 RX MEDLINE=90254161; PubMed=2160278;
 RA Lahti R., Kolakowski L.F. Jr., Heinonen J., Vihinen M., Pohjanoksa K.,
 RA Cooperman B.S.;
 RT "Conservation of functional residues between yeast and E. coli
 RT inorganic pyrophosphatases.";
 RL Biochim. Biophys. Acta 1038:338-345(1990).
 CC -!- CATALYTIC ACTIVITY: Diphosphate + H(2)O = 2 phosphate.
 CC -!- COFACTOR: REQUIRES THE PRESENCE OF DIVALENT METAL CATION.
 CC -!- MAGNESIUM CONFERS THE HIGHEST ACTIVITY.
 CC -!- SUBUNIT: HOMODIMER.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: BELONGS TO THE PPASE FAMILY.

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DR EMBL; X14230; CAA32446.1; -.
 DR PIR; S07894; PWVKL.
 DR HSSP; P00817; IWGI.
 DR InterPro; IPR001596; Pyrophosphatase.
 DR Pfam; PF00719; Pyrophosphatase; 1.
 DR PROSITE; PS00387; PPASE; 1.
 KW Hydrolase; Magnesium.
 FT INIT_MPT 0 0 BY SIMILARITY.
 FT ACT_SITE 56 56 PROBABLE.
 FT BINDING 78 78 INORGANIC PYROPHOSPHATE (BY SIMILARITY).
 SQ SEQUENCE 286 AA; 32034 MW; 11647F4ABD916A2F CRC64;

Query Match 60.7%; Score 34; DB 1; Length 286;
 Best Local Similarity 83.3%; Pred. No. 21;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8

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Db      1111:1
      91 HNYGAF 96

RESULT 10
IPYR_YEAST
ID      IPYR_YEAST      STANDARD;      PRT;      286 AA.
AC      P00817;

DT      21-JUL-1986 (Rel. 01, Created)
DT      01-MAR-1989 (Rel. 10, Last sequence update)
DT      15-JUL-1999 (Rel. 38, Last annotation update)
DE      Inorganic pyrophosphatase (EC 3.6.1.1) (Pyrophosphate phospho-
DE      hydrolase) (Ppase).
GN      IPPI OR PPAL OR PPA OR YBR011C OR YBR0202.
OS      Saccharomyces cerevisiae (Baker's yeast).
OC      Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC      Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX      NCBI_TaxId=4932;

RN      [1]
RN      SEQUENCE FROM N.A.
RC      STRAIN=X2180;
RX      MEDLINE=89083474; PubMed=2849749;
RA      Kolakowski L.F. Jr., Schloesser M., Cooperman B.S.;
RT      "Cloning, molecular characterization and chromosome localization of
RT      the inorganic pyrophosphatase (PPA) gene from S. cerevisiae.";
RL      Nucleic Acids Res. 16:1041-1045(1988).
RN      [2]
RN      SEQUENCE FROM N.A.
RC      STRAIN=S288c;
RA      Entian K.-D., Koetter P., Rose M., Li Z., Thermann R., Brendel M.,
RA      Baur A., Boles E., Miosga T., Schaaff-Gerstenschlaeger I.,
RA      Zimmermann F.K.;
RL      Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
RN      [3]
RN      SEQUENCE.
RX      MEDLINE=78087552; PubMed=340461;
RA      Cohen S.A., Sterner R., Kelm P.S., Heinrikson R.L.;
RT      "Covalent structural analysis of yeast inorganic pyrophosphatase.";
RL      J. Biol. Chem. 253:889-897(1978).
RN      [4]
RN      SEQUENCE OF 25-35 AND 239-251.
RC      STRAIN=S288c;
RX      MEDLINE=95203288; PubMed=7895733;
RA      Garrels J.I., Futch B., Kobayashi R., Latter G.I., Schwender B.,
RA      Volpe T., Warner J.R., McLaughlin C.S.;
RT      "Protein identifications for a Saccharomyces cerevisiae protein
RT      database.";
RL      Electrophoresis 15:1466-1486(1994).
RN      [5]
RN      SEQUENCE OF 239-249.
RC      STRAIN=ATCC 38531 / Y41;
RX      MEDLINE=97089742; PubMed=8935650;
RA      Norbeck J., Blomberg A.;
RT      "Protein expression during exponential growth in 0.7 M NaCl medium of
RT      Saccharomyces cerevisiae.";
RL      FEMS Microbiol. Lett. 137:1-8(1996).
RN      [6]
RN      ACTIVE SITE.
RX      MEDLINE=80109718; PubMed=6101539;
RA      Bond M.W., Chiu N.Y., Cooperman B.S.;
RT      "Identification of an arginine important for enzymatic activity
RT      within the covalent structure of yeast inorganic pyrophosphatase.";
RL      Biochemistry 19:94-102(1980).
RN      [7]
RN      X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
RA      Arutunian E.G., Terzian S.S., Voronova A.A., Kuranova I.P.,
RA      Smirnova E.A., Vainstein B.K., Hohne W.E., Hansen G.;
RT      "X-ray diffraction study of inorganic pyrophosphatase from baker's
RT      yeast at the 3-A resolution.";
RL      Dokl. Akad. Nauk SSSR 258:1481-1492(1981).
RN      [8]
RN      X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX      MEDLINE=97148342; PubMed=8994974;

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RA      Heikinheimo P., Lehtonen J., Baykov A., Lahti R., Cooperman B.S.,
RA      Goldman A.;
RT      "The structural basis for pyrophosphatase catalysis.";
RL      Structure 4:1491-1508(1996).
RN      [9]
RP      X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
RA      Swaminathan K., Cooperman B.S., Lahti R., Voet D.;
RL      Submitted (DEC-1997) to the PDB data bank.
RN      [10]
RP      X-RAY CRYSTALLOGRAPHY (2.15 ANGSTROMS) OF MUTANTS LYS-78 AND LYS-117.
RX      MEDLINE=99056888; PubMed=9878371;
RA      Tuominen V., Heikinheimo P., Kajander T., Torkkel T., Hyttia T.,
RA      Kapyla J., Lahti R., Cooperman B.S., Goldman A.;
RT      "The R78K and D117E active-site variants of Saccharomyces cerevisiae
RT      soluble inorganic pyrophosphatase: structural studies and mechanistic
RT      implications.";
RL      J. Mol. Biol. 284:1565-1580(1998).
RN      [11]
RP      SIMILARITY TO E.COLI AND K.LACTIS PPASES.
RX      MEDLINE=90254161; PubMed=2160278;
RA      Lahti R., Kolakowski L.F. Jr., Heinonen J., Vihinen M., Pohjanoksa K.,
RA      Cooperman B.S.;
RT      "Conservation of functional residues between yeast and E. coli
RT      inorganic pyrophosphatases.";
RL      Biochim. Biophys. Acta 1038:338-345(1990).
CC      -I- CATALYTIC ACTIVITY: Diphosphate + H(2)O = 2 phosphate.
CC      -I- COFACTOR: REQUIRES THE PRESENCE OF DIVALENT METAL CATION.
CC      MAGNESIUM CONFERS THE HIGHEST ACTIVITY. IT BINDS UP TO 4 DIVALENT
CC      CATIONS PER SUBUNIT, WITH THREE REQUIRED FOR ACTIVITY.
CC      -I- SUBUNIT: HOMODIMER.
CC      -I- SUBCELLULAR LOCATION: Cytoplasmic.
CC      -I- SIMILARITY: BELONGS TO THE PPASE FAMILY.
CC      -----
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DR      EMBL; X13253; CAA31629.1; -
DR      EMBL; Z35880; CAA84949.1; -
DR      PIR; S45864; PWB1.
DR      PDB; 1YP; 15-OCT-91.
DR      PDB; 1YPP; 07-DEC-96.
DR      PDB; 1WGI; 19-NOV-97.
DR      PDB; 1WGI; 19-NOV-97.
DR      PDB; 1H0J; 08-APR-98.
DR      PDB; 1H0J; 08-APR-98.
DR      PDB; 1HUK; 08-APR-98.
DR      PDB; 117E; 23-DEC-98.
DR      PDB; 8PRK; 23-DEC-98.
DR      PDB; 2DPA; 07-DEC-98.
DR      SWISS-2DPAGE; P00817; YEAST.
DR      COMPUYEAST-2DPAGE; P00817; -
DR      SGD; S0000215; IPPI.
DR      InterPro; IPR001596; Pyrophosphatase.
DR      Pfam; PF00719; Pyrophosphatase; 1.
DR      PROSITE; PS00387; PPASE; 1.
KW      Hydrolase; Magnesium; 3D-structure.
FT      INIT_MET 0
FT      ACT_SITE 56 56 PROBABLE.
FT      BINDING 78 78 INORGANIC PYROPHOSPHATE.
FT      CONFLICT 40 40 N -> D (IN REF. 3).
FT      CONFLICT 71 71 D -> N (IN REF. 3).
FT      CONFLICT 74 74 MISSING (IN REF. 3).
FT      CONFLICT 123 123 E -> Q (IN REF. 3).
FT      CONFLICT 136 136 Q -> E (IN REF. 3).
FT      CONFLICT 186 186 N -> D (IN REF. 3).
FT      CONFLICT 224 224 D -> N (IN REF. 3).
FT      CONFLICT 266 266 L -> P (IN REF. 2).
FT      STRAND 4 7
FT      STRAND 16 20
FT      STRAND 25 25

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FT TURN 28 30
FT TURN 38 41
FT STRAND 45 45
FT STRAND 55 55
FT STRAND 79 79
FT TURN 97 98
FT TURN 111 112
FT STRAND 121 123
FT TURN 131 132
FT STRAND 135 135
FT STRAND 138 146
FT STRAND 151 158
FT TURN 160 161
FT TURN 165 167
FT HELIX 172 175
FT TURN 176 177
FT TURN 179 180
FT HELIX 182 197
FT STRAND 203 203
FT HELIX 205 207
FT STRAND 210 210
FT HELIX 212 230
FT TURN 231 231
FT TURN 245 246
FT TURN 248 249
FT TURN 251 252
FT TURN 255 260
FT TURN 274 275
SQ SEQUENCE 286 AA; 32184 MW; F29390260B60CB2 CRC64;

Query Match 60.7%; Score 34; DB 1; Length 286;
Best Local Similarity 83.3%; Pred. No. 21;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
    |||||
Db 91 HNYGAF 96

RESULT 11
KHSE_SALTY STANDARD; PRT; 309 AA.
ID Q8XGP5;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Homoserine kinase (EC 2.7.1.39) (HK).
GN THRB OR STM0003 OR STM0003.
OS Salmonella typhimurium, and
OS Salmonella typhi.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=602, 601;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=S.typhimurium; STRAIN=LT2 / SCSCL142 / AFCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RA "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT LT2."
RL Nature 413:852-856(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=S.typhi; STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
Krogh A., Larsen T.S., Leather S., Moulé S., O'Gaora P., Parry C.,
Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
Whitehead S., Barrrell B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
enterica serovar Typhi CT18."
RL Nature 413:848-852(2001).
CC -1- CATALYTIC ACTIVITY: ATP + L-homoserine - ADP + O-phospho-L-
homoserine.
CC -1- PATHWAY: Threonine biosynthesis from aspartate; fourth step.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- SIMILARITY: BELONGS TO THE GHMP KINASE FAMILY. HOMOSERINE KINASE
SUBFAMILY.
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DR EMBL; AE008693; AAL18967.1; -
DR EMBL; AL627265; CAD01156.1; -
DR StyGene; SG2222; thrB
DR InterPro; IPR001745; GHMPkinase_ATP.
DR InterPro; IPR000870; Homoser_Kin.
DR Pfam; PF00288; GHMP_kinases; 1.
DR PRINTS; PR00958; HOMSERKINASE.
DR TIGRFS; TIGR00191; thrB; 1.
DR PROSITE; PS00627; GHMP_KINASES_ATP; 1.
KW Threonine biosynthesis; Transferase; Kinase; ATP-binding;
FT Complete proteome.
FT NP_BIND 91 101 ATP (POTENTIAL).
SQ SEQUENCE 309 AA; 33286 MW; 2B5D570CB35F8911 CRC64;

Query Match 60.7%; Score 34; DB 1; Length 309;
Best Local Similarity 75.0%; Pred. No. 23;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 HNYGSFAD 10
    |||||
Db 47 HNLGRFAD 54

RESULT 12
ALBU_MOUSE STANDARD; PRT; 608 AA.
ID ALBU_MOUSE
AC P07724; Q01802;
DT 01-APR-1988 (Rel. 07, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Serum albumin precursor.
GN ALB OR ALBI.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA van Reeth T., Gabant P., Dreze P., Szpirer J., Szpirer C.;
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yananaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwar H.,

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RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Ouackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE OF 99-516 FROM N.A.
RX MEDLINE=88216123; PubMed=2452956;
RA Minghetti P.P., Law S.W., Dugaiczkyk A.;
RA "The rate of molecular evolution of alpha-fetoprotein approaches that
RT of pseudogenes.";
RL Mol. Biol. Evol. 2:347-358(1985).
RN [4]
RP SEQUENCE OF 477-551 FROM N.A.
RC STRAIN=BA18/C;
RX MEDLINE=90269606; PubMed=1971802;
RA Boccaccio C., Deschatrette J., Meunier-Rotival M.;
RT "Empty and occupied insertion site of the truncated LINE-1 repeat
RT located in the mouse serum albumin-encoding gene.";
RL Gene 88:181-186(1990).
RN [5]
RP SEQUENCE OF 25-44.
RC TISSUE=Liver;
RX MEDLINE=93162044; PubMed=1286668;
RA Giometti C.S., Taylor J., Tollaksen S.L.;
RT "Mouse liver protein database: a catalog of proteins detected by two-
RT dimensional gel electrophoresis.";
RL Electrophoresis 13:970-991(1992).
CC -!- FUNCTION: SERUM ALBUMIN, THE MAIN PROTEIN OF PLASMA, HAS A GOOD
CC BINDING CAPACITY FOR WATER, CA++, NA+, K+, FATTY ACIDS, HORMONES,
CC BILIRUBIN AND DRUGS. ITS MAIN FUNCTION IS THE REGULATION OF THE
CC COLLOIDAL OSMOTIC PRESSURE OF BLOOD.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: PLASMA.
CC -!- SIMILARITY: BELONGS TO THE ALB/AFP/VDB FAMILY.
CC -!- SIMILARITY: CONTAINS 3 ALBUMIN DOMAINS.
CC -----
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CC -----
CC EMBL; AJ011413; CAA09617.1; -;
CC EMBL; M16111; AAA37190.1; -;
CC EMBL; X13060; CAA31458.1; -;
CC EMBL; AK010025; BAB26650.1; -;
CC F01; A05139; A05139.
CC HSP; P02768; IE7B.
CC SWISS-2DPAGE; P07724; MOUSE.
CC MGI; 87991; Alb1.
CC InterPro; IPR00264; Serum_albumin.
CC Pfam; PF00273; transport_prot; 3.
CC PRINTS; PR00802; SERUMALBUMIN.
CC ProDom; PD002486; Serum_albumin; 1.
CC SMART; SM00103; ALBUMIN; 3.
CC PROSITE; PS00212; ALBUMIN; 3.
CC Plasma; Metal-binding; Lipid-binding; Albumin; Repeat; Signal;
CC Copper.
KW SIGNAL. 1 18 BY SIMILARITY.
FT PROPEP 19 24
FT CHAIN , 25 608 SERUM ALBUMIN.

FT DOMAIN 25 205 ALBUMIN 1.
FT DOMAIN 212 397 ALBUMIN 2.
FT DOMAIN 404 595 ALBUMIN 3.
FT METAL 27 27 COPPER.
FT DISULFID 77 86 BY SIMILARITY.
FT DISULFID 99 115 BY SIMILARITY.
FT DISULFID 114 125 BY SIMILARITY.
FT DISULFID 148 193 BY SIMILARITY.
FT DISULFID 192 201 BY SIMILARITY.
FT DISULFID 224 270 BY SIMILARITY.
FT DISULFID 269 277 BY SIMILARITY.
FT DISULFID 289 303 BY SIMILARITY.
FT DISULFID 302 313 BY SIMILARITY.
FT DISULFID 340 385 BY SIMILARITY.
FT DISULFID 384 393 BY SIMILARITY.
FT DISULFID 416 462 BY SIMILARITY.
FT DISULFID 461 472 BY SIMILARITY.
FT DISULFID 485 501 BY SIMILARITY.
FT DISULFID 500 511 BY SIMILARITY.
FT DISULFID 538 583 BY SIMILARITY.
FT DISULFID 582 591 BY SIMILARITY.
FT CONFLICT 27 27 H -> D (IN REF. 5).
FT CONFLICT 33 33 H -> D (IN REF. 5).
FT CONFLICT 41 41 Q -> I (IN REF. 5).
SQ SEQUENCE 608 AA; 68692 MW; 292F7C7ED3A61B4 CRC64;
Query Match 60.7%; Score 34; DB 1; Length 608;
Best Local Similarity 66.7%; Pred. No. 47;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 RHNYGSFAD 10
| | | | |
DB 105 RENYGELAD 113
RESULT 13
COLA_VIBPA STANDARD; PRT; 587 AA.
ID COLA_VIBPA
AC Q56696;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Microbial collagenase precursor (EC 3.4.24.3).
GN PRTVP.
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxID=670;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=93;
RX MEDLINE=96036215; PubMed=7582017;
RA Lee C., Su S., Liaw R.;
RT "Molecular analysis of an extracellular protease gene from Vibrio
RT parahaemolyticus.";
RL Microbiology 141:2569-2576(1995).
CC -!- CATALYTIC ACTIVITY: Digestion of native collagen in the triple
CC helical region at xaa-1-gly bonds. With synthetic peptides, a
CC preference is shown for Gly at P3 and P1', Pro and Ala at P2 and
CC P2'; and hydroxyproline, Ala or Arg at P3'.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M9.
CC -----
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CC -----
CC EMBL; Z46782; CAA86734.1; -;
CC MEROPS; M09.001; -;
CC InterPro; IPR002169; M1collptase.

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DR InterPro; IPR000130; Zn_MTpeptidase.
DR Pfam; PF01752; Peptidase_M9; 1.
DR PRINTS; PR00931; MICOLLPPTASE.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW Hydrolase; Metalloprotease; Zinc; Zymogen; Signal.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 587 MICROBIAL COLLAGENASE.
FT METAL 435 435 ZINC (CATALYTIC) (BY SIMILARITY).
FT ACT_SITE 436 436 BY SIMILARITY.
FT METAL 439 439 ZINC (CATALYTIC) (BY SIMILARITY).
SQ SEQUENCE 587 AA; 66003 MW; 8A94D83E3D2A2BD1 CRC64;

Query Match 59.8%; Score 33.5; DB 1; Length 587;
Best Local Similarity 72.7%; Pred. No. 57;
Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 ARHNYGSFAD 10
Db 443 ARFNQYGSFSD 453

RESULT 14
NCAP_CVHOC
ID NCAP_CVHOC STANDARD; PRT; 448 AA.
AC P33469;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE Nucleocapsid protein.
GN N.
OS Human coronavirus (strain OC43).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=31631;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89243809; PubMed=2541577;
RA Kamahora T., Soe L.H., Lai M.M.C.;
RT "Sequence analysis of nucleocapsid gene and leader RNA of human coronavirus OC43.";
RL Virus Res. 12:1-9(1989).
DR PIR; A60003; A60003.
DR InterPro; IPR001218; Corona_nucleocap.
DR Pfam; PF00937; Corona_nucleoca; 1.
KW Nucleocapsid.
SQ SEQUENCE 448 AA; 49316 MW; 5193AB1AE0D75626 CRC64;

Query Match 58.9%; Score 33; DB 1; Length 448;
Best Local Similarity 85.7%; Pred. No. 54;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 103 RHNRGSF 109

RESULT 15
SYE2_RICPR
ID SYE2_RICPR STANDARD; PRT; 470 AA.
AC Q92CT8;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Glutamyl-tRNA synthetase 2 (EC 6.1.1.17) (Glutamate--tRNA ligase 2) (GLURS 2).
GN GLRX2 OR RP623.
OS Rickettsia prowazekii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=782;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Madrid E;

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RX MEDLINE=99039499; PubMed=9823893;
RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,
RA Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
RT "The genome sequence of Rickettsia prowazekii and the origin of
RT mitochondria.";
RL Nature 396:133-140(1998).
CC -1- CATALYTIC ACTIVITY: ATP + L-glutamate + tRNA(Glu) -> AMP +
CC diphosphate + L-glutamyl-tRNA(Glu).
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-tRNA SYNTHETASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AJ235272; CAAL5066.1; .
CC HSSP; P27000; IGLN.
DR InterPro; IPR004527; GltX_bact.
DR InterPro; IPR000924; Glu_tRNA-synt_1c.
DR InterPro; IPR001412; tRNA-synt_1.
DR Pfam; PF00749; tRNA-synt_1c; 1.
DR PRINTS; PR00987; TRNASYNTHGLU.
DR TIGRFAMS; TIGR00464; gltX_bact; 1.
DR PROSITE; PS00178; AA_tRNA_LIGASE_I; FALSE_NEG.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
KW Complete proteome.
FT SITE 10 20 "HIGH" REGION.
FT SITE 239 243 "KMSKS" REGION.
FT BINDING 242 242 ATP (BY SIMILARITY).
SQ SEQUENCE 470 AA; 53696 MW; DF1CE50A20B8A9FD CRC64;

Query Match 58.9%; Score 33; DB 1; Length 470;
Best Local Similarity 75.0%; Pred. No. 56;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSF 8
Db 31 ARHNNGRF 38

Search completed: November 18, 2002, 17:33:28
Job time : 3.45098 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:01 ; Search time 10.4412 Seconds
(without alignments)
197.341 Million cell updates/sec

Title: US-09-016-061-72

Perfect score: 56

Sequence: 1 ARHNYGSPAD 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvrius.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	49	87.5	839	10	Q9LIE5	Q9LIE5 arabidopsis
2	40	71.4	210	17	O30115	O30115 archaeoglob
3	40	71.4	276	7	Q9GJN0	Q9GJN0 cainan croc
4	39	69.6	162	2	O08236	O08236 ixodes scap
5	39	69.6	162	2	O52253	O52253 rickettsia
6	39	69.6	275	17	Q8U1R5	Q8U1R5 pyrococcus
7	39	69.6	446	5	O62086	O62086 caenorhabdi
8	39	69.6	707	2	O52307	O52307 prevotella
9	38	67.9	89	7	O19495	O19495 gallus gall
10	37	66.1	275	10	Q43476	Q43476 hordeum vul
11	37	66.1	618	10	Q8W127	Q8W127 hordeum vul
12	37	66.1	625	10	Q9MB96	Q9MB96 oryza sativ
13	37	66.1	685	5	Q9V6C3	Q9V6C3 drosophila
14	37	66.1	5317	5	O8PA74	O8PA74 hemiceintrot
15	36	64.3	39	7	P79474	P79474 cervus elap
16	36	64.3	39	7	P79477	P79477 cervus elap

17	36	64.3	39	7	P79478	P79478 cervus elap
18	36	64.3	39	7	P79479	P79479 cervus elap
19	36	64.3	67	7	Q8SP02	Q8SP02 hapalemur g
20	36	64.3	74	6	Q9TMA	Q9TMA bos taurus
21	36	64.3	75	7	Q9GIJ5	Q9GIJ5 bos taurus
22	36	64.3	76	7	Q9TPC2	Q9TPC2 macaca mula
23	36	64.3	77	7	Q9GJ91	Q9GJ91 oviss aries
24	36	64.3	77	7	Q9GJ90	Q9GJ90 oviss aries
25	36	64.3	77	7	Q9GJ82	Q9GJ82 oviss aries
26	36	64.3	78	6	Q97968	Q97968 oviss aries
27	36	64.3	78	6	Q97835	Q97835 oviss aries
28	36	64.3	78	6	Q97839	Q97839 oviss aries
29	36	64.3	78	6	Q97844	Q97844 oviss aries
30	36	64.3	78	7	Q9MWT6	Q9MWT6 leopardus p
31	36	64.3	78	7	Q9MWT5	Q9MWT5 leopardus p
32	36	64.3	78	7	Q9MWT4	Q9MWT4 leopardus p
33	36	64.3	78	7	Q95HD1	Q95HD1 oviss aries
34	36	64.3	78	7	Q95HC6	Q95HC6 oviss aries
35	36	64.3	79	7	Q9MX19	Q9MX19 leopardus p
36	36	64.3	79	7	Q9MX13	Q9MX13 leopardus p
37	36	64.3	79	7	Q9MX03	Q9MX03 leopardus p
38	36	64.3	79	7	Q9MX00	Q9MX00 leopardus p
39	36	64.3	79	7	Q9MW29	Q9MW29 leopardus p
40	36	64.3	79	7	Q9MW28	Q9MW28 leopardus p
41	36	64.3	79	7	Q9MW27	Q9MW27 leopardus p
42	36	64.3	79	7	Q9MWY9	Q9MWY9 leopardus p
43	36	64.3	79	7	Q9MWY8	Q9MWY8 leopardus p
44	36	64.3	79	7	Q9MWY6	Q9MWY6 leopardus p
45	36	64.3	79	7	Q9MWY5	Q9MWY5 leopardus p

ALIGNMENTS

RESULT 1

Q9LIE5
ID Q9LIE5 PRELIMINARY; PRT; 839 AA.
AC Q9LIE5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Far-red impaired response protein, mutator-like transposase-like
DE protein, phytochrome A signaling protein-like.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Magnoliophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=20363099; PubMed=10907853;
RA Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.
RT Sequence features of the regions of 4,251,695 bp covered by ninety pl,
RT TAC and BAC clones.";
RL DNA Res. 7:217-221(2000).
DR EMBL; AP001306; BAB03065.1; .
DR InterPro; IPR004330; FARI.
DR InterPro; IPR001000; Glyco_hydro_10.
DR Pfam; PF03101; FARI; 1.
DR PROSITE; PS00591; GLYCOSYL-HYDROL_F10; UNKNOWN_1.
SQ SEQUENCE 839 AA; 59596 MW; CBBFGDF8B679F8 CRC64;

Query Match 87.5%; Score 49; DB 10; Length 839;

Best Local Similarity 80.0%; Pred. No. 0.44;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;


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QY 1 ARHNYGSFAD 10
DB 274 SRHNYGSFCD 283

RESULT 2
O30115 ID O30115 PRELIMINARY; PRT; 210 AA.
AC O30115;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Hypothetical protein AF0122.
GN AF0122.
OS Archaeoglobus fulgidus.
OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
OC Archaeoglobaceae; Archaeoglobus.
OX NCBI_TaxID=2234;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RX MEDLINE=98049343; PubMed=9389475;
RA Klenk H.-P., Clayton R.J., Tomb J.-F., White O., Nelson K.E.,
RA Richardson D.L., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
RA Fleischmann R.D., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
RA Kirkness E.F., Dougherty B.A., McInerney K., Adams M.D., Loftus B.,
RA Peterson S., Reich C.J., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
RA Overbeek R., Cockayne J.D., Weidman J.F., McDonald L., Oltersback T.,
RA Cotton M.D., Spriggs T., Artlich P., Kaine B.P., Sykes S.M.,
RA Sadow P.M., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RA Venter J.C.;
RT "The complete genome sequence of the hyperthermophilic, sulphate-
RT reducing archaeon Archaeoglobus fulgidus."
RL Nature 390:364-370(1997).
DR EMBL; AE001098; AAB91117.1; -.
DR TIGR; AF0122; -.
DR InterPro; IPR002572; DUF22.
DR Pfam; PF01629; DUF22; 2.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 210 AA; 24129 MW; 5832B214EA77B9BA CRC64;

Query Match 71.4%; Score 40; DB 17; Length 210;
Best Local Similarity 77.8%; Pred. No. 5.4;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAD 10
DB 128 RHAYGSFVD 136

RESULT 3
Q9GJNO ID Q9GJNO PRELIMINARY; PRT; 276 AA.
AC Q9GJNO;
DT 01-WAR-2001 (TREMBLrel. 16, Created)
DT 01-WAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MHC class II beta chain.
GN HCIIIE7A.
OS Caiman crocodilus (Spectacled caiman) (Caiman sclerops).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Crocodylidae; Alligatorinae; Caiman.
OX NCBI_TaxID=8499;
RN [1]
RP SEQUENCE FROM N.A.
RA Voldby J., Vilved L., Due M., Gronlund J., Holmskov U., Teisner B.,
RA Salomonsen J., Brusgaard K., Skjold K.;
RT "Cloning, sequence and genomic structure of MHC class II antigens from
RT the 'spectacled caiman, Caiman crocodilus.'";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF256651; AAF99283.1; -.

HSSP: P13760; 2SEB.
InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR000353; MHC_II_beta.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00969; MHC_II_beta; 1.
DR ProDom; PD000328; MHC_II_beta; 1.
DR SMART; SM00407; Igcl; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Glycoprotein; MHC II; Transmembrane.
SQ SEQUENCE 276 AA; 30366 MW; EA8A4684986AEA6A CRC64;

Query Match 71.4%; Score 40; DB 7; Length 276;
Best Local Similarity 87.5%; Pred. No. 7.4;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFA 9
DB 108 RHNYGVFA 115

RESULT 4
O08236 ID O08236 PRELIMINARY; PRT; 162 AA.
AC O08236;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE RomPA (Fragment).
OS Ixodes scapularis endosymbiont.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae.
OX NCBI_TaxID=47467;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98233883; PubMed=9574696;
RA Weiler S.J., Baldrige G.D., Munderloh U.G., Noda H., Simser J.,
RA Kurtti T.J.;
RT "Phylogenetic placement of rickettsiae from the ticks Amblyomma
RT americanum and Ixodes scapularis."
RL J. Clin. Microbiol. 36:1305-1317(1998).
DR EMBL; AB002268; BAA19525.1; -.
FT NON_TER 1
FT NON_TER 162
SQ SEQUENCE 162 AA; 16211 MW; 995B9A28E3B325B4 CRC64;

Query Match 69.8%; Score 39; DB 2; Length 162;
Best Local Similarity 60.0%; Pred. No. 6.3;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFAD 10
DB 144 AHHDGAFAD 153

RESULT 5
O52253 ID O52253 PRELIMINARY; PRT; 162 AA.
AC O52253;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE 190 kDa antigen (Fragment).
OS Rickettsia cooleyi.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=69410;
RN [1]
RP SEQUENCE FROM N.A.
RA Billings A.N., Teltow G.J., Walker D.H.;
RT "Molecular characterization of a novel spotted fever group rickettsial
RT species from Ixodes scapularis in Texas."
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
```

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DR EMBL; AF031535; AAB95268.1; ..
FT NON_TER 1
FT NON_TER 162
SQ SEQUENCE 162 AA; 16230 MW; 8DF06E97A8478B54 CRC64;

Query Match 69.6%; Score 39; DB 2; Length 162;
Best Local Similarity 60.0%; Pred. No. 6.3;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFAD 10
DB 144 AHDFGAFAD 153
| | | | | |
| | | | | |

RESULT 6
ID Q8UIR5 PRELIMINARY; PRT; 275 AA.
AC Q8UIR5;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Translation initiation factor eIF-2, subunit alpha.
GN PF1140.
OS Pyrococcus furiosus.
OC Archaea: Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=2261;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VC1 / DSM 3638 / ATCC 43587 / JCM 8422;
RA Wells R.B., Dunn D.M., Robb F.T., Brown J.R.;
RT "The complete sequence of the Pyrococcus furiosus genome.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE010224; AAL81264.1; -.
KW Initiation factor; Complete proteome.
SQ SEQUENCE 275 AA; 31917 MW; 1AEE323D1DC5F8FF CRC64;

Query Match 69.6%; Score 39; DB 17; Length 275;
Best Local Similarity 75.0%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFAD 10
DB 23 HNYGAFD 30
| | | | |
| | | | |

RESULT 7
ID O62086 PRELIMINARY; PRT; 446 AA.
AC O62086;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE C31H5.6 protein.
GN C31H5.6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Kershaw J.K.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; Z93778; CAB07846.1; -.
DR InterPro; IPR000379; Set_estrs_site.
SQ SEQUENCE 446 AA; 50763 MW; 82AD969CDAD753DE CRC64;

Query Match 69.6%; Score 39; DB 2; Length 707;
Best Local Similarity 66.7%; Pred. No. 35;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFA 9
DB 51 RHNYGSHA 58
| | | | |
| | | | |

RESULT 8
ID Q52307 PRELIMINARY; PRT; 707 AA.
AC Q52307;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Xylanase.
OS Prevotella ruminicola (Bacteroides ruminicola).
OC Bacteria; CFB group; Bacteroidetes; Bacteroidales; Prevotellaceae;
OC Prevotella.
OX NCBI_TaxID=839;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D31D;
RA Whitehead T.R.;
RT "Cloning and comparison of xylanase genes from ruminal and colonic
Bacteroides species.";
RL Curr. Microbiol. 23:15-19(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=D31D;
RX MEDLINE=97201063; PubMed=9048892;
RA Flint H.J., Whitehead T.R., Martin J.C., Gasparic A.;
RT "Interrupted catalytic domain structures in xylanases from two
distinctly related strains of prevotella ruminicola.";
RL Biochim. Biophys. Acta 1337:161-165(1997).
DR EMBL; U53926; AAB81559.1; -.
DR HSP; P23360; IFXM.
DR InterPro; IPR000583; GATase_2.
DR PFam; PF00331; Glyco_hydro_10; 3.
DR PRINTS; PR00134; GLHYDLASE10.
DR PROSITE; PS00443; GATASE_TYPE_II; UNKNOWN1.
SQ SEQUENCE 707 AA; 78252 MW; 8484E75C60869DB5 CRC64;

Query Match 69.6%; Score 39; DB 2; Length 707;
Best Local Similarity 66.7%; Pred. No. 35;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAD 10
DB 694 KHYGGFAD 702
| | | | |
| | | | |

RESULT 9
ID O19495 PRELIMINARY; PRT; 89 AA.
AC O19495;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II beta 1 domain (Fragment).
GN B-LBI.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=15.151-5; TISSUE=BURSA;
RX MEDLINE=98179131; PubMed=9510552;

```

RA Pharr G.T., Dodgson J.B., Hunt H.D., Bacon L.D.:
 RT "Class II MHC cDNAs in 1515 B-congenic chickens."
 RL Immunogenetics 47:350-354(1998).
 DR EMBL; U91532; AAC15813.1; -.
 DR InterPro; IPR000353; MHC_II_beta.
 DR Pfam; PF00969; MHC_II_beta; 1.
 DR ProDom; PD000328; MHC_II_beta; 1.
 KW Glycoprotein; MHC II; Transmembrane.
 FT NON_TER 1
 FT NON_TER 89 89
 SQ SEQUENCE 89 AA; 10724 MW; BC7D558B6AEB1379 CRC64;

Query Match 67.9%; Score 38; DB 7; Length 89;
 Best Local Similarity 85.7%; Pred. No. 5;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
 Db 75 RHNYGDF 81

RESULT 10
 Q43476 PRELIMINARY; PRT; 275 AA.
 AC Q43476;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Mammalian acyl CoA oxidase homologous (Fragment).
 GN CDR29.
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Specmatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticeae; Hordeum.
 OX NCBI_TaxID=4513;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=CV. ARDA; TISSUE=GREEN LEAF;
 RA Grossi M., Gulli M., Stanca A.M., Cattivelli L.;
 RT "Characterization of two barley genes that respond rapidly to
 RT dehydration stress."
 RL Plant Sci. 105:71-80(1995).
 DR EMBL; X84055; CAA58874.1; -.
 DR InterPro; IPR001552; Acyl-CoA_dh.
 DR InterPro; IPR005202; GRAS.
 DR Pfam; PF00441; Acyl-CoA_dh; 1.
 DR Pfam; PF03514; GRAS; 1.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 275 AA; 30689 MW; 332811FD05827472 CRC64;

Query Match 66.1%; Score 37; DB 10; Length 275;
 Best Local Similarity 70.0%; Pred. No. 29;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARHNYGSFAD 10
 Db 1 ANHNSGSFLD 10

RESULT 11
 Q8W127 PRELIMINARY; PRT; 618 AA.
 AC Q8W127;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Nuclear transcription factor SLN1.
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Specmatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticeae; Hordeum.
 OX NCBI_TaxID=4513;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=CV. MOREX;
 RA Chandler P., Marion-Poll A., Ellis M., Gubler F.;
 RT "Mutants at the slender 1 locus of 'Himalaya' barley: molecular and
 RT physiological characterization."
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF460219; AAL66734.1; -.
 DR InterPro; IPR005202; GRAS.
 DR Pfam; PF03514; GRAS; 1.
 SQ SEQUENCE 618 AA; 65206 MW; 5E862C8E8207E045 CRC64;

Query Match 66.1%; Score 37; DB 10; Length 618;
 Best Local Similarity 70.0%; Pred. No. 75;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARHNYGSFAD 10
 Db 471 ANHNSGSFLD 480

RESULT 12
 Q9MB96 PRELIMINARY; PRT; 625 AA.
 AC Q9MB96;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE OSGAI (Gibberellin-insensitive protein OSGAI).
 GN OSGAI.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoidae; Oryzeae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=CV. NIPPONBARE;
 RX MEDLINE=20179680; PubMed=10713441;
 RA Ogawa M., Kusano T., Katsumi M., Sano H.;
 RT "Rice gibberellin-insensitive gene homolog, OSGAI, encodes a nuclear-
 RT localized protein capable of gene activation at transcriptional
 RT level."
 RL Gene 245:21-29(2000).
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN=CV. NIPPONBARE;
 RA Buell C.R., Yuan Q., Ouyang S., Moffat K.S., Hill J.N., Gansberger K.,
 RA Brenner M., Burgess S., Hance M., Shvartsbeyn M., Tsitrin T.,
 RA Riggs F., Hsiao J., Zismann V., Blunt S., Pai G., VanAken S.E.,
 RA Uterback T.R., Feldblyum T.V., Quackenbush J., Salzberg S.L.,
 RA White O., Fraser C.M.;
 RT "Oryza sativa chromosome 3 BAC OSJNB0022E02 genomic sequence."
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB030956; BAA90749.1; -.
 DR EMBL; AC087797; AAK50137.1; -.
 DR InterPro; IPR005202; GRAS.
 DR Pfam; PF03514; GRAS; 1.
 SQ SEQUENCE 625 AA; 65406 MW; 034FF02719D42E97 CRC64;

Query Match 66.1%; Score 37; DB 10; Length 625;
 Best Local Similarity 70.0%; Pred. No. 76;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARHNYGSFAD 10
 Db 481 ANHNSGSFLD 490

RESULT 13
 Q9V6C3 PRELIMINARY; PRT; 685 AA.
 AC Q9V6C3;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)

```
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE CG8828 protein (LD47477P).
GN CG8828
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abail J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Dou L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleab J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nunoo J., Pacleab J., Paragab V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003822; AAF58505.1; -
DR EMBL; AY052018; AAK93442.1; -
DR FlyBase; FBgn0033740; CG8828.
SQ SEQUENCE 685 AA; 77978 MW; 4808C2FDEF7E3A91 CRC64;

Query Match 66.1%; Score 37; DB 5; Length 685;
Best Local Similarity 77.8%; Pred. No. 85;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSPAD 10
Db 654 RYNNGSPAD 662

Search completed: November 18, 2002, 17:40:47
Job time : 10.4912 secs
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RESULT 14
Q8TA74 PRELIMINARY; PRT; 5317 AA.
ID Q8TA74
AC Q8TA74;
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Ryanodine receptor.
OS Hemicentrotus pulcherrimus (Sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
OC Hemicentrotus.
OX NCBI_TaxID=7650;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21821894; PubMed=11832393;
RA Shiwa M., Murayama T., Ogawa Y.;
RT "Molecular cloning and characterization of ryanodine receptor from
RT unfertilized sea urchin eggs.";
RL Am. J. Physiol. Regul. Integr. Comp. Physiol. 282:R727-R737(2002).
DR EMBL; AB051576; BAB84714.1; -
KW Receptor.
SQ SEQUENCE 5317 AA; 597209 MW; 2FA8A1D8CB5E28A78 CRC64;

Query Match 66.1%; Score 37; DB 5; Length 5317;
Best Local Similarity 85.7%; Pred. No. 9.2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGS 7
Db 3329 ARHNYGA 3335
```

```
RESULT 15
P79474 PRELIMINARY; PRT; 39 AA.
ID P79474
AC P79474;
DT 01-MAY-1997 (TReMBLrel. 03, Created)
DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE MHC class II DRB (Fragment).
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
OC Cervidae; Cervinae; Cervus.
OX NCBI_TaxID=9860;
RN [1]
RP SEQUENCE FROM N.A.
RA Swarbrick P.A., Crawford A.M.;
RT "The MHC class II DRB intron 2 microsatellite of red deer.";
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U63077; AAB37777.1; -
DR InterPro; IPR000353; MHC_II_beta.
DR Pfam; PF00969; MHC_II_beta; 1.
DR ProDom; PD000328; MHC_II_beta; 1.
KW Glycoprotein; MHC II; Transmembrane.
FT NON_TER 1
FT NON_TER 39
SQ SEQUENCE 39 AA; 4767 MW; CAF3680999733D1D CRC64;

Query Match 64.3%; Score 36; DB 7; Length 39;
Best Local Similarity 85.7%; Pred. No. 4.8;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
Db 25 RHNYGVF 31
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:21:57 ; Search time 13.8235 Seconds
(without alignments)
96.394 Million cell updates/sec

Title: US-09-016-061-72
Perfect score: 56
Sequence: 1 ARHNYGSEAD 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	56	100.0	10	AAW76026	LM609 grafted anti
2	56	100.0	10	AAW76026	Mutant VH CDR3 pep
3	52	92.9	10	AAW76027	LM609 grafted anti
4	52	92.9	10	AAW76027	Mutant VH CDR3 pep
5	50	89.3	10	AAW76024	LM609 grafted anti
6	50	89.3	10	AAW76025	LM609 grafted anti
7	50	89.3	10	AAW76028	LM609 grafted anti
8	50	89.3	10	AAW76029	LM609 grafted anti
9	50	89.3	10	AAW76030	LM609 grafted anti
10	50	89.3	10	AAW76010	LM609 grafted anti

11	50	89.3	10	22	AAW76026	LM609 grafted anti
12	50	89.3	10	22	AAW76026	Mutant VH CDR3 pep
13	50	89.3	10	22	AAW76026	Mutant VH CDR3 pep
14	50	89.3	10	22	AAW76026	Mutant VH CDR3 pep
15	50	89.3	10	22	AAW76026	Mutant VH CDR3 pep
16	50	89.3	10	22	AAW76026	Mutant VH CDR3 pep
17	50	89.3	117	19	AAW76001	Vitaxin antibody h
18	50	89.3	117	19	AAW76003	LM609 antibody hea
19	50	89.3	117	20	AAW76031	Murine monoclonal
20	50	89.3	117	20	AAW76031	Humanised LM609 an
21	50	89.3	117	22	AAW76037	A heavy chain vari
22	50	89.3	117	22	AAW76037	A heavy chain vari
23	50	89.3	117	22	AAW76037	Vitaxin heavy chai
24	50	89.3	117	22	AAW76037	Antibody LM609 hea
25	50	89.3	118	20	AAW76038	Humanised LM609 an
26	50	89.3	118	20	AAW76038	Humanised LM609 an
27	50	89.3	118	20	AAW76038	Humanised LM609 an
28	50	89.3	118	20	AAW76038	Humanised LM609 an
29	50	89.3	130	20	AAW76039	Murine monoclonal
30	47	83.9	10	19	AAW76021	LM609 grafted anti
31	47	83.9	10	22	AAW76039	Mutant VH CDR3 pep
32	46	82.1	10	19	AAW76039	LM609 grafted anti
33	46	82.1	10	19	AAW76040	LM609 grafted anti
34	46	82.1	10	19	AAW76022	LM609 grafted anti
35	46	82.1	10	19	AAW76023	LM609 grafted anti
36	46	82.1	10	22	AAW76038	Mutant VH CDR3 pep
37	46	82.1	10	22	AAW76038	Mutant VH CDR3 pep
38	46	82.1	10	22	AAW76039	Multiple mutant VH
39	46	82.1	10	22	AAW76039	Multiple mutant VH
40	45	80.4	10	19	AAW76037	LM609 grafted anti
41	45	80.4	10	19	AAW76020	LM609 grafted anti
42	45	80.4	10	22	AAW76038	Mutant VH CDR3 pep
43	45	80.4	10	22	AAW76039	Multiple mutant VH
44	42	75.0	110	20	AAW84099	Vitronectin alpha-
45	42	75.0	117	20	AAW84093	Murine vitronectin

ALIGNMENTS

RESULT 1
AAW76026
ID AAW76026 standard; Protein; 10 AA.
XX AAW76026;
XX AC
XX AC
DT 02-NOV-1998 (first entry)
XX
DE LM609 grafted antibody V-H region CDR3 protein fragment #8.
XX
KW Vitaxin; antibody; variable region; heavy chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
XX
OS Mus sp.
XX
XX WO9833919-A2.
XX
PD 06-AUG-1998.
XX
PF 30-JAN-1998; 98WO-US01826.
XX
PR 30-JAN-1997; 97US-0791391.
XX
PA (IXSY-) IXSYS INC.
XX
PI Glaser SM, Huse WD;
XX
DR WPI; 1998-437472/37.
DR N-PSDB; AAW49863.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
XX Claim 62; Page 41; 129pp; English.
XX
XX AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
CC antibodies contain non-murine framework regions so are suitable for use
CC in humans. Enhanced types of LM609 have affinity more than 90 times
CC greater than that of parent the parent antibody.
XX
XX Sequence 10 AA;
SQ
Query Match 100.0%; Score 56; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0032;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ARHNYGSFAD 10
|||||
Db 1 ARHNYGSFAD 10
RESULT 2
AAB61384
ID AAB61384 standard; peptide; 10 AA.
XX
AC AAB61384;
XX
XX 03-APR-2001 (first entry)
XX
XX Mutant VH CDR3 peptide #7.
XX
XX LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
KW inflammatory; cancer; retina; restenosis; osteoporosis.
KW
XX Unidentified.
OS
XX WO200078815-A1.
PN
XX 28-DEC-2000.
PD
XX 23-JUN-2000; 2000WO-US17454.
PF
XX 24-JUN-1999; 99US-0339922.
PR
XX (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX
XX Huse WD, Wu H;
PI
XX WPI; 2001-050110/06.
XX
XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
PT osteoporosis -
XX
XX Disclosure; Page 41; 132pp; English.
XX
XX The present invention relates to enhanced LM609 grafted antibodies
CC exhibiting selective binding affinity to alphavbeta_3 integrin or
CC their functional fragments. The antibodies or their functional
CC fragments can be used in the diagnosis and treatment of
CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory

CC diseases (such as psoriasis and chronic articular rheumatism),
CC disorders associated with inappropriate or inopportune invasion of
CC vessels (such as diabetic retinopathy, neovascular glaucoma and
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
CC diseases (such as macular degeneration), restenosis and
CC osteoporosis.
XX
XX Sequence 10 AA;
SQ
Query Match 100.0%; Score 56; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0032;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ARHNYGSFAD 10
|||||
Db 1 ARHNYGSFAD 10
RESULT 3
AAW76027
ID AAW76027 standard; Protein; 10 AA.
XX
AC AAW76027;
XX
XX 02-NOV-1998 (first entry)
XX
XX LM609 grafted antibody V-H region CDR3 protein fragment #9.
XX
XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
XX
XX Mus sp.
OS
XX WO9833919-A2.
PN
XX 06-AUG-1998.
PD
XX 30-JAN-1998; 98WO-US01826.
PF
XX 30-JAN-1997; 97US-0791391.
PR
XX (IXSY-) IXSYS INC.
XX
XX Glaser SM, Huse WD;
PI
XX WPI; 1998-437472/37.
DR
XX N-PSDB; AAV49864.
XX
XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
XX Claim 62; Page 41; 129pp; English.
XX
XX AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
CC antibodies contain non-murine framework regions so are suitable for use
CC in humans. Enhanced types of LM609 have affinity more than 90 times
CC greater than that of parent the parent antibody.
XX
XX Sequence 10 AA;
SQ

Query Match 92.9%; Score 52; DB 19; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.015;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFAD 10
 DB 1 ARHNYGSFAE 10
 |||||

RESULT 4

AAB61385
 ID AAB61385 standard; peptide; 10 AA.

AC AAB61385;

DT 03-APR-2001 (first entry)

DE Mutant VH CDR3 peptide #8.

KW LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis.

OS Unidentified.

PN WO200078815-A1.

PD 28-DEC-2000.

PF 23-JUN-2000; 2000WO-US17454.

PR 24-JUN-1999; 99US-0339922.

PA (MOLE-) APPLIED MOLECULAR EVOLUTION.

PI Huse WD, Wu H;

DR WPI; 2001-050110/06.

Enhanced LM609 grafted antibodies exhibiting selective binding affinity to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of angiogenesis, inflammatory diseases e.g. psoriasis, cancers and osteoporosis -

PS Disclosure; Page 41; 132pp; English.

The present invention relates to enhanced LM609 grafted antibodies exhibiting selective binding affinity to alphavbeta_3 integrin or their functional fragments. The antibodies or their functional fragments can be used in the diagnosis and treatment of alphavbeta_3-mediated diseases such as angiogenesis, inflammatory diseases (such as psoriasis and chronic articular rheumatism), disorders associated with inappropriate or inopportune invasion of vessels (such as diabetic retinopathy, neovascular glaucoma and cancer disorders such as tumours and Kaposi's sarcoma), retinal diseases (such as macular degeneration), restenosis and osteoporosis.

SQ Sequence 10 AA;

Query Match 92.9%; Score 52; DB 22; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.015;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFAD 10
 DB 1 ARHNYGSFAE 10
 |||||

RESULT 5

AAW76024

ID AAW76024 standard; Protein; 10 AA.

XX

AAW76024;

DT 02-NOV-1998 (first entry)

DE LM609 grafted antibody V-H region CDR3 protein fragment #6.

KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.

OS Mus SP.

PN WO9833919-A2.

PD 06-AUG-1998.

PF 30-JAN-1998; 98WO-US01826.

PR 30-JAN-1997; 97US-0791391.

PA (IXSY-) IXSYS INC.

PI Glaser SM, Huse WD;

DR WPI; 1998-437472/37.

DR N-PSDB; AAV49861.

Humanised antibody, Vitaxin, that binds selectively to alphavbeta3 integrin - and related grafted antibodies based on murine monoclonal LM609, also related nucleic acid, used to treat, prevent or diagnose angiogenesis or restenosis

PS Claim 62; Page 41; 129pp; English.

AAW76007-W76040 are protein fragments of the grafted monoclonal antibody LM609 heavy and light chain variable region. LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3 and can be used to inhibit binding of alphavbeta3 to a ligand and thus block integrin-mediated signal transduction. This is useful in the treatment, prevention and diagnosis of alphavbeta3-mediated disease, specifically angiogenesis and restenosis (but also e.g. (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis etc.). The antibodies contain non-murine framework regions so are suitable for use in humans. Enhanced types of LM609 have affinity more than 90 times greater than that of parent the parent antibody.

SQ Sequence 10 AA;

Query Match 89.3%; Score 50; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.033;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
 DB 1 ARHNYGSFA 9
 |||||

RESULT 6

AAW76025

ID AAW76025 standard; Protein; 10 AA.

AC AAW76025;

DT 02-NOV-1998 (first entry)

DE LM609 grafted antibody V-H region CDR3 protein fragment #7.

KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;

KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 XX complementarity determining region.

OS Mus sp.
 XX WO9833919-A2.
 PN
 XX
 PD 06-AUG-1998.
 XX
 PF 30-JAN-1998; 98WO-US01826.
 XX
 PR 30-JAN-1997; 97US-0791391.
 XX
 PA (IXSY-) IXSYS INC.
 XX
 PI Glaser SM, Huse WD;
 XX
 DR WPI: 1998-437472/37.
 DR N-PSDB; AAV49862.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 PS Claim 62; Page 41; 129pp; English.

CC AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
 CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
 CC antibodies contain non-murine framework regions so are suitable for use
 CC in humans. Enhanced types of LM609 have affinity more than 90 times
 CC greater than that of parent the parent antibody.

XX Sequence 10 AA;
 SQ
 Query Match 89.3%; Score 50; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.033;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
 Db | | | | | | | | | |
 1 ARHNYGSFA 9

RESULT 7
 AAW76028
 ID AAW76028 standard; Protein; 10 AA.
 XX
 AC AAW76028;
 XX
 DT 02-NOV-1998 (first entry)
 XX
 DE LM609 grafted antibody V-H region CDR3 protein fragment #10.
 XX
 XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.

XX Mus sp.
 OS
 XX WO9833919-A2.
 PN

XX 06-AUG-1998.
 XX
 XX 30-JAN-1998; 98WO-US01826.
 XX
 PR 30-JAN-1997; 97US-0791391.
 XX
 PA (IXSY-) IXSYS INC.
 XX
 PI Glaser SM, Huse WD;
 XX
 DR WPI: 1998-437472/37.
 DR N-PSDB; AAV49865.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX

PS Claim 62; Page 41; 129pp; English.

XX AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
 CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
 CC antibodies contain non-murine framework regions so are suitable for use
 CC in humans. Enhanced types of LM609 have affinity more than 90 times
 CC greater than that of parent the parent antibody.

XX Sequence 10 AA;

Query Match 89.3%; Score 50; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.033;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
 Db | | | | | | | | | |
 1 ARHNYGSFA 9

RESULT 8
 AAW76029
 ID AAW76029 standard; Protein; 10 AA.
 XX
 AC AAW76029;
 XX
 DT 02-NOV-1998 (first entry)
 XX

DE LM609 grafted antibody V-H region CDR3 protein fragment #11.
 XX
 XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.

OS Mus sp.
 XX
 PN WO9833919-A2.
 XX
 PD 06-AUG-1998.
 XX
 PF 30-JAN-1998; 98WO-US01826.
 XX
 PR 30-JAN-1997; 97US-0791391.
 XX
 PA (IXSY-) IXSYS INC.


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XX Glaser SM, Huse WD;
XX WPI: 1998-437472/37.
XX N-PSDB; AAV49866.
XX
XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
XX integrin - and related grafted antibodies based on murine monoclonal
XX LM609, also related nucleic acid, used to treat, prevent or diagnose
XX angiogenesis or restenosis
XX
XX Claim 62; Page 41; 129pp; English.
XX
XX AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
XX LM609 heavy and light chain variable region. LM609 and the antibody
XX vitaxin bind selectively to integrin alphavbeta3 and can be used to
XX inhibit binding of alphavbeta3 to a ligand and thus block
XX integrin-mediated signal transduction. This is useful in the treatment,
XX prevention and diagnosis of alphavbeta3-mediated disease, specifically
XX angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
XX diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
XX rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
XX antibodies contain non-murine framework regions so are suitable for use
XX in humans. Enhanced types of LM609 have affinity more than 90 times
XX greater than that of parent the parent antibody.
XX
XX Sequence 10 AA;
XX
XX Query Match 89.3%; Score 50; DB 19; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 0.033;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 ARHNYGSFA 9
XX | | | | | | | |
XX Db 1 ARHNYGSFA 9
XX
XX RESULT 9
XX AAW76030
XX ID AAW76030 standard; Protein; 10 AA.
XX AC AAW76030;
XX DT 02-NOV-1998 (first entry)
XX DE LM609 grafted antibody V-H region CDR3 protein fragment #12.
XX XX
XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
XX LM609; inhibitor; integrin-mediated signal transduction; treatment;
XX diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
XX neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
XX macular degeneration; osteoporosis; primer; V-H region; CDR;
XX complementarity determining region.
XX
XX OS Mus sp.
XX XX
XX PN WO9833919-A2.
XX XX
XX PD 06-AUG-1998.
XX XX
XX PF 30-JAN-1998; 98WO-US01826.
XX XX
XX PR 30-JAN-1997; 97US-0791391.
XX XX
XX PA (IXSY-) IXSYS INC.
XX XX
XX PI Glaser SM, Huse WD;
XX XX
XX DR WPI: 1998-437472/37.
XX N-PSDB; AAV49867.
XX
XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
XX integrin - and related grafted antibodies based on murine monoclonal
XX LM609 heavy and light chain variable region. LM609 and the antibody
XX vitaxin bind selectively to integrin alphavbeta3 and can be used to
XX
XX Sequence 10 AA;
XX
XX Query Match 89.3%; Score 50; DB 19; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 0.033;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 ARHNYGSFA 9
XX | | | | | | | |
XX Db 1 ARHNYGSFA 9
XX
XX RESULT 10
XX AAW76010
XX ID AAW76010 standard; Protein; 10 AA.
XX AC AAW76010;
XX DT 02-NOV-1998 (first entry)
XX DE LM609 grafted antibody V-H region CDR3 protein fragment #1.
XX XX
XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
XX LM609; inhibitor; integrin-mediated signal transduction; treatment;
XX diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
XX neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
XX macular degeneration; osteoporosis; primer; V-H region; CDR;
XX complementarity determining region.
XX
XX OS Mus sp.
XX XX
XX PN WO9833919-A2.
XX XX
XX PD 06-AUG-1998.
XX XX
XX PF 30-JAN-1998; 98WO-US01826.
XX XX
XX PR 30-JAN-1997; 97US-0791391.
XX XX
XX PA (IXSY-) IXSYS INC.
XX XX
XX PI Glaser SM, Huse WD;
XX XX
XX DR WPI: 1998-437472/37.
XX N-PSDB; AAV49847.
XX
XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
XX integrin - and related grafted antibodies based on murine monoclonal
XX LM609, also related nucleic acid, used to treat, prevent or diagnose
XX angiogenesis or restenosis
XX
XX Disclosure; Page 40; 129pp; English.
XX
XX AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
XX LM609 heavy and light chain variable region. LM609 and the antibody
XX vitaxin bind selectively to integrin alphavbeta3 and can be used to

```

CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
 CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
 CC antibodies contain non-murine framework regions so are suitable for use
 CC in humans. Enhanced types of LM609 have affinity more than 90 times
 CC greater than that of parent the parent antibody.

XX Sequence 10 AA;

Query Match 89.3%; Score 50; DB 19; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.033;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9

Db 1 ARHNYGSFA 9

RESULT 11

AAB61368

ID AAB61368 standard; peptide; 10 AA.

XX AC

XX AC

XX AAB61368;

DT 03-APR-2001 (first entry)

DE LM609 VH CDR3 peptide.

XX LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;

KW inflammatory; cancer; retina; restenosis; osteoporosis.

XX Unidentified.

OS WO200078815-A1.

PN 28-DEC-2000.

XX 23-JUN-2000; 2000WO-US17454.

XX 24-JUN-1999; 99US-0339922.

XX (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX Huse WD, Wu H;

XX WPI; 2001-050110/06.

XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity

PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of

PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and

PT osteoporosis -

XX Disclosure; Page 39; 132pp; English.

XX The present invention relates to enhanced LM609 grafted antibodies

CC exhibiting selective binding affinity to alphavbeta_3 integrin or

CC their functional fragments. The antibodies or their functional

CC fragments can be used in the diagnosis and treatment of

CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory

CC diseases (such as psoriasis and chronic articular rheumatism),

CC disorders associated with inappropriate or inopportune invasion of

CC vessels (such as diabetic retinopathy, neovascular glaucoma and

CC cancer disorders such as tumours and Kaposi's sarcoma), retinal

CC diseases (such as macular degeneration), restenosis and

XX osteoporosis.

XX Sequence 10 AA;

Query Match 89.3%; Score 50; DB 22; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.033;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9

Db 1 ARHNYGSFA 9

RESULT 13

AAB61383

ID AAB61383 standard; peptide; 10 AA.

XX AC

XX AAB61383;

XX 03-APR-2001 (first entry)

DT 03-APR-2001 (first entry)

XX Sequence 10 AA;

Query Match 89.3%; Score 50; DB 22; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.033;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9

Db 1 ARHNYGSFA 9

RESULT 13

AAB61383

ID AAB61383 standard; peptide; 10 AA.

XX AC

XX AAB61383;

XX 03-APR-2001 (first entry)

DT 03-APR-2001 (first entry)

XX Sequence 10 AA;

Query Match 89.3%; Score 50; DB 22; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.033;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9

Db 1 ARHNYGSFA 9

RESULT 13

AAB61383

ID AAB61383 standard; peptide; 10 AA.

XX AC

XX AAB61383;

XX 03-APR-2001 (first entry)

DT 03-APR-2001 (first entry)

XX Sequence 10 AA;

Query Match 89.3%; Score 50; DB 22; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.033;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9

Db 1 ARHNYGSFA 9

RESULT 13

AAB61383

ID AAB61383 standard; peptide; 10 AA.

XX AC

XX AAB61383;

XX 03-APR-2001 (first entry)

DT 03-APR-2001 (first entry)

XX Sequence 10 AA;

Query Match 89.3%; Score 50; DB 22; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.033;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9

Db 1 ARHNYGSFA 9

RESULT 13

AAB61383

ID AAB61383 standard; peptide; 10 AA.

XX AC

XX AAB61383;

XX 03-APR-2001 (first entry)

DT 03-APR-2001 (first entry)

XX Sequence 10 AA;

Query Match 89.3%; Score 50; DB 22; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.033;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9

Db 1 ARHNYGSFA 9

RESULT 13

AAB61383

ID AAB61383 standard; peptide; 10 AA.

XX AC

XX AAB61383;

XX 03-APR-2001 (first entry)

DT 03-APR-2001 (first entry)

XX Sequence 10 AA;

Query Match 89.3%; Score 50; DB 22; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.033;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9

Db 1 ARHNYGSFA 9

RESULT 13

AAB61383

ID AAB61383 standard; peptide; 10 AA.

XX AC

XX AAB61383;

XX 03-APR-2001 (first entry)

DT 03-APR-2001 (first entry)

XX Sequence 10 AA;

Query Match 89.3%; Score 50; DB 22; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.033;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9

Db 1 ARHNYGSFA 9

RESULT 13

AAB61383

ID AAB61383 standard; peptide; 10 AA.

XX AC

XX AAB61383;

XX 03-APR-2001 (first entry)

DT 03-APR-2001 (first entry)

XX Sequence 10 AA;

Query Match 89.3%; Score 50; DB 22; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.033;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9

Db 1 ARHNYGSFA 9

RESULT 13

AAB61383

ID AAB61383 standard; peptide; 10 AA.

XX AC

XX AAB61383;

XX 03-APR-2001 (first entry)

DT 03-APR-2001 (first entry)

XX Sequence 10 AA;

Query Match 89.3%; Score 50; DB 22; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.033;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9

Db 1 ARHNYGSFA 9

RESULT 13

AAB61383

ID AAB61383 standard; peptide; 10 AA.

XX AC

XX AAB61383;

XX 03-APR-2001 (first entry)

DT 03-APR-2001 (first entry)

XX Sequence 10 AA;

Query Match 89.3%; Score 50; DB 22; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.033;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9

Db 1 ARHNYGSFA 9

RESULT 13

AAB61383

ID AAB61383 standard; peptide; 10 AA.

XX AC

XX AAB61383;

XX 03-APR-2001 (first entry)

DT 03-APR-2001 (first entry)

XX Sequence 10 AA;

Query Match 89.3%; Score 50; DB 22; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.033;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9

Db 1 ARHNYGSFA 9

RESULT 13

AAB61383

ID AAB61383 standard; peptide; 10 AA.

XX AC

XX AAB61383;

XX 03-APR-2001 (first entry)

DT 03-APR-2001 (first entry)

XX Sequence 10 AA;

Query Match 89.3%; Score 50; DB 22; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.033;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9

Db 1 ARHNYGSFA 9

RESULT 13

AAB61383

ID AAB61383 standard; peptide; 10 AA.

XX AC

XX AAB61383;

XX 03-APR-2001 (first entry)

DT 03-APR-2001 (first entry)

XX Sequence 10 AA;

Query Match 89.3%; Score 50; DB 22; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.033;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9

Db 1 ARHNYGSFA 9

RESULT 13

AAB61383

ID AAB61383 standard; peptide; 10 AA.

XX AC

XX AAB61383;

XX 03-APR-2001 (first entry)

DT 03-APR-2001 (first entry)

XX Sequence 10 AA;

Query Match 89.3%; Score 50; DB 22; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.033;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9

Db 1 ARHNYGSFA 9

RESULT 13

AAB61383

ID AAB61383 standard; peptide; 10 AA.

XX AC

XX AAB61383;

XX 03-APR-2001 (first entry)

DT 03-APR-2001 (first entry)

XX Sequence 10 AA;

Query Match 89.3%; Score 50; DB 22; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.033;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9

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XX DE Mutant VH CDR3 peptide #6.
XX LM609; grafted antibody; alphaVbeta_3 integrin; angiogenesis;
KW inflammatory; cancer; retina; restenosis; osteoporosis.
XX OS Unidentified.
XX PN WO200078815-A1.
XX PD 28-DEC-2000.
XX PF 23-JUN-2000; 2000WO-US17454.
XX PR 24-JUN-1999; 99US-0339922.
XX PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX PI Huse WD, Wu H;
XX DR WPI; 2001-050110/06.
XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
PT osteoporosis.
XX Disclosure; Page 41; 132pp; English.
XX The present invention relates to enhanced LM609 grafted antibodies
CC exhibiting selective binding affinity to alphaVbeta_3 integrin or
CC their functional fragments. The antibodies or their functional
CC fragments can be used in the diagnosis and treatment of
CC alphaVbeta_3-mediated diseases such as angiogenesis, inflammatory
CC diseases (such as psoriasis and chronic articular rheumatism),
CC disorders associated with inappropriate or inopportune invasion of
CC vessels (such as diabetic retinopathy, neovascular glaucoma and
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
CC diseases (such as macular degeneration), restenosis and
XX osteoporosis.
XX Sequence 10 AA;
XX Query Match 89.3%; Score 50; DB 22; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 0.033;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 ARHNYGSFA 9
XX DB 1 ARHNYGSFA 9
XX RESULT 14
XX AAB61386
XX ID AAB61386 standard; peptide; 10 AA.
XX AC AAB61386;
XX DT 03-APR-2001 (first entry)
XX DE Mutant VH CDR3 peptide #9.
XX LM609; grafted antibody; alphaVbeta_3 integrin; angiogenesis;
KW inflammatory; cancer; retina; restenosis; osteoporosis.
XX OS Unidentified.
XX PN WO200078815-A1.
XX PD 28-DEC-2000.
XX PF 23-JUN-2000; 2000WO-US17454.
XX PR 24-JUN-1999; 99US-0339922.
XX PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX PI Huse WD, Wu H;
XX DR WPI; 2001-050110/06.
XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
PT osteoporosis.
XX Disclosure; Page 41; 132pp; English.
XX The present invention relates to enhanced LM609 grafted antibodies
CC exhibiting selective binding affinity to alphaVbeta_3 integrin or
CC their functional fragments. The antibodies or their functional
CC fragments can be used in the diagnosis and treatment of
CC alphaVbeta_3-mediated diseases such as angiogenesis, inflammatory
CC diseases (such as psoriasis and chronic articular rheumatism),
CC disorders associated with inappropriate or inopportune invasion of
CC vessels (such as diabetic retinopathy, neovascular glaucoma and
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
CC diseases (such as macular degeneration), restenosis and
XX osteoporosis.
XX Sequence 10 AA;
XX Query Match 89.3%; Score 50; DB 22; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 0.033;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 ARHNYGSFA 9
XX DB 1 ARHNYGSFA 9
XX RESULT 15
XX AAB61387
XX ID AAB61387 standard; peptide; 10 AA.
XX AC AAB61387;
XX DT 03-APR-2001 (first entry)
XX DE Mutant VH CDR3 peptide #10.
XX LM609; grafted antibody; alphaVbeta_3 integrin; angiogenesis;
KW inflammatory; cancer; retina; restenosis; osteoporosis.
XX OS Unidentified.
XX PN WO200078815-A1.
XX PD 28-DEC-2000.
XX PF 23-JUN-2000; 2000WO-US17454.
XX PR 24-JUN-1999; 99US-0339922.
XX PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX PI Huse WD, Wu H;
XX DR WPI; 2001-050110/06.
XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
PT osteoporosis.
XX Disclosure; Page 41; 132pp; English.

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PR 24-JUN-1999; 99US-0339922.
XX (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX Huse WD, Wu H;
XX WPI; 2001-050110/06.
XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
PT osteoporosis.
XX Disclosure; Page 41; 132pp; English.
XX The present invention relates to enhanced LM609 grafted antibodies
CC exhibiting selective binding affinity to alphaVbeta_3 integrin or
CC their functional fragments. The antibodies or their functional
CC fragments can be used in the diagnosis and treatment of
CC alphaVbeta_3-mediated diseases such as angiogenesis, inflammatory
CC diseases (such as psoriasis and chronic articular rheumatism),
CC disorders associated with inappropriate or inopportune invasion of
CC vessels (such as diabetic retinopathy, neovascular glaucoma and
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
CC diseases (such as macular degeneration), restenosis and
XX osteoporosis.
XX Sequence 10 AA;
XX Query Match 89.3%; Score 50; DB 22; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 0.033;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 ARHNYGSFA 9
XX DB 1 ARHNYGSFA 9
XX RESULT 15
XX AAB61387
XX ID AAB61387 standard; peptide; 10 AA.
XX AC AAB61387;
XX DT 03-APR-2001 (first entry)
XX DE Mutant VH CDR3 peptide #10.
XX LM609; grafted antibody; alphaVbeta_3 integrin; angiogenesis;
KW inflammatory; cancer; retina; restenosis; osteoporosis.
XX OS Unidentified.
XX PN WO200078815-A1.
XX PD 28-DEC-2000.
XX PF 23-JUN-2000; 2000WO-US17454.
XX PR 24-JUN-1999; 99US-0339922.
XX PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX PI Huse WD, Wu H;
XX DR WPI; 2001-050110/06.
XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
PT osteoporosis.
XX Disclosure; Page 41; 132pp; English.

```

XX The present invention relates to enhanced LM609 grafted antibodies
CC exhibiting selective binding affinity to alphavbeta_3 integrin or
CC their functional fragments. The antibodies or their functional
CC fragments can be used in the diagnosis and treatment of
CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
CC diseases (such as psoriasis and chronic articular rheumatism),
CC disorders associated with inappropriate or inopportune invasion of
CC vessels (such as diabetic retinopathy, neovascular glaucoma and
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
CC diseases (such as macular degeneration), restenosis and
CC osteoporosis.

XX

SQ Sequence 10 AA:

Query Match 89.3%; Score 50; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
| | | | | | | | | |
Db 1 ARHNYGSFA 9

Search completed: November 18, 2002, 17:31:38
Job time : 13.8235 secs

GenCore version 5.1.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:54:45 ; Search time 1.96078 Seconds
(without alignments)
76.811 Million cell updates/sec

Title: US-09-016-061-72

Perfect score: 56

Sequence: 1 ARHNGYSPAD 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 97044 seqs, 15060890 residues

Total number of hits satisfying chosen parameters: 97044

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications AA.*
- 1: /cgn2_6/ptodata/1/pubpaa/us08_NEW_PUB.pep.*
 - 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
 - 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
 - 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
 - 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
 - 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
 - 7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
 - 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
 - 9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
 - 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
 - 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
 - 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
 - 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
 - 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	ID	Description
1	50	89.3	117	8	US-08-790-540A-2	Sequence 2, Appli
2	50	89.3	117	8	US-08-790-540A-6	Sequence 6, Appli
3	50	89.3	117	8	US-08-791-391A-2	Sequence 2, Appli
4	50	89.3	117	8	US-08-791-391A-6	Sequence 6, Appli
5	38	67.9	464	10	US-09-791-171-62	Sequence 62, Appl
6	36	64.3	14	1	US-08-677-599B-22	Sequence 22, Appl
7	36	64.3	101	10	US-09-764-853-432	Sequence 432, App
8	34	60.7	30	10	US-09-839-884-40	Sequence 40, Appl
9	34	60.7	287	10	US-09-415-540-5	Sequence 5, Appli
10	34	60.7	309	10	US-09-815-242-13711	Sequence 13711, A
11	34	60.7	407	9	US-09-895-913A-136	Sequence 136, App
12	33	58.9	14	1	US-08-677-599B-21	Sequence 21, Appl
13	33	58.9	58	10	US-09-925-299-1363	Sequence 1363, Ap
14	33	58.9	269	10	US-09-764-853-654	Sequence 654, App
15	33	58.9	571	10	US-09-216-393-327	Sequence 327, App
16	32	57.1	14	1	US-08-677-599B-11	Sequence 11, Appl
17	32	57.1	14	1	US-08-677-599B-12	Sequence 12, Appl
18	32	57.1	14	1	US-08-677-599B-13	Sequence 13, Appl
19	32	57.1	14	1	US-08-677-599B-14	Sequence 14, Appl

Query Match 89.3%; Score 50; DB 8; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.011;

20	32	57.1	14	1	US-08-677-599B-15	Sequence 15, Appl
21	32	57.1	14	1	US-08-677-599B-16	Sequence 16, Appl
22	32	57.1	14	1	US-08-677-599B-17	Sequence 17, Appl
23	32	57.1	14	1	US-08-677-599B-18	Sequence 18, Appl
24	32	57.1	14	1	US-08-677-599B-19	Sequence 19, Appl
25	32	57.1	14	1	US-08-677-599B-20	Sequence 20, Appl
26	32	57.1	14	1	US-08-677-599B-23	Sequence 23, Appl
27	32	57.1	15	10	US-09-756-983-11	Sequence 11, Appl
28	32	57.1	25	1	US-08-677-599B-8	Sequence 8, Appli
29	32	57.1	93	12	US-10-081-281-121	Sequence 121, App
30	32	57.1	94	10	US-09-766-378A-37	Sequence 37, Appl
31	32	57.1	181	10	US-09-815-837-103	Sequence 103, App
32	32	57.1	183	10	US-09-815-837-16	Sequence 16, Appl
33	32	57.1	184	10	US-09-815-837-15	Sequence 15, Appl
34	32	57.1	185	10	US-09-815-837-13	Sequence 13, Appl
35	32	57.1	185	10	US-09-815-837-14	Sequence 14, Appl
36	32	57.1	186	10	US-09-815-837-17	Sequence 17, Appl
37	32	57.1	186	10	US-09-815-837-19	Sequence 19, Appl
38	32	57.1	186	10	US-09-815-837-20	Sequence 20, Appl
39	32	57.1	187	10	US-09-815-837-18	Sequence 18, Appl
40	32	57.1	189	10	US-09-815-837-21	Sequence 21, Appl
41	32	57.1	189	10	US-09-815-837-22	Sequence 22, Appl
42	32	57.1	193	10	US-09-815-837-23	Sequence 23, Appl
43	32	57.1	193	10	US-09-815-837-24	Sequence 24, Appl
44	32	57.1	196	10	US-09-741-669-368	Sequence 368, App
45	32	57.1	196	10	US-09-912-020-376	Sequence 376, App

ALIGNMENTS

RESULT 1
US-08-790-540A-2
; Sequence 2, Application US/08790540A
; Patent No. US20010011125A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,540A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9901
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-790-540A-2

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
|||||

Db 97 ARHNYGSFA 105

RESULT 2
US-08-790-540A-6
; Sequence 6, Application US/08790540A
; Patent No. US2001001125A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TELECOMMUNICATION INFORMATION:
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,540A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-790-540A-6

Query Match 89.3%; Score 50; DB 8; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
|||||

Db 97 ARHNYGSFA 105

RESULT 3
US-08-791-391A-2
; Sequence 2, Application US/08791391A
; Patent No. US20010016645A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TELECOMMUNICATION INFORMATION:
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,391A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-391A-2

Query Match 89.3%; Score 50; DB 8; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
|||||

Db 97 ARHNYGSFA 105

RESULT 4
US-08-791-391A-6
; Sequence 6, Application US/08791391A
; Patent No. US20010016645A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TELECOMMUNICATION INFORMATION:
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,391A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-391A-6

Query Match 89.3%; Score 50; DB 8; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
Db 97 ARHNYGSFA 105

RESULT 5

US-09-791-171-62
; Sequence 62, Application US/09791171
; Patent No. US20020094336A1
; GENERAL INFORMATION:
; APPLICANT: ANDERSEN, Peter
; APPLICANT: NIELSEN, Rikke
; APPLICANT: OETTINGER, Thomas
; APPLICANT: RASMUSSEN, Peter Birk
; APPLICANT: ROSENKRANDS, Ida
; APPLICANT: WELDLINGH, Karln
; APPLICANT: FLORIO, Walter
; TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
; FILE REFERENCE: 670001-2002.1
; CURRENT APPLICATION NUMBER: US/09/791,171
; CURRENT FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 09/050,739
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 0376/97
; PRIOR FILING DATE: 1997-04-02
; PRIOR APPLICATION NUMBER: 1277/97
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/044,624
; PRIOR FILING DATE: 1997-04-18
; PRIOR APPLICATION NUMBER: 60/070,488
; PRIOR FILING DATE: 1998-01-05
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 62
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-791-171-62

Query Match 67.9%; Score 38; DB 10; Length 464;
Best Local Similarity 75.0%; Pred. No. 7.6;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSPAD 10
Db 110 HGYGTSPAD 117

RESULT 6

US-08-677-599B-22
; Sequence 22, Application US/08677599B
; Patent No. US20020155117A1
; GENERAL INFORMATION:
; APPLICANT: Sucia-Foca, Nicole
; TITLE OF INVENTION: METHODS FOR DETECTING ORGAN ALLOGRAFT
; TITLE OF INVENTION: REJECTION AND USES THEREOF
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/677,599B
; FILING DATE: 08-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq., John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 50161-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212/378/0400
; TELEFAX: 212/391/0525
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-677-599B-22

Query Match 64.3%; Score 36; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.47;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYG 6
Db 9 ARHNYG 14

RESULT 7

US-09-764-853-432
; Sequence 432, Application US/09764853
; Patent No. US20020090672A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P206
; CURRENT APPLICATION NUMBER: US/09/764,853
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 939
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 432
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-853-432

Query Match 64.3%; Score 36; DB 10; Length 101;
Best Local Similarity 85.7%; Pred. No. 3.7;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 64 RHNYSSF 70

RESULT 8

US-09-839-884-40
; Sequence 40, Application US/09839884
; Patent No. US20020076739A1
; GENERAL INFORMATION:
; APPLICANT: Aebersold, Rudolf H.
; APPLICANT: Gelb, Michael H.
; APPLICANT: Gygi, Steven
; APPLICANT: Scott, C R
; APPLICANT: Turecek, Frantisek
; APPLICANT: Gerber, Scott A
; APPLICANT: Rist, Beate
; TITLE OF INVENTION: Rapid Quantitative Analysis of Proteins or Protein
; TITLE OF INVENTION: Function in Complex Mixture

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; FILE REFERENCE: 64-98A
; CURRENT APPLICATION NUMBER: US/09/839,884
; CURRENT FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: 09/383,062
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 60/097,788
; PRIOR FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40
; LENGTH: 30
; TYPE: PRT
; ORGANISM: yeast
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (2)
; OTHER INFORMATION: C at position 2 is ICAT-labeled cysteinyl residue.
US-09-839-884-40

Query Match          60.7%; Score 34; DB 10; Length 30;
Best Local Similarity 83.3%; Pred. No. 2.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      3 HNYGSP 8
        |||||
DB      10 HNYGAF 15

RESULT 9
US-09-415-540-5
; Sequence 5, Application US/09415540
; Patent No. US20010010911A1
; GENERAL INFORMATION:
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: A NOVEL HUMAN PYROPHOSPHATASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 317A Porter Drive
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/415,540
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/741,437
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0148 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 855-0555
; TELEFAX: (415) 845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 287 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 4199
US-09-415-540-5
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Query Match          60.7%; Score 34; DB 10; Length 287;
Best Local Similarity 83.3%; Pred. No. 25;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      3 HNYGSP 8
        |||||
DB      92 HNYGAF 97

RESULT 10
US-09-815-242-13711
; Sequence 13711, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13711
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Salmonella typhi
US-09-815-242-13711

Query Match          60.7%; Score 34; DB 10; Length 309;
Best Local Similarity 75.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3 HNYGSPAD 10
        |||||
DB      47 HNLGRPAD 54

RESULT 11
US-09-895-913A-136
; Sequence 136, Application US/09895913A
; Patent No. US20020160456A1
; GENERAL INFORMATION:
; APPLICANT: Kleanthous, Harold
; APPLICANT: Al-Garawi, Amal
; APPLICANT: Miller, Charles
; APPLICANT: Tomb, Jean Francois
; APPLICANT: Oomen, Raymond P.
; TITLE OF INVENTION: Identification of Polynucleotides
; FILE REFERENCE: Encoding No. US20020160456A1el Helicobacter Polypeptides in t
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; CURRENT APPLICATION NUMBER: US/09/895,913A
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 08/881,227
; PRIOR FILING DATE: 1997-06-24
; NUMBER OF SEQ ID NOS: 368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 136
; LENGTH: 407
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-895-913A-136

Query Match      60.7%; Score 34; DB 9; Length 407;
Best Local Similarity 85.7%; Pred. No. 36;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  4 NYGSFAD 10
Db  45 NYGSFKD 51

RESULT 12
US-08-677-599B-21
; Sequence 21, Application US/08677599B
; Patent No. US20020155117A1
; GENERAL INFORMATION:
; APPLICANT: Sucia-Foca, Nicole
; TITLE OF INVENTION: METHODS FOR DETECTING ORGAN ALLOGRAFT
; TITLE OF INVENTION: REJECTION AND USES THEREOF
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/677,599B
; FILING DATE: 08-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq., John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 50161-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212/278/0400
; TELEFAX: 212/391/0525
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-677-599B-21

Query Match      58.9%; Score 33; DB 1; Length 14;
Best Local Similarity 83.3%; Pred. No. 1.7;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY  1 ARHNYG 6
Db  9 SRHNYG 14

RESULT 13
US-09-925-299-1363
```

```
; Sequence 1363, Application US/09925299
; Patent No. US20020055627A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1363
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (11)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (56)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-299-1363

Query Match      58.9%; Score 33; DB 10; Length 58;
Best Local Similarity 50.0%; Pred. No. 7.4;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY  1 ARHNYGSFAD 10
Db  15 ARHSENFHSD 24

RESULT 14
US-09-764-853-654
; Sequence 654, Application US/09764853
; Patent No. US20020090672A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJ206
; CURRENT APPLICATION NUMBER: US/09/764,853
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 939
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 654
; LENGTH: 269
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-853-654

Query Match      58.9%; Score 33; DB 10; Length 269;
Best Local Similarity 60.0%; Pred. No. 36;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY  1 ARHNYGSFAD 10
Db  238 ARHSGSGFGD 247

RESULT 15
US-09-216-393-327
; Sequence 327, Application US/09216393
; Patent No. US20010014447A1
; GENERAL INFORMATION:
; APPLICANT: Milhausen, Michael James
; TITLE OF INVENTION: TOXOPLASMA GONDI PROTEINS, NUCLEIC ACID MOLECULES, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: TX-1-C2
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; CURRENT APPLICATION NUMBER: US/09/216,393
; CURRENT FILING DATE: 1998-12-18
; EARLIER APPLICATION NUMBER: 08/994,825
; EARLIER FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 364
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 327
; LENGTH: 571
; TYPE: PRT
; ORGANISM: Toxoplasma gondii
US-09-216-393-327

Query Match 58.9%; Score 33; DB 10; Length 571;
Best Local Similarity 71.4%; Pred. No. 79;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 NYGSFAD 10
| | | | |
Db 33 NYGAFSD 39

Search completed: November 18, 2002, 18:45:17
Job time : 2.96078 secs

GenCore version 5.1.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:01 ; Search time 4.2402 Seconds
(without alignments)
69.390 Million cell updates/sec

Title: US-09-016-061-72

Perfect score: 56

Sequence: 1 ARHNYGSPAD 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	64.3	94	3	US-09-147-550-14
2	36	64.3	94	3	US-09-147-550-45
3	36	64.3	94	3	US-09-147-550-48
4	36	64.3	94	3	US-09-147-550-77
5	36	64.3	94	3	US-09-147-550-84
6	36	64.3	94	3	US-09-147-550-90
7	36	64.3	94	3	US-09-147-550-101
8	36	64.3	94	4	US-09-557-917-14
9	36	64.3	94	4	US-09-557-917-45
10	36	64.3	94	4	US-09-557-917-48
11	36	64.3	94	4	US-09-557-917-77
12	36	64.3	94	4	US-09-557-917-84
13	36	64.3	94	4	US-09-557-917-90
14	36	64.3	94	4	US-09-557-917-101
15	36	64.3	119	3	US-08-767-128-6
16	34	60.7	165	4	US-08-858-207A-510
17	34	60.7	191	4	US-09-443-041A-24
18	34	60.7	236	4	US-09-443-041A-30
19	34	60.7	260	4	US-09-443-041A-10
20	34	60.7	261	4	US-09-443-041A-26
21	34	60.7	269	4	US-09-443-041A-28
22	34	60.7	271	4	US-09-443-041A-32
23	34	60.7	271	4	US-09-443-041A-33
24	34	60.7	286	2	US-08-809-267-3
25	34	60.7	286	5	PCT-US95-13662A-3
26	34	60.7	287	2	US-08-741-437-5
27	34	60.7	287	2	US-09-134-593-5

ALIGNMENTS

RESULT 1

US-09-147-550-14
; Sequence 14, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-14

Query Match 64.3%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
| | | | |
Db 80 RHNYGVF 86

RESULT 2

US-09-147-550-45
; Sequence 45, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979

; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-45

Query Match 64.3%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
|||||
Db 80 RHNYGVF 86

RESULT 3

US-09-147-550-48
; Sequence 48, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko

; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-48

Query Match 64.3%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
|||||
Db 80 RHNYGVF 86

RESULT 4

US-09-147-550-77
; Sequence 77, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko

; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 77
; LENGTH: 94

; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-77

Query Match 64.3%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
|||||
Db 80 RHNYGVF 86

RESULT 5

US-09-147-550-84
; Sequence 84, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko

; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-84

Query Match 64.3%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
|||||
Db 80 RHNYGVF 86

RESULT 6

US-09-147-550-90
; Sequence 90, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko

; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 90
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-90

Query Match 64.3%; Score 36; DB 3; Length 94;

Best Local Similarity 85.7%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
Db 80 RHNYGVF 86

RESULT 7
US-09-147-550-101
; Sequence 101, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; PRIOR FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-101

Query Match 64.3%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
Db 80 RHNYGVF 86

RESULT 8
US-09-557-917-14
; Sequence 14, Application US/09557917
; Patent No. 6284457
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-14

Query Match 64.3%; Score 36; DB 4; Length 94;
Best Local Similarity 85.7%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8

Qy 2 RHNYGSF 8
Db 80 RHNYGVF 86

RESULT 9
US-09-557-917-45
; Sequence 45, Application US/09557917
; Patent No. 6284457
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-45

Query Match 64.3%; Score 36; DB 4; Length 94;
Best Local Similarity 85.7%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
Db 80 RHNYGVF 86

RESULT 10
US-09-557-917-48
; Sequence 48, Application US/09557917
; Patent No. 6284457
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-48

Query Match 64.3%; Score 36; DB 4; Length 94;
Best Local Similarity 85.7%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8

Db 80 RHNYGVF 86
|||||

RESULT 11
US-09-557-917-77
; Sequence 77, Application US/09557917
; Patent No. 6284457
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 77
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-77

Query Match 64.3%; Score 36; DB 4; Length 94;
Best Local Similarity 85.7%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

Qy 2 RHNYGSF 8
|||||

RESULT 12
US-09-557-917-84
; Sequence 84, Application US/09557917
; Patent No. 6284457
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-84

Query Match 64.3%; Score 36; DB 4; Length 94;
Best Local Similarity 85.7%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

Qy 2 RHNYGSF 8
|||||

Db 80 RHNYGVF 86

RESULT 13
US-09-557-917-90
; Sequence 90, Application US/09557917
; Patent No. 6284457
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 90
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-90

Query Match 64.3%; Score 36; DB 4; Length 94;
Best Local Similarity 85.7%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

Qy 2 RHNYGSF 8
|||||

RESULT 14
US-09-557-917-101
; Sequence 101, Application US/09557917
; Patent No. 6284457
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-101

Query Match 64.3%; Score 36; DB 4; Length 94;
Best Local Similarity 85.7%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

Qy 2 RHNYGSF 8
|||||

Db 80 RHNYGVF 86

Search completed: November 18, 2002, 17:43:38
Job time : 5.2402 secs

RESULT 15
US-08-767-128-6
; Sequence 6, Application US/08767128
; Patent No. 6111079
; GENERAL INFORMATION:
; APPLICANT: WYLIE, DWANE E.
; APPLICANT: LOPEZ, OSVALDO
; APPLICANT: MURRAY, PETER JOSEPH
; APPLICANT: GOEBEL, PETER
; TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
; TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
; STREET: 3100 No. 6111079west Center, 90 South Seventh St
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/767,128
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE: 04-DEC-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/09258
; FILING DATE: 05-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/541,373
; FILING DATE: 10-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/462,798
; FILING DATE: 05-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G.
; REGISTRATION NUMBER: 35,093
; REFERENCE/DOCKET NUMBER: 8648.49USF1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/371-5278
; TELEFAX: 612/332-9081
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: Internal
; ORIGINAL SOURCE:
US-08-767-128-6

Query Match 64.3%; Score 36; DB 3; Length 119;
Best Local Similarity 66.7%; Pred. No. 27;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 ARHNYGSFA 9
Db 97 ARHNYGYA 105

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:01 ; Search time 4.90196 Seconds
(without alignments)
196.114 Million cell updates/sec

Title: US-09-016-061-74

Perfect score: 55

Sequence: 1 ARHNYGSFAE 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR-73:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	39	70.9	446	2	T19625
2	39	70.9	723	2	F83173
3	38	69.1	275	2	G75130
4	38	69.1	275	2	D71087
5	37	67.3	347	2	S43771
6	36	65.5	82	2	I51106
7	36	65.5	89	2	S38688
8	36	65.5	89	2	S38683
9	36	65.5	89	2	S38684
10	36	65.5	210	1	B69265
11	36	65.5	225	2	I47095
12	36	65.5	326	2	S47248
13	35	63.6	195	2	G86742
14	35	63.6	287	1	PWBV
15	35	63.6	287	1	PWVKL
16	35	63.6	507	2	H82580
17	34	61.8	108	2	S26316
18	34	61.8	110	2	S26317
19	34	61.8	189	2	D75026
20	34	61.8	182	2	D71211
21	34	61.8	364	2	C64326
22	34	61.8	464	2	B70828
23	34	61.8	484	2	G72395
24	34	61.8	1052	2	AF2959
25	34	61.8	1341	2	H98323
26	33	60.0	80	2	I54469
27	33	60.0	80	2	I68777
28	33	60.0	81	2	I54550
29	33	60.0	85	2	I59634

30 33 60.0 89 2 S38676 MHC class II histo
31 33 60.0 89 2 S38680 MHC class II histo
32 33 60.0 89 2 S57512 MHC class II histo
33 33 60.0 123 2 C25239 MHC class II histo
34 33 60.0 127 2 G70105 conserved hypothet
35 33 60.0 167 2 T16454 hypothetical prote
36 33 60.0 191 2 H84544 hypothetical prote
37 33 60.0 200 2 D32526 class II histocomp
38 33 60.0 220 2 T46055 hypothetical prote
39 33 60.0 220 2 AEL301 phosphoglycerate d
40 33 60.0 220 2 AEL1673 phosphoglycerate d
41 33 60.0 237 2 C27060 class II histocomp
42 33 60.0 266 2 I54287 gene HLA-DRB1 prot
43 33 60.0 266 2 A27618 class II histocomp
44 33 60.0 266 2 I54295 lymphocyte antigen
45 33 60.0 275 2 T04480 acyl-CoA oxidase h

ALIGNMENTS

RESULT 1

T19625

hypothetical protein C31H5.6 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000

C:Accession: T19625

R:Kershaw, J.

submitted to the EMBL Data Library, April 1997

A:Reference number: Z19153

A:Accession: T19625

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-446 <WIL>

A:Cross-references: EMBL:Z93778; PIDN:CAB07846.1; GSPDB:GN00019; CESP:C31H5.6

A:Experimental source: clone C31H5

C:Genetics:

A:Gene: CESP:C31H5.6

A:Map position: 1

A:Introns: 49/2; 85/1; 120/2; 183/3; 218/3; 255/3; 285/2; 331/3; 360/3

C:Superfamily: Caenorhabditis elegans hypothetical protein W03D8.8

Query Match 70.9%; Score 39; DB 2; Length 446;
Best Local Similarity 87.5%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSFA 9

Db 51 RHNYGSHA 58

RESULT 2

F83173

outer membrane protein OprC PA3790 [imported] - Pseudomonas aeruginosa (strain PA01)

C:Species: Pseudomonas aeruginosa

C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C:Accession: F83173

R:Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.;

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L

.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa

A:Reference number: A82950; MUID:20437337; PMID:10984043

A:Accession: F83173

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-723 <STO>

A:Cross-references: GB:AE004797; GB:AE004091; NID:g9949950; PIDN:AAG07177.1; GSPDB:GN

A:Experimental source: strain PA01

C:Genetics:

A:Gene: oprC; PA3790

Query Match 70.9%; Score 39; DB 2; Length 723;

Best Local Similarity 75.0%; Pred. No. 19;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSPAE 10
|||||
Db 407 HNYGAFGE 414

RESULT 3
G75130
translation initiation factor aif-2, subunit alpha (aif2a) PAB0568 - Pyrococcus abyssi
C:Species: Pyrococcus abyssi
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C:Accession: G75130
R:anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure
A:Reference number: A75001
A:Accession: G75130
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-275 <KAW>
A:Cross-references: GB:AJ248285; GB:AL096836; NID:g5458067; PIDN:CAB49760.1; PID:g545827
A:Experimental source: strain Orsay
C:Genetics:
A:Gene: aif2a; PAB0568
C:Superfamily: translation initiation factor eIF-2 alpha chain

Query Match 69.1%; Score 38; DB 2; Length 275;
Best Local Similarity 75.0%; Pred. No. 11;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSPAE 10
|||||
Db 23 HNYGAFLE 30

RESULT 4
D71087
probable translation initiation factor eIF-2 alpha chain - Pyrococcus horikoshii
C:Species: Pyrococcus horikoshii
C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000
C:Accession: D71087
R:Kawarayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
DNA Res. 5, 55-76, 1998
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic
A:Reference number: A71000; MUID:98344137; PMID:9679194
A:Accession: D71087
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-275 <KAW>
A:Cross-references: GB:AP000004; NID:g3236131; PIDN:BAA30058.1; PID:g3257375
A:Experimental source: strain OY3
A:Note: this accession replaces an interim accession for a sequence replaced by GenBank
C:Genetics:
A:Gene: PH0961
C:Superfamily: translation initiation factor eIF-2 alpha chain

Query Match 69.1%; Score 38; DB 2; Length 275;
Best Local Similarity 75.0%; Pred. No. 11;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSPAE 10
|||||
Db 23 HNYGAFLE 30

RESULT 5
S43771
phosphatidylcholine desaturase (EC 1.3.1.35) - Synechococcus sp. (strain PCC 7002)
N:Alternate names: Delta-12 desaturase; fatty acid desaturase (EC 1.14.99.-) [misidentified]
C:Species: Synechococcus sp.

A:Variety: PCC 7002
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-2000
C:Accession: S43771
R:Sakamoto, T.; Wada, H.; Nishida, I.; Ohmori, M.; Murata, N.
Plant Mol. Biol. 24, 643-650, 1994
A:Title: Identification of conserved domains in the Delta-12 desaturases of cyanobact
A:Reference number: S43770; MUID:94207189; PMID:8155883
A:Accession: S43771
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-347 <SAK>
A:Cross-references: GB:D13779; NID:g488510; PIDN:BAA02922.1; PID:g488511
C:Superfamily: omega-3 fatty acid desaturase
C:Keywords: oxidoreductase

Query Match 67.3%; Score 37; DB 2; Length 347;
Best Local Similarity 70.0%; Pred. No. 22;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSFAE 10
|||||
Db 334 AEHNYISFAQ 343

RESULT 6
I51106
Major Histocompatibility Complex class IIB - ring-necked pheasant (fragment)
C:Species: Phasianus colchicus (ring-necked pheasant)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 23-Jul-1999
C:Accession: I51106
R:Wittzell, H.; von Schantz, T.; Zoorob, R.; Auffray, C.
Immunogenetics 39, 395-403, 1994
A:Title: Molecular characterization of three Mhc class II B haplotypes in the ring-ne
A:Reference number: I51103; MUID:94245280; PMID:7910588
A:Accession: I51106
A>Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: DNA
A:Residues: 1-82 <WIT>
A:Cross-references: EMBL:X75406; NID:g496926; PIDN:CAA53160.1; PID:g496927
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 65.5%; Score 36; DB 2; Length 82;
Best Local Similarity 85.7%; Pred. No. 8.2;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
|||||
Db 75 RHNYGVF 81

RESULT 7
S38688
MHC class II histocompatibility antigen HLA-DR-08 beta chain - northern lesser bushba
C:Species: Galago senegalensis (northern lesser bushbaby)
C:Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 19-May-2000
C:Accession: S38688
R:Figueroa, F.; O'Huigin, C.; Tichy, H.; Klein, J.
submitted to the EMBL Data Library, November 1993
A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduce
A:Reference number: S38676
A:Accession: S38688
A:Molecule type: DNA
A:Residues: 1-89 <FIG>
A:Cross-references: EMBL:Z27158
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 65.5%; Score 36; DB 2; Length 89;
Best Local Similarity 85.7%; Pred. No. 8.9;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
|||||
Db 75 RHNYGVF 81

```
RESULT 8
S38683
MHC class II histocompatibility antigen HLA-DR-03 beta chain - northern lesser bushbaby
C:Species: Galago senegalensis (northern lesser bushbaby)
C:Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 19-May-2000
C:Accession: S38683
R:Figueroa, F.; O'Huigin, C.; Tichy, H.; Klein, J.
submitted to the EMBL Data Library, November 1993
A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduced f
A:Reference number: S38676
A:Accession: S38683
A:Molecule type: DNA
A:Residues: 1-89 <FIG>
A:Cross-references: EMBL:Z27153
C:Superfamily: class II histocompatibility antigen; Immunoglobulin homology

Query Match 65.5%; Score 36; DB 2; Length 89;
Best Local Similarity 85.7%; Pred. No. 8.9;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
Db 75 RHNYGVF 81

RESULT 9
S38684
MHC class II histocompatibility antigen HLA-DR-04 beta chain - northern lesser bushbaby
C:Species: Galago senegalensis (northern lesser bushbaby)
C:Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 19-May-2000
C:Accession: S38684
R:Figueroa, F.; O'Huigin, C.; Tichy, H.; Klein, J.
submitted to the EMBL Data Library, November 1993
A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduced f
A:Reference number: S38676
A:Accession: S38684
A:Molecule type: DNA
A:Residues: 1-89 <FIG>
A:Cross-references: EMBL:Z27154
C:Superfamily: class II histocompatibility antigen; Immunoglobulin homology

Query Match 65.5%; Score 36; DB 2; Length 89;
Best Local Similarity 85.7%; Pred. No. 8.9;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
Db 75 RHNYGVF 81

RESULT 10
B69265
conserved hypothetical protein AF0122 - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C:Accession: B69265
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
A:Reference number: A69250; MUID:98049343; PMID:9389475
A:Accession: B69265
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-210 <KLE>
A:Cross-references: GB:AE001098; GB:AE000782; MID:g2689421; PIDN:AA891117.1; PID:g265053
C:Superfamily: conserved hypothetical protein AF0119
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```
Query Match 65.5%; Score 36; DB 1; Length 210;
Best Local Similarity 66.7%; Pred. No. 21;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RHNYGSFAE 10
Db 128 RHAYGSFVD 136

RESULT 11
M47095
MHC class II OVAR-DR-beta-3 - sheep (fragment)
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 15-Oct-1996 #sequence_revision 15-Oct-1996 #text_change 21-Jan-2000
C:Accession: I47095
R:Fabb, S.A.; Maddox, J.F.; Gogolin-Ewens, K.J.; Baker, L.; Wu, M.J.; Brandon, M.R.
Anim. Genet. 24, 249-255, 1993
A:Title: Isolation, characterization and evolution of ovine major histocompatibility
A:Reference number: I47075; MUID:94057592; PMID:7902039
A:Accession: I47095
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-225 <FAB>
A:Cross-references: GB:L04790; MID:g458880; PIDN:AAA16562.1; PID:g458881
C:Genetics:
A:Gene: OVAR-DRB3
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology
F:98-163/Domain: immunoglobulin homology <IMMS>

Query Match 65.5%; Score 36; DB 2; Length 225;
Best Local Similarity 85.7%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
Db 68 RHNYGVF 74

RESULT 12
S47248
site-specific DNA-methyltransferase (cytosine-specific) (EC 2.1.1.73) phi3TII - phage
C:Species: phage phi-3T
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-May-2000
C:Accession: S47248; S50099
R:Noyer-Weidner, M.; Walter, J.; Terschuereen, P.A.; Chal, S.; Trautner, T.A.
submitted to the EMBL Data Library, August 1994
A:Description: M.phi3TII: a new monospecific C5-DNA-methyltransferase with pronounced
A:Reference number: S47248
A:Accession: S47248
A:Molecule type: DNA
A:Residues: 1-326 <NOY>
A:Cross-references: EMBL:X80202; MID:g535136; PIDN:CAA56493.1; PID:g535137
R:Noyer-Weidner, M.; Walter, J.; Terschuereen, P.A.; Chal, S.; Trautner, T.A.
Nucleic Acids Res. 22, 4066-4072, 1994
A:Title: M.phi3TII: a new monospecific DNA (cytosine-C5) methyltransferase with prono
A:Reference number: S50099; MUID:95023172; PMID:7937131
A:Accession: S50099
A:Molecule type: DNA
A:Residues: 1-90,120-130,177-237 <NOW>
A:Cross-references: EMBL:X80202
C:Genetics:
A:Gene: M.phi3TII
C:Superfamily: site-specific methyltransferase (cytosine-specific) ECORII
C:Keywords: methyltransferase; S-adenosylmethionine

Query Match 65.5%; Score 36; DB 2; Length 326;
Best Local Similarity 55.6%; Pred. No. 32;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RHNYGSFAE 10
Db 52 RHNFGDYVE 60
```

RESULT 13

G86742
conserved hypothetical protein yjgF [imported] - Lactococcus lactis subsp. lactis (strain
C:Species: Lactococcus lactis subsp. lactis
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 17-May-2002
C:Accession: G86742
R:Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss
A:Reference number: A86625; MUID:21235186; PMID:11337471
A:Accession: G86742
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-195 <STO>
A:Cross-references: GB:AE005176; PID:g12723879; PIDN:AAK05041.1; GSPDB:GN00146
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: yjgF
C:Superfamily: hypothetical protein b1011

Query Match 63.6%; Score 35; DB 2; Length 195;

Best Local Similarity 62.3%; Pred. No. 30;

Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSF 8

||||:|

Db 103 AKHNGAF 110

RESULT 14

PMWY
inorganic diphosphatase (EC 3.6.1.1) - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein YBR011c; protein YBR0202; pyrophosphate phosphohydrolase
C:Species: Saccharomyces cerevisiae
C:Date: 30-Nov-1980 #sequence_revision 09-Sep-1994 #text_change 03-Jun-2002
C:Accession: S45864; S07679; A01014; S29189
R:Entian, K.D.; Koetter, P.; Rose, M.; Li, Z.; Thermann, R.; Brendel, M.; Baur, A.; Boile
submitted to the Protein Sequence Database, August 1994
A:Reference number: S45862

A:Accession: S45864

A:Molecule type: DNA

A:Residues: 1-287 <ENT>

A:Cross-references: EMBL:X13253; NID:g4198; PIDN:CAA31629.1; PID:g536206; GSPDB:GN000

A:Experimental source: strain S288C

R:Kolakowski Jr., L.F.; Schloesser, M.; Cooperman, B.S.

Nucleic Acids Res. 16, 10441-10452, 1988

A:Title: Cloning, molecular characterization and chromosome localization of the inorganic

A:Reference number: S07679; MUID:89083474; PMID:2849749

A:Accession: S07679

A:Molecule type: DNA

A:Residues: 1-266, 'L', 268-287 <KOL>

A:Cross-references: EMBL:X13253; NID:g4198; PIDN:CAA31629.1; PID:g4199

R:Cohen, S.A.; Sterner, R.; Keim, P.S.; Heinrichson, R.L.

J. Biol. Chem. 253, 889-897, 1978

A:Title: Covalent structural analysis of yeast inorganic pyrophosphatase.

A:Reference number: A92241; MUID:78087552; PMID:340461

A:Accession: A01014

A:Molecule type: protein

A:Residues: 2-40, 'D', 42-71, 'N', 73, 75-117, 'N', 119-123, 'Q', 125-136, 'E', 138-186, 'D', 188-224

A:Note: this is the final paper in a series

A:Note: no disulfide bonds are present

R:Raznikov, A.V.; Sklyankina, V.A.; Awaeva, S.M.

FEBS Lett. 308, 62-64, 1992

A:Title: Tyrosine-89 is important for enzymatic activity of S. cerevisiae inorganic pyro

A:Reference number: S29189; MUID:92354770; PMID:1322842

A:Accession: S29189

A:Molecule type: protein

A:Residues: 83-105, 'E', 107-112 <RAZ>

R:Bond, M.-C.; Chiu, N.Y.; Cooperman, B.S.

Biochemistry 19, 94-102, 1980

A:Title: Identification of an arginine important for enzymatic activity within the coval

A:Reference number: A90443

A:Contents: annotation; active site
C:Genetics:
A:Gene: SGD:IPP1; PPA; MIPS:YBR011c
A:Cross-references: SGD:S0000215; MIPS:YBR011c
A:Map position: 2R
C:Function:
A:Description: catalyzes hydrolysis of pyrophosphate to orthophosphate
A:Note: requires divalent metal cation
C:Superfamily: inorganic pyrophosphatase
C:Keywords: homodimer; hydrolase
E;2-287/Product: inorganic pyrophosphate #status experimental <MA>
F;79/Binding site: pyrophosphate (Arg) #status experimental

Query Match 63.6%; Score 35; DB 1; Length 287;

Best Local Similarity 62.5%; Pred. No. 44;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFAE 10

||||:|

Db 92 HNYGAFPO 99

RESULT 15

PMVKL

inorganic diphosphatase (EC 3.6.1.1) - yeast (Kluyveromyces marxianus var. lactis)
C:Species: Kluyveromyces marxianus var. lactis, Candida sphaerica
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 03-Jun-2002
C:Accession: S07894

R:Stark, M.J.R.; Milner, J.S.

Yeast 5, 35-50, 1989

A:Title: Cloning and analysis of the Kluyveromyces lactis TRP1 gene: a chromosomal lo

A:Reference number: S07892; MUID:89189093; PMID:2538971

A:Accession: S07894

A:Molecule type: DNA

A:Residues: 1-287 <STA>

A:Cross-references: EMBL:X14230; NID:g2900; PIDN:CAA32446.1; PID:g2903

C:Genetics:

A:Gene: IPP

C:Superfamily: inorganic pyrophosphatase

C:Keywords: hydrolase

F;79,151/Active site: Arg, Glu #status predicted

Query Match 63.6%; Score 35; DB 1; Length 287;

Best Local Similarity 62.5%; Pred. No. 44;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFAE 10

||||:|

Db 92 HNYGAFPO 99

Search completed: November 18, 2002, 17:47:07

Job time : 5.90196 secs

GenCore version 5.1.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:00 : Search time 2.45098 Seconds
(without alignments)
169.223 Million cell updates/sec

Title: US-09-016-061-74

Perfect score: 55

Sequence: 1 ARHNYGSFAE 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	38	69.1	275	1	IF2A_PVRAB	Q9v0e4 pyrococcus
2	38	69.1	275	1	IF2A_PVRHO	O58655 pyrococcus
3	37	67.3	223	1	CCSA_LOTJA	Q9bbp4 lotus japon
4	35	63.6	284	1	IPYR_PICPA	G13505 pichia past
5	35	63.6	286	1	IPYR_KIULA	P13998 kluyveromyc
6	35	63.6	286	1	IPYR_YEAST	P00817 saccharomyc
7	34	61.8	364	1	SUCC_METJA	O57663 methanococc
8	34	61.8	464	1	DLDH_MYCTU	O53747 mycobacteri
9	33	60.0	448	1	NCAP_CVHOC	P33469 human coron
10	33	60.0	470	1	SYE2_RICPR	Q9zc58 rickettsia
11	33	60.0	473	1	SYE_AQUAE	O67271 aquifex aeo
12	33	60.0	682	1	VG50_BPML5	Q05262 mycobacteri
13	33	60.0	1267	1	VL3_REOVL	P17378 reovirus (t
14	33	60.0	1267	1	VL3_REOVL	P17376 reovirus (t
15	32	58.2	65	1	CCSA_OENBE	P15565 oenothera b
16	32	58.2	65	1	CCSA_PEA	P31172 pisum sativ
17	32	58.2	196	1	WBJJ_ECOLI	P37750 escherichia
18	32	58.2	198	1	HB2G_HUMAN	P01911 homo sapien
19	32	58.2	220	1	SDHE_BACSU	O34635 bacillus su
20	32	58.2	262	1	VP2_BPCHP	P19193 bacterioph
21	32	58.2	266	1	HB2A_HUMAN	P01913 homo sapien
22	32	58.2	266	1	HB2B_HUMAN	P01912 homo sapien
23	32	58.2	266	1	HB2C_HUMAN	P01914 homo sapien
24	32	58.2	266	1	HB2D_CANFA	P18470 canis famil
25	32	58.2	266	1	HB2D_HUMAN	P13759 homo sapien
26	32	58.2	266	1	HB2E_HUMAN	P04229 homo sapien
27	32	58.2	266	1	HB2F_HUMAN	P13758 homo sapien
28	32	58.2	266	1	HB2H_HUMAN	P13760 homo sapien
29	32	58.2	266	1	HB2I_HUMAN	P20039 homo sapien
30	32	58.2	266	1	HB2J_HUMAN	P13761 homo sapien
31	32	58.2	305	1	YN45_DEIRA	Q9rry7 deinococcus
32	32	58.2	310	1	PANE_AQUAE	O67619 aquifex aeo
33	32	58.2	313	1	CCSA_TOBAC	P12216 nicotiana t

ALIGNMENTS

RESULT 1

IF2A_PVRAB
ID IF2A_PVRAB STANDARD; PRT; 275 AA.
AC Q9V0E4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable translation initiation factor 2 alpha subunit (eIF-2-alpha).
GN EIF2A OR PAB0568.
OS Pyrococcus abyssi.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=29292;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GE5 / Orsay;
RA Heilig R.;
RT "Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure and evolution."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: EIF-2 FUNCTIONS IN THE EARLY STEPS OF PROTEIN SYNTHESIS BY FORMING A TERNARY COMPLEX WITH GTP AND INITIATOR TRNA (BY SIMILARITY).
CC -!- SUBUNIT: HETEROPRIMER COMPOSED OF AN ALPHA, A BETA, AND A GAMMA CHAIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE EIF-2-ALPHA FAMILY.
CC -!- SIMILARITY: CONTAINS 1 SI MOTIF DOMAIN.

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DR EMBL; AJ248285; CAB49760.1; -.
DR HSSP; P05055; ISRO.
DR InterPro; IPR003029; S1.
DR Pfam; PF00575; S1; 1.
DR SMART; SM00316; S1; 1.
DR PROSITE; PS50126; S1; 1.
KW Initiation factor; Protein biosynthesis; RNA-binding;
FT Complete proteome.
FT DOMAIN 12 83 S1 MOTIF.
SQ SEQUENCE 275 AA; 31912 MW; B2659F3A49879B4F CRC64;

Query Match 69.1%; Score 38; DB 1; Length 275;
Best Local Similarity 75.0%; Pred. No. 2.6;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 HNYGSFAE 10

Db 23 HNYGAFLE 30

```

RESULT 2
ID IF2A_PIRHO STANDARD; PRT; 275 AA.
AC O58655;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE Probable translation initiation factor 2 alpha subunit (eIF-2-alpha).
GN EIF2A OR pI40961.
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=53953;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=98344137; PubMed=9679194;
RA Kawarabayashi Y., Sawada M., Horikawa H., Halkawa Y., Hino Y.,
RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
RA Funahashi T., Tanaka T., Kudo Y., Yamazaki J., Kushida N., Oguchi A.,
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RA Masuchi Y., Shizuya H., Kikuchi H.;
RT "Complete sequence and gene organization of the genome of a hyper-
thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
RL DNA Res. 5:55-76(1998).
CC -1- FUNCTION: EIF-2 FUNCTIONS IN THE EARLY STEPS OF PROTEIN SYNTHESIS
CC BY FORMING A TERNARY COMPLEX WITH GTP AND INITIATOR TRNA
CC (BY SIMILARITY).
CC -1- SUBUNIT: HETEROTRIMER COMPOSED OF AN ALPHA, A BETA, AND A GAMMA
CC CHAIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE EIF-2-ALPHA FAMILY.
CC -1- SIMILARITY: CONTAINS 1 SI MOTIF DOMAIN.
CC
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CC
CC EMBL; AP000004; BAA30058.1; -.
DR HSP; P05055; 1SR0.
DR InterPro; IPR003029; S1.
DR Pfam; PF00575; S1; 1.
DR SMART; SM00316; S1; 1.
DR PROSITE; PS0126; S1; 1.
KW Initiation factor; Protein biosynthesis; RNA-binding;
KW Complete proteome.
FT DOMAIN 12 83 SI MOTIF.
SQ SEQUENCE 275 AA; 31980 MW; 6AAAD15F10FFB436 CRC64;

Query Match 69.1%; Score 38; DB 1; Length 275;
Best Local Similarity 75.0%; Pred. No. 2.6;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFAE 10
DB 23 HNYGAFLE 30

RESULT 3
CCSA_LOTJA STANDARD; PRT; 323 AA.
ID CCSA_LOTJA
AC Q9BBP4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Cytochrome c biogenesis protein ccsa.
GN CCSA.
OS Lotus japonicus.
OG Chloroplast.

```

```

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Lotaeae; Lotus.
OX NCBI_TaxID=34305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Accession MG-20;
RX MEDLINE=21082929; PubMed=11214967;
RA Kato T., Kaneko T., Sato S., Nakamura Y., Tabata S.;
RT "Complete structure of the chloroplast genome of a legume, Lotus
japonicus."
RL DNA Res. 7:323-330(2000).
CC -1- FUNCTION: REQUIRED DURING CYTOCHROME BIOGENESIS AT THE STEP OF
CC HEME ATTACHMENT (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CCMF/CYCK/CCIL/NRFE/CCSA FAMILY.
CC
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CC
CC EMBL; AP0002983; BAB33244.1; -.
DR InterPro; IPR002541; CytC_asm.
DR Pfam; PF01578; CytC_asm; 1.
KW Cytochrome c-type biogenesis; Chloroplast.
SQ SEQUENCE 323 AA; 37185 MW; 5A034E3E2829FE35 CRC64;

Query Match 67.3%; Score 37; DB 1; Length 323;
Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
DB 315 HNYGSF 320

RESULT 4
IPYR_PICPA STANDARD; PRT; 284 AA.
ID IPYR_PICPA
AC O13505;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Inorganic pyrophosphatase (EC 3.6.1.1) (pyrophosphate phospho-
DE hydrolase) (ppase).
DE IPPI.
GN IPPI.
OS Pichia pastoris (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Pichia.
OX NCBI_TaxID=4922;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL Y-11430;
RX MEDLINE=99034033; PubMed=9818724;
RA Cosano I.C., Alvarez P., Molina M., Nombela C.;
RT "Cloning and sequence analysis of the Pichia pastoris TRP1, IPPI and
RT HIS3 genes."
RL Yeast 14:861-867(1998).
CC -1- CATALYTIC ACTIVITY: Diphosphate + H(2)O = 2 phosphate.
CC -1- COFACTOR: REQUIRE THE PRESENCE OF DIVALENT METAL CATION.
CC MAGNESIUM CONFERS THE HIGHEST ACTIVITY.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE PPASE FAMILY.
CC
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CC -----

DR EMBL; AJ001000; CAA04453.1; --

DR HSSP; P00817; IWGI.

DR InterPro; IPR001596; Pyrophosphatase.

DR Pfam; PF00719; Pyrophosphatase; 1.

DR PROSITE; PS00387; PPASE; 1.

KW Hydrolase; Magnesium. 0 BY SIMILARITY.

FT INIT_MET 0 56 PROBABLE.

FT ACT_SITE 56 78 INORGANIC PYROPHOSPHATE (BY SIMILARITY).

FT BINDING 78 78 INORGANIC PYROPHOSPHATE (BY SIMILARITY).

SQ SEQUENCE 284 AA; 31937 MW; 3DAD27970D775D6 CRC64;

Query Match 63.6%; Score 35; DB 1; Length 284;

Best Local Similarity 62.5%; Pred. No. 11;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 HNYGSFAE 10

DB 91 HNYGAFFQ 98

|||||:

RESULT 5

IPYR_KLUJLA STANDARD; PRT; 286 AA.

AC P13998;

DT 01-JAN-1990 (Rel. 13, Created)

DT 01-JAN-1990 (Rel. 13, Last sequence update)

DT 01-OCT-1994 (Rel. 30, Last annotation update)

DE Inorganic pyrophosphatase (EC 3.6.1.1) (Pyrophosphate phospho-

DE hydrolase) (Ppase).

GN IPPI OR IPP.

OS Kluyveromyces lactis (Yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.

OX NCBI_TaxID=28985;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=89189093; PubMed=2538971;

RA Stark M.J.R., Milner J.S.;

RT "Cloning and analysis of the Kluyveromyces lactis TRP1 gene: a

RT chromosomal locus flanked by genes encoding inorganic pyrophosphatase

RT and histone H3.;"

RL Yeast 5:35-50(1989).

RN [2]

RP SIMILARITY TO E. COLI AND YEAST PPASES.

RX MEDLINE=90254161; PubMed=2160278;

RA Lahti R., Kolakowski L.F. Jr., Heinonen J., Vihinen M., Pohjanoksa K.,

RA Cooperman B.S.;

RT "Conservation of functional residues between yeast and E. coli

RT inorganic pyrophosphatases.;"

RL Biochim. Biophys. Acta 1038:338-345(1990).

CC -1- CATALYTIC ACTIVITY: Diphosphate + H(2)O = 2 phosphate.

CC -1- COPACTOR: REQUIRES THE PRESENCE OF DIVALENT METAL CATION.

CC MAGNESIUM CONFERS THE HIGHEST ACTIVITY.

CC -1- SUBUNIT: HOMODIMER.

CC -1- SUBCELLULAR LOCATION: Cytoplasmic.

CC -1- SIMILARITY: BELONGS TO THE PPASE FAMILY.

CC -----

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CC -----

DR EMBL; X14230; CAA32446.1; --

DR PIR; S07894; PWVKL.

DR HSSP; P00817; IWGI.

DR InterPro; IPR001596; Pyrophosphatase.

DR Pfam; PF00719; Pyrophosphatase; 1.

DR PROSITE; PS00387; PPASE; 1.

KW Hydrolase; Magnesium. 0 BY SIMILARITY.

FT INIT_MET 0 56 PROBABLE.

FT ACT_SITE 56 78 INORGANIC PYROPHOSPHATE (BY SIMILARITY).

FT BINDING 78 78 INORGANIC PYROPHOSPHATE (BY SIMILARITY).

SQ SEQUENCE 286 AA; 32034 MW; 11647F4ABD916A2F CRC64;

Query Match 63.6%; Score 35; DB 1; Length 286;

Best Local Similarity 62.5%; Pred. No. 11;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 HNYGSFAE 10

DB 91 HNYGAFFQ 98

|||||:

RESULT 6

IPYR_YEAST STANDARD; PRT; 286 AA.

AC P00817;

DT 21-JUL-1986 (Rel. 01, Created)

DT 01-MAR-1989 (Rel. 10, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Inorganic pyrophosphatase (EC 3.6.1.1) (Pyrophosphate phospho-

DE hydrolase) (Ppase).

GN IPPI OR PPAL OR PPA OR YBR011C OR YBR0202.

OS Saccharomyces cerevisiae (Baker's yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.

OX NCBI_TaxID=4932;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=89083474; PubMed=2849749;

RA Kolakowski L.F. Jr., Schloesser M., Cooperman B.S.;

RT "Cloning, molecular characterization and chromosome localization of

RT the inorganic pyrophosphatase (PPA) gene from *S. cerevisiae*.;"

RL Nucleic Acids Res. 16:10441-10452(1988).

RN [2]

RP SEQUENCE FROM N.A.

RX STRAIN=S288C;

RA Entian K.-D., Koetter P., Rose M., Li Z., Therman R., Brendel M.,

RA Baur A., Boles E., Miosga T., Schaaff-Gerstenschlaeger I.,

RA Zimmermann F.K.;

RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE.

RX MEDLINE=78097552; PubMed=340461;

RA Cohen S.A., Sterner R., Keim P.S., Heinrichson R.L.;

RT "Covalent structural analysis of yeast inorganic pyrophosphatase.;"

RL J. Biol. Chem. 253:889-897(1978).

RN [4]

RP SEQUENCE OF 25-35 AND 239-251.

RX STRAIN=S288C;

RX MEDLINE=95203288; PubMed=7895733;

RA Garrels J.I., Fitcher B., Kobayashi R., Latter G.I., Schwender B.,

RA Volpe T., Warner J.R., McLaughlin C.S.;

RT "Protein identifications for a Saccharomyces cerevisiae protein

RT database.;"

RL Electrophoresis 15:1466-1486(1994).

RN [5]

RP SEQUENCE OF 239-249.

RX STRAIN=ATCC 38531 / Y41;

RX MEDLINE=97089742; PubMed=8935650;

RA Norbeck J., Blomberg A.;

RT "Protein expression during exponential growth in 0.7 M NaCl medium of

RT Saccharomyces cerevisiae.;"

RL FEMS Microbiol. Lett. 137:1-8(1996).

RN [6]

RP ACTIVE SITE.

RX MEDLINE=80109718; PubMed=6101539;

RA Bond M.W., Chiu N.Y., Cooperman B.S.;

RT "Identification of an arginine important for enzymatic activity

INIT_MET	0	0
ACT_SITE	56	56
		PROBABLE.

RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., G
RA Scott J.L., Geoghagen N.S.M., Weidman J.E., Fuhrmann J.L.,

```

RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii";
RL Science 273:1058-1073(1996).
CC -!- CATALYTIC ACTIVITY: ATP + succinate + CoA = ADP + succinyl-CoA +
CC phosphate.
CC -!- PATHWAY: Tricarboxylic acid cycle.
CC -!- SUBUNIT: Composed of an alpha chain and a beta chain (By
CC similarity).
CC -!- SIMILARITY: BELONGS TO THE SUCCINYL-COA SYNTHETASE BETA SUBUNIT
CC FAMILY.
CC -----
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CC -----
CC EMBL; U67477; AAB98195.1; -.
CC HSSP; P07460; 2SCU.
CC TIGR; MJ0210; -.
CC InterPro; IPR003135; ATP-grasp.
CC InterPro; IPR000303; CoA_ligase.
CC Pfam; PF00549; ligase-CoA; 1.
CC TIGRFAMs; TIGR01016; sucCoABeta; 1.
CC PROSITE; PS01217; SUCCINYL-CoA_LIG_3; 1.
KW Ligase; Tricarboxylic acid cycle; Complete proteome.
SQ SEQUENCE 364 AA; 40907 MW; 16937FC54694770C CRC64;

Query Match 61.8%; Score 34; DB 1; Length 364;
Best Local Similarity 66.7%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 RHNYGSFAE 10
DB 215 RHNYEEFEE 223

RESULT 8
DLDH_MYCTU ID DLDH_MYCTU STANDARD; PRT; 464 AA.
AC O53747;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Dihydrolipoamide dehydrogenase (EC 1.8.1.4) (E3 component of alpha
DE keto acid dehydrogenase complexes).
GN LPD OR RVO462 OR MT0478 OR MTV038.06.
OS Mycobacterium tuberculosis
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37Rv;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eigmler K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Rellwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RL Nature 393:537-544(1998).
RN [2]

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RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwin M.L., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: LIPOAMIDE DEHYDROGENASE IS A COMPONENT OF THE ALPHA-
CC KETOCID DEHYDROGENASE COMPLEXES (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: Dihydrolipoamide + NAD(+) = lipoamide + NADH.
CC -!- COFACTOR: FAD (BY SIMILARITY).
CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (potential).
CC -!- MISCELLANEOUS: THE ACTIVE SITE IS A REDOX-ACTIVE DISULFIDE BOND.
CC -!- SIMILARITY: BELONGS TO THE PYRIDINE NUCLEOTIDE-DISULFIDE
CC OXIDOREDUCTASES CLASS-I.
CC -----
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CC -----
CC EMBL; AL021933; CAAL7417.1; -.
CC EMBL; AE006950; AAK44702.1; -.
CC HSSP; P11959; 1EBD.
CC TIGR; MT0478; -.
CC Tuberculist; RV0462; -.
CC InterPro; IPR001327; FAD_pyr_redox.
CC InterPro; IPR000205; NAD_binding.
CC InterPro; IPR001100; pyr_redox.
CC InterPro; IPR004099; pyr_redox_dim.
CC Pfam; PF00070; pyr_redox; 1.
CC Pfam; PF02852; pyr_redox_dim; 1.
CC PRINTS; PR00368; FADPNR.
CC PRINTS; PR00411; PNDRDTASEI.
CC ProDom; PD000139; FAD_pyr_redox; 1.
CC Redox-active center; PYRIDINE_REDOX_1; 1.
KW Redox-active center; Glycolysis; Oxidoreductase; NAD; Flavoprotein;
KW FAD; Complete proteome.
FT NP_BIND 5 34 FAD (ADP PART) (PROBABLE).
FT DISULFID 41 46 REDOX-ACTIVE (BY SIMILARITY).
FT NP_BIND 299 309 FAD (FLAVIN PART) (BY SIMILARITY).
FT ACT_SITE 443 443 BY SIMILARITY.
SQ SEQUENCE 464 AA; 49239 MW; DD93D95DC6F76B22 CRC64;

Query Match 61.8%; Score 34; DB 1; Length 464;
Best Local Similarity 62.5%; Pred. No. 29;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFAE 10
DB 110 HGYGTFAD 117

RESULT 9
NCAP_CVHOC ID NCAP_CVHOC STANDARD; PRT; 448 AA.
AC P33469;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE Nucleocapsid protein.
GN N.
OS Human coronavirus (strain OC43).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=31631;

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RN [1]
RX MEDLINE-89243809; PubMed=2541577;
RA Kanahora T., Soe L.H., Lai M.M.C.;
RT "Sequence analysis of nucleocapsid gene and leader RNA of human
RT coronavirus OC43.";
RL Virus Res. 12:1-9(1989).
DR PIR; A60003; A60003.
DR InterPro; IPR001218; Corona_nucleocap.
DR Pfam; PF00937; Corona_nucleoca; 1.
KW Nucleocapsid.
SQ SEQUENCE 448 AA; 49316 MW; 5193AB1AE0D75626 CRC64;

Query Match 60.0%; Score 33; DB 1; Length 448;
Best Local Similarity 85.7%; Pred. No. 44;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 103 RHNRGSF 109

RESULT 10
SYE2_RICPR
ID SYE2_RICPR STANDARD; PRT; 470 AA.
AC Q9ZCT8;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Glutamyl-tRNA synthetase 2 (EC 6.1.1.17) (Glutamate--tRNA ligase 2)
DE (Glurs 2).
GN GLTX2 OR RP623.
OS Rickettsia prowazekii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsieae; Rickettsia.
OX NCBI_TaxID=782;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-99039499; PubMed=9823893;
RA Anderson S.G.E., Zomorodipour A., Andersson J.O.,
RA Sichteritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
RT "The genome sequence of Rickettsia prowazekii and the origin of
RT mitochondria.";
RL Nature 396:133-140(1998).
CC -!- CATALYTIC ACTIVITY: ATP + L-glutamate + tRNA(Glu) = AMP +
CC diphosphate + L-glutamyl-tRNA(Glu).
CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
CC -----
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CC -----
CC EMBL; AJ235272; CAAL15066.1; -.
CC HSP; P27000; IGLN.
CC InterPro; IPR004527; GltX_bact.
CC InterPro; IPR000924; GltX_bact.
CC InterPro; IPR001412; tRNA-synt_1c.
CC Pfam; PF00749; tRNA-synt_1c; 1.
CC PRINTS; PR00987; TRNASYNTHGLU.
CC TIGRFAMs; TIGR00464; gltX_bact; 1.
CC PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
CC Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
CC Complete proteome.
CC SITE 10 20 "HIGH" REGION.
CC SITE 242 246 "KMSKS" REGION.
CC FT BINDING 245 ATP (BY SIMILARITY).
CC SQ SEQUENCE 473 AA; 55121 MW; 5CB4D1590973E07A CRC64;

Query Match 60.0%; Score 33; DB 1; Length 473;
Best Local Similarity 75.0%; Pred. No. 46;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSF 8
Db 31 ARHNGKF 38

RESULT 11
SYE_AQUAE
ID SYE_AQUAE STANDARD; PRT; 473 AA.
AC O67271;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Glutamyl-tRNA synthetase (EC 6.1.1.17) (Glutamate--tRNA ligase)
DE (Glurs).
GN GLTX OR AQ_1221.
OS Aquifex aeolicus.
OC Bacteria; Aquificae; Aquificae (class); Aquificales; Aquificaceae;
OC Aquifex.
OX NCBI_TaxID=63363;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-98196666; PubMed=9537320;
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Snead M.A., Keller M., Auja M., Huber R.,
RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus.";
RL Nature 392:353-358(1998).
CC -!- CATALYTIC ACTIVITY: ATP + L-glutamate + tRNA(Glu) = AMP +
CC diphosphate + L-glutamyl-tRNA(Glu).
CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
CC -----
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CC -----
CC EMBL; AF000729; AAC07230.1; -.
CC HSP; P27000; IGLN.
CC InterPro; IPR004527; GltX_bact.
CC InterPro; IPR000924; GltX_bact.
CC InterPro; IPR001412; tRNA-synt_1c.
CC Pfam; PF00749; tRNA-synt_1c; 1.
CC PRINTS; PR00987; TRNASYNTHGLU.
CC TIGRFAMs; TIGR00464; gltX_bact; 1.
CC PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
CC Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
CC Complete proteome.
CC SITE 10 20 "HIGH" REGION.
CC SITE 242 246 "KMSKS" REGION.
CC FT BINDING 245 ATP (BY SIMILARITY).
CC SQ SEQUENCE 473 AA; 55121 MW; 5CB4D1590973E07A CRC64;

Query Match 60.0%; Score 33; DB 1; Length 473;
Best Local Similarity 75.0%; Pred. No. 46;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSF 8
Db 31 ARHNGKF 38

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RESULT 12
V050_BPML5
ID V050_BPML5 STANDARD; PRT; 682 AA.
AC Q05262;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Putative adenosylcobalamin-dependent ribonucleotide reductase
DE (EC 1.17.4.2) (GP50).
GN 50.
OS Mycobacteriophage L5.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
OC L5-like viruses.
OX NCBI_TaxID=31757;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93211282; PubMed=8459766;
RA Hatfull G.F., Sarkis G.J.;
RT "DNA sequence, structure and gene expression of mycobacteriophage L5:
RT a phage system for mycobacterial genetics.";
RL Mol. Microbiol. 7:395-405(1993).
CC -!- CATALYTIC ACTIVITY: 2'-deoxyribonucleoside triphosphate + oxidized
CC thiorodoxin + H(2)O = ribonucleoside triphosphate + reduced
CC thiorodoxin.
CC -----
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CC -----
CC EMBL: Z18946; CAA79426.1; -
CC PIR: S30995; S30995.
CC InterPro: IPR001230; Prenyl_site.
CC InterPro: IPR000788; Ribonucleo_red.
CC Pfam: PF02867; ribonuc_red_lgc; 1.
CC Oxidoreductase; DNA replication.
SQ SEQUENCE 682 AA; 76331 MW; 8D2A71B873BC04A8 CRC64;

Query Match 60.0%; Score 33; DB 1; Length 682;
Best Local Similarity 66.7%; Pred. No. 68;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
|: |||||
Db 311 AREGYGSFA 319

RESULT 13
VL3_REOVD
ID VL3_REOVD STANDARD; PRT; 1267 AA.
AC P17378;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last annotation update)
DE Minor core protein lambda 3.
GN L1.
OS Reovirus (type 3 / strain Dearing).
OC Viruses; dsRNA viruses; Reoviridae; Orthoreovirus.
OX NCBI_TaxID=10886;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89163254; PubMed=2922925;
RA Wiener J.R., Joklik W.K.;
RT "The sequences of the reovirus serotype 1, 2, and 3 L1 genome
RT segments and analysis of the mode of divergence of the reovirus
RT serotypes.";
RL Virology 169:194-203(1989).
CC -!- MISCELLANEOUS: IT IS UNLIKELY THAT CORES CONTAIN MORE THAN 12
CC MOLECULES OF PROTEIN LAMBDA 3.
CC -!- SIMILARITY: VERY HIGH WITH OTHER REOVIRUS TYPES.
CC PIR: A30121; MWXR31.
KW Core protein.
SQ SEQUENCE 1267 AA; 142354 MW; 157E8FD4D664FCDB CRC64;

Query Match 60.0%; Score 33; DB 1; Length 1267;
Best Local Similarity 55.6%; Pred. No. 1.3e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFAE 10
|: |||||
Db 1043 RHSYSSFSK 1051

RESULT 15
CCSA_OENBE
ID CCSA_OENBE STANDARD; PRT; 65 AA.
AC P31565;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Cytochrome c biogenesis protein ccsa (Fragment).
GN CCSA.
OS Oenothera bertiana (Bertero's evening primrose).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
```

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CC MOLECULES OF PROTEIN LAMBDA 3.
CC -!- SIMILARITY: VERY HIGH WITH OTHER REOVIRUS TYPES.
CC -----
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CC -----
CC EMBL: M24734; AAA47234.1; -
CC PIR: C30121; MWXR33.
KW Core protein.
SQ SEQUENCE 1267 AA; 142269 MW; FC9FDA3CEF527148 CRC64;

Query Match 60.0%; Score 33; DB 1; Length 1267;
Best Local Similarity 55.6%; Pred. No. 1.3e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFAE 10
|: |||||
Db 1043 RHSYSSFSK 1051

RESULT 14
VL3_REOVL
ID VL3_REOVL STANDARD; PRT; 1267 AA.
AC P17376;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last annotation update)
DE Minor core protein lambda 3.
GN L1.
OS Reovirus (type 1 / strain Lang).
OC Viruses; dsRNA viruses; Reoviridae; Orthoreovirus.
OX NCBI_TaxID=10884;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89163254; PubMed=2922925;
RA Wiener J.R., Joklik W.K.;
RT "The sequences of the reovirus serotype 1, 2, and 3 L1 genome
RT segments and analysis of the mode of divergence of the reovirus
RT serotypes.";
RL Virology 169:194-203(1989).
CC -!- MISCELLANEOUS: IT IS UNLIKELY THAT CORES CONTAIN MORE THAN 12
CC MOLECULES OF PROTEIN LAMBDA 3.
CC -!- SIMILARITY: VERY HIGH WITH OTHER REOVIRUS TYPES.
CC PIR: A30121; MWXR31.
KW Core protein.
SQ SEQUENCE 1267 AA; 142354 MW; 157E8FD4D664FCDB CRC64;

Query Match 60.0%; Score 33; DB 1; Length 1267;
Best Local Similarity 55.6%; Pred. No. 1.3e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFAE 10
|: |||||
Db 1043 RHSYSSFSK 1051

RESULT 15
CCSA_OENBE
ID CCSA_OENBE STANDARD; PRT; 65 AA.
AC P31565;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Cytochrome c biogenesis protein ccsa (Fragment).
GN CCSA.
OS Oenothera bertiana (Bertero's evening primrose).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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OC  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC  eurosids II; Myrtales; Onagraceae; Oenothera.
OX  NCBI_TaxID=3950;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=931169690; PubMed=8435856;
RA  Nimzyk R., Schoendorf T., Hachtel W.;
RT  "In-frame length mutations associated with short tandem repeats are
RT  located in unassigned open reading frames of Oenothera chloroplast
RT  DNA.";
RL  Curr. Genet. 23:265-270(1993).
CC  -!- FUNCTION: REQUIRED DURING CYTOCHROME BIOGENESIS AT THE STEP OF
CC  HEME ATTACHMENT (BY SIMILARITY).
CC  -!- SIMILARITY: BELONGS TO THE CCMF/CYCK/CCL1/NRFE/CCSA FAMILY.
CC  -----
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CC  -----
DR  EMBL; X64617; CAA45900.1; -.
DR  EMBL; X64614; CAA45894.1; -.
DR  PIR; S19981; S19981.
DR  PIR; S19988; S19988.
DR  InterPro; IPR002541; CytC_asm.
DR  Pfam; PF01578; CytC_asm; 1.
KW  Cytochrome c-type biogenesis; Chloroplast.
FT  NON_TER 1
SQ  SEQUENCE 65 AA; 7441 MW; 343E66DDA1492C0C CRC64;

Query Match      58.2%; Score 32; DB 1; Length 65;
Best Local Similarity 83.3%; Pred. No. 9.2;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY  3 HNYGSF 8
Db  57 HSYGSF 62

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Search completed: November 18, 2002, 17:33:28
 Job time : 2.45098 secs

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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:01 ; Search time 10.4412 Seconds
(without alignments)
197.341 Million cell updates/sec

Title: US-09-016-061-74

Perfect score: 55

Sequence: 1 ARHNYGSPAE 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	81.8	839	10 Q9LIE5	Q9lie5 arabidopsis
2	40	72.7	276	7 Q9GIN0	Q9gin0 cainan croc
3	39	70.9	446	5 O62086	O62086 caenorhabd
4	39	70.9	723	16 P72121	P72121 pseudomonas
5	38	69.1	89	7 O19495	O19495 gallus gall
6	38	69.1	433	10 Q9C5G3	Q9c5g3 arabidopsis
7	37	67.3	347	2 Q55231	Q55231 synecococc
8	37	67.3	5317	5 O8TA74	O8ta74 hemocentrot
9	36	65.5	39	7 P79474	P79474 cervus elap
10	36	65.5	39	7 P79477	P79477 cervus elap
11	36	65.5	39	7 P79478	P79478 cervus elap
12	36	65.5	39	7 P79479	P79479 cervus elap
13	36	65.5	67	7 Q8SP02	Q8sp02 hapalemur g
14	36	65.5	74	6 Q9TPT4	Q9tpt4 bos taurus
15	36	65.5	75	7 Q9GIJ5	Q9giJ5 bos taurus
16	36	65.5	76	7 Q9TPC2	Q9tpc2 macaca mula

ALIGNMENTS

RESULT 1

Q9LIE5 ID Q9LIE5 PRELIMINARY; PRT; 839 AA.
AC Q9LIE5; Q9LIE5; 839 AA.
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Far-red impaired response protein, mutator-like transposase-like protein, phytochrome A signaling protein-like.
DE Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=20363099; PubMed=10907853;
RA Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. II. Sequence features of the regions of 4,251,695 bp covered by ninety P1, TAC and BAC clones.";
RL DNA Res. 7:217-221(2000).
DR EMBL; AP001306; BAB03065.1;
DR InterPro; IPR004330; FARI.
DR InterPro; IPR001000; Glyco_hydro_10.
DR Pfam; PF03101; FARI; 1.
DR PROSITE; PS00591; GLYCOSYL_HYDROL_F10; UNKNOWN_1.
SQ SEQUENCE 839 AA; 95996 MW; CBBF6DF8B679F8 CRC64;

Query Match 81.8%; Score 45; DB 10; Length 839;

Best Local Similarity 70.0%; Pred. No. 2.4;

Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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QY 1 ARHNGSFAE 10
Db 274 SRHNGSFCD 283
      :|||||||:
      274 SRHNGSFCD 283

RESULT 2
O9GJNO PRELIMINARY; PRT; 276 AA.
ID O9GJNO
AC O9GJNO;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MHC class II beta chain.
GN HClIBETA.
OS Calman crocodilus (Spectacled calman) (Calman sclerops).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Crocodylidae; Alligatorinae; Calman.
OX NCBI_TaxID=8499;
RN [1]
RN SEQUENCE FROM N.A.
RA Voldby J., Vitved L., Due M., Gronlund J., Holmskov U., Telsner B.,
RA Salomonsen J., Brusgaard K., Skjoldt K.;
RT "Cloning, sequence and genomic structure of MHC class II antigens from
RT the spectacled calman, Calman crocodilus.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF256651; AAF99283.1; -.
DR HSSP; P13760; 2SER.
DR InterPro; IPR003006; Iq_c1.
DR InterPro; IPR003006; Iq_MHC.
DR InterPro; IPR000353; MHC_II_beta.
DR Pfam; PF00047; Iq; 1.
DR Pfam; PF00969; MHC_II_beta; 1.
DR ProDom; PD000328; MHC_II_beta; 1.
DR SMART; SM00407; IGc1; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Glycoprotein; MHC II; Transmembrane.
SQ SEQUENCE 276 AA; 30366 MW; EABA4684986AEAA6A CRC64;

Query Match 72.7%; Score 40; DB 7; Length 276;
Best Local Similarity 87.5%; Pred. No. 6.8;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFA 9
Db 108 RHNYGVFA 115
      :|||||:
      108 RHNYGVFA 115

RESULT 3
O62086 PRELIMINARY; PRT; 446 AA.
AC O62086
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE C3IH5.6 protein.
GN C3IH5.6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RN SEQUENCE FROM N.A.
RA Kershaw J.K.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; Z93778; CAB07846.1; -.
DR InterPro; IPR000379; Ser_estrs_site.
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```
SQ SEQUENCE 446 AA; 50763 MW; 82AD969CDAD753DE CRC64;

Query Match 70.9%; Score 39; DB 5; Length 446;
Best Local Similarity 87.5%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFA 9
Db 51 RHNYGSHA 58
      :|||||:
      51 RHNYGSHA 58

RESULT 4
P72121 PRELIMINARY; PRT; 723 AA.
ID P72121
AC P72121;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Outer membrane protein C precursor (Outer membrane protein OPRC).
GN OPRC OR PA3790.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=96349120; PubMed=8760927;
RA Yoneyama H., Nakae T.;
RT "Protein C (OPRC) of the outer membrane of Pseudomonas aeruginosa is a
RT copper-regulated channel protein.";
RL Microbiology 142:2137-2144(1996).
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
DR EMBL; D28119; BAA05664.1; -.
DR EMBL; AE004797; AAG07177.1; -.
DR InterPro; IPR001005; Myb_DNA_binding.
DR InterPro; IPR000531; TonB_boxC.
DR Pfam; PF00593; TonB_boxC; 1.
DR PROSITE; PS00037; MYB_1; UNKNOWN_1.
KW Signal; Complete proteome.
FT SIGNAL 1 55 POTENTIAL.
FT CHAIN 56 723 MATURE PROTEIN C.
SQ SEQUENCE 723 AA; 79303 MW; E9FC33618E830A3E CRC64;

Query Match 70.9%; Score 39; DB 16; Length 723;
Best Local Similarity 75.0%; Pred. No. 32;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFAE 10
Db 407 HNYGAFCE 414
      :|||||:
      407 HNYGAFCE 414

RESULT 5
O19495 PRELIMINARY; PRT; 89 AA.
ID O19495
AC O19495;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MHC class II beta 1 domain (Fragment).
```

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GN B-LBI
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=15.151-5; TISSUE=BURSA;
RX MEDLINE=98179131; Pubmed=9510552;
RA Pharr G.T., Dodgson J.B., Hunt H.D., Bacon L.D.;
RT "Class II MHC cDNAs in 1515 B-congenic chickens.";
RL Immunogenetics 47:350-354(1998).
DR EMBL; U91532; AAC15813.1; -.
DR InterPro; IPR000353; MHC_II_beta.
DR Pfam; PF00969; MHC_II_beta; 1.
DR ProDom; PD000328; MHC_II_beta; 1.
KW Glycoprotein; MHC II; Transmembrane.
FT NON_TER 1
FT NON_TER 89
SQ SEQUENCE 89 AA; 10724 MW; BC7D558B6AEB1379 CRC64;

Query Match 69.1%; Score 38; DB 7; Length 89;
Best Local Similarity 85.7%; Pred. No. 4.7;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
DB 75 RHNYGDF 81

RESULT 6
ID Q9CSG3 PRELIMINARY; PRT; 433 AA.
AC Q9CSG3;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative major surface glycoprotein.
GN MFO20.3/AT5G42620.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
RA Goldsmith A.D., Lee J.M., Quach H.B., Toriumi M., Yu G., Bowser L.,
RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
RA Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RT "Full length cDNA of gene MFO20.3/AT5g42620 (GI:101717140).";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF360272; AAK25982.1; -.
DR InterPro; IPR001577; Peptidase_M8.
DR Pfam; PF01457; Peptidase_M8; 1.
DR PRINTS; PR00782; LSHMANOLYSIN.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
SQ SEQUENCE 433 AA; 48711 MW; EC907C8174665D11 CRC64;

Query Match 69.11%; Score 38; DB 10; Length 433;
Best Local Similarity 50.0%; Pred. No. 28;
Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFAE 10
DB 345 SRHHYGAFSQ 354

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RESULT 7
Q55231 PRELIMINARY; PRT; 347 AA.
ID Q55231;
AC Q55231;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Delta 12 desaturase.
DR DESA.
OS Synechococcus sp. (strain PCC 7002) (Agmenellum quadruplicatum).
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX NCBI_TaxID=32049;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94207189; Pubmed=8155883;
RA Sakamoto T., Wada H., Nishida I., Ohmori M., Murata N.;
RT "Identification of conserved domains in the delta 12 desaturases of
cyanobacteria.";
RL Plant Mol. Biol. 24:643-650(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA Sakamoto T., Bryant D.A.;
RT "Molecular characterization of the ammonium transporter gene of
Synechococcus sp. PCC7002.";
RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; D13779; BAA02922.1; -.
DR EMBL; U36388; AAF21445.1; -.
DR InterPro; IPR000595; CNMP_Binding.
DR InterPro; IPR001225; FA_desaturase.
DR Pfam; PF00487; FA_desaturase; 1.
DR ProDom; PD001081; FA_desaturase; 2.
DR PROSITE; PS00888; CNMP_BINDING_1; UNKNOWN_1.
SQ SEQUENCE 347 AA; 40655 MW; EC099B226A9B96D9 CRC64;

Query Match 67.3%; Score 37; DB 2; Length 347;
Best Local Similarity 70.0%; Pred. No. 35;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSFAE 10
DB 334 AEHNYISFAQ 343

RESULT 8
Q8TA74 PRELIMINARY; PRT; 5317 AA.
ID Q8TA74
AC Q8TA74;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Ryanodine receptor.
OS Hemicotrotus pulcherrimus (Sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoida; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
OC Hemicotrotus.
OX NCBI_TaxID=7650;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21821894; Pubmed=11832393;
RA Shiwa M., Murayama T., Ogawa Y.;
RT "Molecular cloning and characterization of ryanodine receptor from
unfertilized sea urchin eggs.";
RL Am. J. Physiol. Regul. Integr. Comp. Physiol. 282:R727-R737(2002).
DR EMBL; AB051576; BAB84714.1; -.
KW Receptor.
SQ SEQUENCE 5317 AA; 597209 MW; 2FA8A1D8C8E28A78 CRC64;

Query Match 67.3%; Score 37; DB 5; Length 5317;
Best Local Similarity 85.7%; Pred. No. 7.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGS 7
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Db 3329 ARNYGA 3335

RESULT 9
P79474
ID P79474 PRELIMINARY; PRT; 39 AA.
AC P79474;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MHC class II DRB (Fragment).
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervioidea;
OC Cervidae; Cervinae; Cervus.
OX NCBI_TaxID=9860;
RN [1]
RP SEQUENCE FROM N.A.
RA Swabrick P.A., Crawford A.M.;
RT "The MHC class II DRB intron 2 microsatellite of red deer.";
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U63077; AAB37777.1; -.
DR InterPro: IPR000353; MHC_II_beta.
DR Pfam: PF00969; MHC_II_beta; 1.
DR ProDom: PD000328; MHC_II_beta; 1.
KW Glycoprotein; MHC II; Transmembrane.
FT NON_TER 1
FT NON_TER 39
SQ SEQUENCE 39 AA; 4767 MW; CAF3680999733DID CRC64;

Query Match 65.5%; Score 36; DB 7; Length 39;
Best Local Similarity 85.7%; Pred. No. 4.6;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
| | | | |
Db 25 RHNYGVF 31

RESULT 10
P79477
ID P79477 PRELIMINARY; PRT; 39 AA.
AC P79477;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MHC class II DRB (Fragment).
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervioidea;
OC Cervidae; Cervinae; Cervus.
OX NCBI_TaxID=9860;
RN [1]
RP SEQUENCE FROM N.A.
RA Swabrick P.A., Crawford A.M.;
RT "The MHC class II DRB intron 2 microsatellite of red deer.";
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U63080; AAB37780.1; -.
DR InterPro: IPR000353; MHC_II_beta.
DR Pfam: PF00969; MHC_II_beta; 1.
DR ProDom: PD000328; MHC_II_beta; 1.
KW Glycoprotein; MHC II; Transmembrane.
FT NON_TER 1
FT NON_TER 39
SQ SEQUENCE 39 AA; 4806 MW; C2188A16752A3C1D CRC64;

Query Match 65.5%; Score 36; DB 7; Length 39;
Best Local Similarity 85.7%; Pred. No. 4.6;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
| | | | |
Db 25 RHNYGVF 31

RESULT 11
P79478
ID P79478 PRELIMINARY; PRT; 39 AA.
AC P79478;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MHC class II DRB (Fragment).
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervioidea;
OC Cervidae; Cervinae; Cervus.
OX NCBI_TaxID=9860;
RN [1]
RP SEQUENCE FROM N.A.
RA Swabrick P.A., Crawford A.M.;
RT "The MHC class II DRB intron 2 microsatellite of red deer.";
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U63081; AAB37781.1; -.
DR InterPro: IPR000353; MHC_II_beta.
DR Pfam: PF00969; MHC_II_beta; 1.
DR ProDom: PD000328; MHC_II_beta; 1.
KW Glycoprotein; MHC II; Transmembrane.
FT NON_TER 1
FT NON_TER 39
SQ SEQUENCE 39 AA; 4806 MW; C2188A16752A3C1D CRC64;

Query Match 65.5%; Score 36; DB 7; Length 39;
Best Local Similarity 85.7%; Pred. No. 4.6;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
| | | | |
Db 25 RHNYGVF 31

RESULT 12
P79479
ID P79479 PRELIMINARY; PRT; 39 AA.
AC P79479;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MHC class II DRB (Fragment).
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervioidea;
OC Cervidae; Cervinae; Cervus.
OX NCBI_TaxID=9860;
RN [1]
RP SEQUENCE FROM N.A.
RA Swabrick P.A., Crawford A.M.;
RT "The MHC class II DRB intron 2 microsatellite of red deer.";
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U63082; AAB37782.1; -.
DR InterPro: IPR000353; MHC_II_beta.
DR Pfam: PF00969; MHC_II_beta; 1.
DR ProDom: PD000328; MHC_II_beta; 1.
KW Glycoprotein; MHC II; Transmembrane.
FT NON_TER 1
FT NON_TER 39
SQ SEQUENCE 39 AA; 4806 MW; C2188A16752A3C1D CRC64;

Query Match 65.5%; Score 36; DB 7; Length 39;
Best Local Similarity 85.7%; Pred. No. 4.6;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
| | | | |
Db 25 RHNYGVF 31

RESULT 13

Q8SP02

ID Q8SP02 PRELIMINARY; PRT; 67 AA.
 AC Q8SP02;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE MHC class II antigen (Fragment).
 GN HAGG-DRB.
 OS Hapalemur griseus griseus.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Strepsirrhini; Lemnidae; Hapalemur.
 OX NCBI_TaxID=122219;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Go Y., Satou Y., Kawamoto Y., Rakotoarisoa G., Randrianjafy A.,
 RA Koyama N., Hirai H.;
 RT "Mhc-DRB genes evolution in lemurs.";
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB078220; BAB88434.1; -;
 FT NON_TER 1
 FT NON_TER 67
 SQ SEQUENCE 67 AA; 8083 MW; 559300839F0EFA52 CRC64;

Query Match 65.5%; Score 36; DB 7; Length 67;
 Best Local Similarity 85.7%; Pred. No. 8.4;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8

|||||
 Db 59 RHNYGVF 65

RESULT 14

Q9TTM4

ID Q9TTM4 PRELIMINARY; PRT; 74 AA.
 AC Q9TTM4;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE MHC(BOLA) class II DR-beta chain (Fragment).
 GN BOLA-DRB3.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-JAPANESE BLACK;
 RA Takeshima S., Ikegami M., Morita M., Nakai Y., Aida Y.;
 RT "Identification of BOLA-DRB3 exon 2 of Japanese black cattle.";
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB033388; BAA85470.1; -;
 DR InterPro; IPR000353; MHC_II_beta.
 DR Pfam; PF00969; MHC_II_beta; 1.
 DR ProDom; PD000328; MHC_II_beta; 1.
 KW Glycoprotein; MHC II; Transmembrane.
 FT NON_TER 1
 FT NON_TER 74
 SQ SEQUENCE 74 AA; 9132 MW; C5834842F0E38BA6 CRC64;

Query Match 65.5%; Score 36; DB 6; Length 74;
 Best Local Similarity 85.7%; Pred. No. 9.4;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8

|||||
 Db 68 RHNYGVF 74

RESULT 15

Q9GIJ5

ID Q9GIJ5 PRELIMINARY; PRT; 75 AA.
 AC Q9GIJ5;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE MHC(BOLA) class II DR-beta chain (Fragment).
 GN BOLA-DRB3.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-JAPANESE BLACK; TISSUE-PERIPHERAL BLOOD LYMPHOCYTE;
 RA Takeshima S., Ikegami M., Saitou N., Morita M., Inoko T., Aida Y.;
 RT "Nature and origin of polymorphism in BOLA-DRB3 gene.";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB053167; BAB20423.1; -;
 DR InterPro; IPR000353; MHC_II_beta.
 DR Pfam; PF00969; MHC_II_beta; 1.
 DR ProDom; PD000328; MHC_II_beta; 1.
 KW Glycoprotein; MHC II; Transmembrane.
 FT NON_TER 1
 FT NON_TER 75
 SQ SEQUENCE 75 AA; 9260 MW; C58310BD57BB7401 CRC64;

Query Match 65.5%; Score 36; DB 7; Length 75;
 Best Local Similarity 85.7%; Pred. No. 9.6;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8

|||||
 Db 69 RHNYGVF 75

Search completed: November 18, 2002, 17:40:48
 Job time : 11.4912 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 18, 2002, 17:21:57 ; Search time 13.8235 Seconds
(without alignments)
96.394 Million cell updates/sec

Title: US-09-016-061-74

Perfect score: 55

Sequence: 1 ARHNYGSFAE 10

Scoring table: BLOSUM62

Gapop 10.0., Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	55	100.0	10	AAW76027	LM609 grafted anti
2	55	100.0	10	AAW76027	Mutant VH CDR3 pep
3	52	94.5	10	AAW76026	LM609 grafted anti
4	52	94.5	10	AAW76024	Mutant VH CDR3 pep
5	50	90.9	10	AAW76024	LM609 grafted anti
6	50	90.9	10	AAW76025	LM609 grafted anti
7	50	90.9	10	AAW76028	LM609 grafted anti
8	50	90.9	10	AAW76029	LM609 grafted anti
9	50	90.9	10	AAW76030	LM609 grafted anti
10	50	90.9	10	AAW76010	LM609 grafted anti

11	50	90.9	10	22	AAW76027	LM609 grafted anti
12	50	90.9	10	22	AAW76027	Mutant VH CDR3 pep
13	50	90.9	10	22	AAW76027	Mutant VH CDR3 pep
14	50	90.9	10	22	AAW76027	Mutant VH CDR3 pep
15	50	90.9	10	22	AAW76027	Mutant VH CDR3 pep
16	50	90.9	10	22	AAW76027	Mutant VH CDR3 pep
17	50	90.9	117	19	AAW76001	Vitaxin antibody h
18	50	90.9	117	19	AAW76003	LM609 antibody hea
19	50	90.9	117	20	AAW76031	Murine monoclonal
20	50	90.9	117	20	AAW76037	Humanised LM609 an
21	50	90.9	117	22	AAW76038	A heavy chain vari
22	50	90.9	117	22	AAW76038	A heavy chain vari
23	50	90.9	117	22	AAW76038	Vitaxin heavy chai
24	50	90.9	117	22	AAW76038	Antibody LM609 hea
25	50	90.9	118	20	AAW76038	Humanised LM609 an
26	50	90.9	118	20	AAW76038	Humanised LM609 an
27	50	90.9	118	20	AAW76038	Humanised LM609 an
28	50	90.9	118	20	AAW76038	Humanised LM609 an
29	50	90.9	130	20	AAW76039	Murine monoclonal
30	49	89.1	10	19	AAW76039	LM609 grafted anti
31	49	89.1	10	22	AAW76039	Multiple mutant VH
32	47	85.5	10	19	AAW76021	LM609 grafted anti
33	47	85.5	10	22	AAW76021	Mutant VH CDR3 pep
34	46	83.6	10	19	AAW76040	LM609 grafted anti
35	46	83.6	10	19	AAW76022	LM609 grafted anti
36	46	83.6	10	19	AAW76023	LM609 grafted anti
37	46	83.6	10	22	AAW76023	Mutant VH CDR3 pep
38	46	83.6	10	22	AAW76023	Mutant VH CDR3 pep
39	46	83.6	10	22	AAW76023	Multiple mutant VH
40	45	81.8	10	19	AAW76037	LM609 grafted anti
41	45	81.8	10	19	AAW76020	LM609 grafted anti
42	45	81.8	10	22	AAW76020	Mutant VH CDR3 pep
43	45	81.8	10	22	AAW76020	Multiple mutant VH
44	42	76.4	110	20	AAW84099	Vitronectin alpha-
45	42	76.4	117	20	AAW84093	Murine vitronectin

ALIGNMENTS

RESULT 1

AAW76027
ID AAW76027 standard; Protein; 10 AA.

AC AAW76027;

DT 02-NOV-1998 (first entry)

DE LM609 grafted antibody V-H region CDR3 protein fragment #9.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.

OS Mus sp.

PN WO9833919-A2.

XX 06-AUG-1998.

PF 30-JAN-1998; 98WO-US01826.

PR 30-JAN-1997; 97US-0791391.

PA (IXSY-) IXSYS INC.

PI Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

DR N-PSDB; AAV49864.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
XX
PS Claim 62; Page 41; 129pp; English.
XX
XX AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
CC antibodies contain non-murine framework regions so are suitable for use
CC in humans. Enhanced types of LM609 have affinity more than 90 times
CC greater than that of parent the parent antibody.
XX
XX Sequence 10 AA;

Query Match 100.0%; Score 55; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0039;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFAE 10
| | | | | | | | | |
Db 1 ARHNYGSFAE 10
| | | | | | | | | |

RESULT 2
AAB61385
ID AAB61385 standard; peptide; 10 AA.
XX
AC AAB61385;
XX
XX 03-APR-2001 (first entry)
XX
XX Mutant VH CDR3 peptide #8.
XX
XX LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
KW inflammatory; cancer; retina; restenosis; osteoporosis.
KW
XX
XX Unidentified.
XX
XX WO200078815-A1.
XX
XX 28-DEC-2000.
XX
XX 23-JUN-2000; 2000WO-US17454.
XX
XX 24-JUN-1999; 99US-0339922.
XX
XX (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX
XX Huse WD, Wu H;
XX
XX WPI: 2001-050110/06.
XX
XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
PT osteoporosis -
XX
XX Disclosure; Page 41; 132pp; English.
XX
XX The present invention relates to enhanced LM609 grafted antibodies
CC exhibiting selective binding affinity to alphavbeta_3 integrin or
CC their functional fragments. The antibodies or their functional
CC fragments can be used in the diagnosis and treatment of
CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory

CC diseases (such as psoriasis and chronic articular rheumatism),
CC disorders associated with inappropriate or inopportune invasion of
CC vessels (such as diabetic retinopathy, neovascular glaucoma and
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
CC diseases (such as macular degeneration), restenosis and
CC osteoporosis.
XX
XX Sequence 10 AA;

Query Match 100.0%; Score 55; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0039;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFAE 10
| | | | | | | | | |
Db 1 ARHNYGSFAE 10
| | | | | | | | | |

RESULT 3
AAW76026
ID AAW76026 standard; Protein; 10 AA.
XX
AC AAW76026;
XX
XX 02-NOV-1998 (first entry)
XX
XX LM609 grafted antibody V-H region CDR3 protein fragment #8.
XX
XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
XX
XX Mus sp.
XX
XX WO9833919-A2.
XX
XX 06-AUG-1998.
XX
XX 30-JAN-1998; 98WO-US01826.
XX
XX 30-JAN-1997; 97US-0791391.
XX
XX (IXSY-) IXSYS INC.
XX
XX Glaser SM, Huse WD;
XX
XX WPI: 1998-437472/37.
XX
XX N-PSDB; AAV49863.
XX
XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
XX
XX Claim 62; Page 41; 129pp; English.
XX
XX AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
CC antibodies contain non-murine framework regions so are suitable for use
CC in humans. Enhanced types of LM609 have affinity more than 90 times
CC greater than that of parent the parent antibody.
XX
XX Sequence 10 AA;

Query Match 94.5%; Score 52; DB 19; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.013;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFAE 10
 Db 1 ARHNYGSFAD 10
 |||||

RESULT 4

AAB61384
 ID AAB61384 standard; peptide; 10 AA.

XX AC AAB61384;

DT 03-APR-2001 (first entry)

DE Mutant VH CDR3 peptide #7.

KW LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis.

XX OS Unidentified.

PN WO200078815-A1.

PD 28-DEC-2000.

PF 23-JUN-2000; 2000WO-US17454.

PR 24-JUN-1999; 99US-0339922.

PA (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX Huse WD, Wu H;

DR WPI; 2001-050110/06.

Enhanced LM609 grafted antibodies exhibiting selective binding affinity to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of angiogenesis, inflammatory diseases e.g. psoriasis, cancers and osteoporosis.

PS Disclosure; Page 41; 132pp; English.

The present invention relates to enhanced LM609 grafted antibodies exhibiting selective binding affinity to alphavbeta_3 integrin or their functional fragments. The antibodies or their functional fragments can be used in the diagnosis and treatment of diseases (such as psoriasis and chronic articular rheumatism), disorders associated with inappropriate or inopportune invasion of vessels (such as diabetic retinopathy, neovascular glaucoma and cancer disorders such as tumours and Kaposi's sarcoma), retinal osteoporosis.

XX Sequence 10 AA;

Query Match 94.5%; Score 52; DB 22; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.013;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFAE 10
 Db 1 ARHNYGSFAD 10
 |||||

RESULT 5

AAW76024

ID AAW76024 standard; Protein; 10 AA.

XX

AC AAW76024;

DT 02-NOV-1998 (first entry)

DE LM609 grafted antibody V-H region CDR3 protein fragment #6.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.

OS Mus SP.

PN WO9833919-A2.

PD 06-AUG-1998.

PF 30-JAN-1998; 98WO-US01826.

PR 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

XX Glaser SM, Huse WD;

DR WPI; 1998-437472/37.

DR N-PSDB; AAV49861.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3 integrin - and related grafted antibodies based on murine monoclonal LM609, also related nucleic acid, used to treat, prevent or diagnose angiogenesis or restenosis

PS Claim 62; Page 41; 129pp; English.

AAW76007-W76040 are protein fragments of the grafted monoclonal antibody LM609 heavy and light chain variable region. LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3 and can be used to inhibit binding of alphavbeta3 to a ligand and thus block integrin-mediated signal transduction. This is useful in the treatment, prevention and diagnosis of alphavbeta3-mediated disease, specifically angiogenesis and restenosis (but also e.g. (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis etc.). The antibodies contain non-murine framework regions so are suitable for use in humans. Enhanced types of LM609 have affinity more than 90 times greater than that of parent the parent antibody.

XX Sequence 10 AA;

Query Match 90.9%; Score 50; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.028;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
 Db 1 ARHNYGSFA 9
 |||||

RESULT 6

AAW76025

ID AAW76025 standard; Protein; 10 AA.

XX AC AAW76025;

DT 02-NOV-1998 (first entry)

DE LM609 grafted antibody V-H region CDR3 protein fragment #7.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;

KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.

OS Mus sp.

XX WO9833919-A2.

PN 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

PF 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

XX Glaser SM, Huse WD;

PI WPI; 1998-437472/37.

DR N-PSDB; AAV49862.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

XX Claim 62; Page 41; 129pp; English.

CC AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
 CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
 CC antibodies contain non-murine framework regions so are suitable for use
 CC in humans. Enhanced types of LM609 have affinity more than 90 times
 CC greater than that of parent the parent antibody.

XX Sequence 10 AA;

Query Match 90.9%; Score 50; DB 19; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.028;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9

DB 1 ARHNYGSFA 9

RESULT 7

AAW76028

ID AAW76028 standard; Protein; 10 AA.

XX AAW76028;

XX 02-NOV-1998 (first entry)

DE LM609 grafted antibody V-H region CDR3 protein fragment #10.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.

OS Mus sp.

XX WO9833919-A2.

XX 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

XX Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

DR N-PSDB; AAV49865.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

XX Claim 62; Page 41; 129pp; English.

CC AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
 CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
 CC antibodies contain non-murine framework regions so are suitable for use
 CC in humans. Enhanced types of LM609 have affinity more than 90 times
 CC greater than that of parent the parent antibody.

XX Sequence 10 AA;

Query Match 90.9%; Score 50; DB 19; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.028;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9

DB 1 ARHNYGSFA 9

RESULT 8

AAW76029

ID AAW76029 standard; Protein; 10 AA.

XX AAW76029;

XX 02-NOV-1998 (first entry)

DE LM609 grafted antibody V-H region CDR3 protein fragment #11.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.

OS Mus sp.

XX WO9833919-A2.

XX 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

XX PI Glaser SM, Huse WD;
 XX DR WPI: 1998-437472/37.
 XX DR N-PSDB; AAV49866.
 XX PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 XX PT integrin - and related grafted antibodies based on murine monoclonal
 XX PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 XX PT angiogenesis or restenosis
 XX PS Claim 62; Page 41; 129pp; English.
 XX CC AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
 XX CC LM609 heavy and light chain variable region. LM609 and the antibody
 XX CC vitaxin bind selectively to integrin alphaVbeta3 and can be used to
 XX CC inhibit binding of alphaVbeta3 to a ligand and thus block
 XX CC integrin-mediated signal transduction. This is useful in the treatment,
 XX CC prevention and diagnosis of alphaVbeta3-mediated disease, specifically
 XX CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 XX CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
 XX CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
 XX CC antibodies contain non-murine framework regions so are suitable for use
 XX CC in humans. Enhanced types of LM609 have affinity more than 90 times
 XX CC greater than that of parent the parent antibody.
 XX SQ Sequence 10 AA;
 Query Match 90.9%; Score 50; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.028;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ARHNYGSFA 9
 Db | | | | | | | | | |
 1 ARHNYGSFA 9
 RESULT 9
 AAW76030
 ID AAW76030 standard; Protein; 10 AA.
 AC AAW76030;
 XX 02-NOV-1998 (first entry)
 DE LM609 grafted antibody V-H region CDR3 protein fragment #12.
 XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 XX OS Mus sp.
 XX WO9833919-A2.
 PN 06-AUG-1998.
 PD 30-JAN-1998; 98WO-US01826.
 PF 30-JAN-1997; 97US-0791391.
 PR (IXSY-) IXSYS INC.
 PA Glaser SM, Huse WD;
 XX WPI: 1998-437472/37.
 XX DR N-PSDB; AAV49867.
 XX PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 XX PT integrin - and related grafted antibodies based on murine monoclonal
 XX PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 XX PT angiogenesis or restenosis
 XX PS Disclosure; Page 40; 129pp; English.
 XX CC AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
 XX CC LM609 heavy and light chain variable region. LM609 and the antibody
 XX CC vitaxin bind selectively to integrin alphaVbeta3 and can be used to

PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX Claim 62; Page 41; 129pp; English.
 CC AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphaVbeta3 and can be used to
 CC inhibit binding of alphaVbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphaVbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
 CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
 CC antibodies contain non-murine framework regions so are suitable for use
 CC in humans. Enhanced types of LM609 have affinity more than 90 times
 CC greater than that of parent the parent antibody.
 XX SQ Sequence 10 AA;
 Query Match 90.9%; Score 50; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.028;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ARHNYGSFA 9
 Db | | | | | | | | | |
 1 ARHNYGSFA 9
 RESULT 10
 AAW76010
 ID AAW76010 standard; Protein; 10 AA.
 AC AAW76010;
 XX 02-NOV-1998 (first entry)
 DE LM609 grafted antibody V-H region CDR3 protein fragment #1.
 XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 XX OS Mus sp.
 XX WO9833919-A2.
 PN 06-AUG-1998.
 PD 30-JAN-1998; 98WO-US01826.
 PF 30-JAN-1997; 97US-0791391.
 PR (IXSY-) IXSYS INC.
 PA Glaser SM, Huse WD;
 XX WPI: 1998-437472/37.
 XX DR N-PSDB; AAV49847.
 XX PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 XX PT integrin - and related grafted antibodies based on murine monoclonal
 XX PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 XX PT angiogenesis or restenosis
 XX PS Disclosure; Page 40; 129pp; English.
 XX CC AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
 XX CC LM609 heavy and light chain variable region. LM609 and the antibody
 XX CC vitaxin bind selectively to integrin alphaVbeta3 and can be used to

CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
 CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
 CC antibodies contain non-murine framework regions so are suitable for use
 CC in humans. Enhanced types of LM609 have affinity more than 90 times
 CC greater than that of parent the parent antibody.
 XX
 SQ Sequence 10 AA;

Query Match 90.9%; Score 50; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.028;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
 DB 1 ARHNYGSFA 9

RESULT 11

AAB61368
 ID AAB61368 standard; peptide; 10 AA.

XX
 AC AAB61368;

XX
 DT 03-APR-2001 (first entry)

XX
 DE LM609 VH CDR3 peptide.

XX
 KW LM609; grafted antibody; alphaVbeta_3 integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis.

XX
 OS Unidentified.

XX
 PN WO200078815-A1.

XX
 PD 28-DEC-2000.

XX
 PF 23-JUN-2000; 2000WO-US17454.

XX
 PR 24-JUN-1999; 99US-0339922.

XX
 PA (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX
 PI Huse WD, Wu H;

XX
 WPI; 2001-050110/06.

XX
 DR Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -

XX
 PS Disclosure; Page 39; 132pp; English.

XX
 CC The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphavbeta_3 integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.

XX
 SQ Sequence 10 AA;

Query Match 90.9%; Score 50; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.028;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ARHNYGSFA 9
 DB 1 ARHNYGSFA 9

RESULT 12

AAB61382
 ID AAB61382 standard; peptide; 10 AA.

XX
 AC AAB61382;

XX
 DT 03-APR-2001 (first entry)

XX
 DE Mutant VH CDR3 peptide #5.

XX
 KW LM609; grafted antibody; alphaVbeta_3 integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis.

XX
 OS Unidentified.

XX
 PN WO200078815-A1.

XX
 PD 28-DEC-2000.

XX
 PF 23-JUN-2000; 2000WO-US17454.

XX
 PR 24-JUN-1999; 99US-0339922.

XX
 PA (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX
 PI Huse WD, Wu H;

XX
 WPI; 2001-050110/06.

XX
 DR Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -

XX
 PS Disclosure; Page 41; 132pp; English.

XX
 CC The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphavbeta_3 integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.

XX
 SQ Sequence 10 AA;

Query Match 90.9%; Score 50; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.028;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
 DB 1 ARHNYGSFA 9

RESULT 13

AAB61383
 ID AAB61383 standard; peptide; 10 AA.

XX
 AC AAB61383;

XX
 DT 03-APR-2001 (first entry)

XX The present invention relates to enhanced LM609 grafted antibodies
CC exhibiting selective binding affinity to alphavbeta_3 integrin or
CC their functional fragments. The antibodies or their functional
CC fragments can be used in the diagnosis and treatment of
CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
CC diseases (such as psoriasis and chronic articular rheumatism),
CC disorders associated with inappropriate or inopportune invasion of
CC vessels (such as diabetic retinopathy, neovascular glaucoma and
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
CC diseases (such as macular degeneration), restenosis and
CC osteoporosis.

XX

SQ Sequence 10 AA;

Query Match 90.9%; Score 50; DB 22; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.028;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9

|||||||

Db 1 ARHNYGSFA 9

Search completed: November 18, 2002, 17:31:38
Job time : 13.8235 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:54:45 ; Search time 1.96078 Seconds
(without alignments)
76.811 Million cell updates/sec

Title: US-09-016-061-74

Perfect score: 55

Sequence: 1 ARHNYGSPAE 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 97044 seqs, 15060890 residues

Total number of hits satisfying chosen parameters: 97044

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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4: /cgn2.6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
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11: /cgn2.6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
12: /cgn2.6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
13: /cgn2.6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
14: /cgn2.6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	50	90.9	117	8	US-08-790-540A-2
2	50	90.9	117	8	US-08-790-540A-6
3	50	90.9	117	8	US-08-791-391A-2
4	50	90.9	117	8	US-08-791-391A-6
5	36	65.5	14	1	US-08-677-599B-22
6	36	65.5	101	10	US-09-764-853-432
7	35	63.6	30	10	US-09-839-884-40
8	35	63.6	287	10	US-09-415-540-5
9	34	61.8	464	10	US-09-791-171-62
10	33	60.0	14	1	US-08-677-599B-21
11	32	58.2	14	1	US-08-677-599B-11
12	32	58.2	14	1	US-08-677-599B-12
13	32	58.2	14	1	US-08-677-599B-13
14	32	58.2	14	1	US-08-677-599B-14
15	32	58.2	14	1	US-08-677-599B-15
16	32	58.2	14	1	US-08-677-599B-16
17	32	58.2	14	1	US-08-677-599B-17
18	32	58.2	14	1	US-08-677-599B-18
19	32	58.2	14	1	US-08-677-599B-19

20	32	58.2	14	1	US-08-677-599B-20	Sequence 20, Appl
21	32	58.2	14	1	US-08-677-599B-23	Sequence 23, Appl
22	32	58.2	15	10	US-09-756-983-11	Sequence 11, Appl
23	32	58.2	25	1	US-08-677-599B-8	Sequence 8, Appl
24	32	58.2	93	12	US-10-081-281-121	Sequence 121, Appl
25	32	58.2	94	10	US-09-766-378A-37	Sequence 37, Appl
26	32	58.2	181	10	US-09-815-837-103	Sequence 103, Appl
27	32	58.2	183	10	US-09-815-837-16	Sequence 16, Appl
28	32	58.2	184	10	US-09-815-837-15	Sequence 15, Appl
29	32	58.2	185	10	US-09-815-837-13	Sequence 13, Appl
30	32	58.2	185	10	US-09-815-837-14	Sequence 14, Appl
31	32	58.2	186	10	US-09-815-837-17	Sequence 17, Appl
32	32	58.2	186	10	US-09-815-837-19	Sequence 19, Appl
33	32	58.2	186	10	US-09-815-837-20	Sequence 20, Appl
34	32	58.2	187	10	US-09-815-837-18	Sequence 18, Appl
35	32	58.2	189	10	US-09-815-837-21	Sequence 21, Appl
36	32	58.2	189	10	US-09-815-837-22	Sequence 22, Appl
37	32	58.2	193	10	US-09-815-837-23	Sequence 23, Appl
38	32	58.2	193	10	US-09-815-837-24	Sequence 24, Appl
39	32	58.2	196	10	US-09-741-669-368	Sequence 368, Appl
40	32	58.2	196	10	US-09-912-020-376	Sequence 376, Appl
41	32	58.2	199	10	US-09-815-837-56	Sequence 56, Appl
42	32	58.2	199	10	US-09-815-837-60	Sequence 60, Appl
43	32	58.2	207	12	US-10-081-281-93	Sequence 93, Appl
44	32	58.2	208	10	US-09-815-837-102	Sequence 102, Appl
45	32	58.2	209	10	US-09-815-837-58	Sequence 58, Appl

ALIGNMENTS

RESULT 1

US-08-790-540A-2

; Sequence 2, Application US/08790540A

; Patent No. US2001001125A1

; GENERAL INFORMATION:

; APPLICANT: Huse, William D.

; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human

; NUMBER OF SEQUENCES: 24

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Campbell & Flores LLP

; STREET: 4370 La Jolla Village Drive, Suite 700

; CITY: San Diego

; STATE: California

; COUNTRY: United States

; ZIP: 92122

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/790,540A

; FILING DATE: 30-JAN-1997

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: Campbell, Cathryn A.

; REGISTRATION NUMBER: 31,815

; REFERENCE/DOCKET NUMBER: P-IX 2405

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (619) 535-9001

; TELEFAX: (619) 535-8949

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 117 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-790-540A-2

Query Match 90.9%; Score 50; DB 8; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.0063;

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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
   |||||
Db 97 ARHNYGSFA 105

RESULT 2
US-08-790-540A-6
; Sequence 6, Application US/08790540A
; Patent No. US2001001125A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TELECOMMUNICATION INFORMATION:
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,540A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-790-540A-6

Query Match 90.9%; Score 50; DB 8; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.0063;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
   |||||
Db 97 ARHNYGSFA 105

RESULT 3
US-08-791-391A-2
; Sequence 2, Application US/08791391A
; Patent No. US20010016645A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TELECOMMUNICATION INFORMATION:
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,391A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-391A-2

Query Match 90.9%; Score 50; DB 8; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.0063;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
   |||||
Db 97 ARHNYGSFA 105

RESULT 4
US-08-791-391A-6
; Sequence 6, Application US/08791391A
; Patent No. US20010016645A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TELECOMMUNICATION INFORMATION:
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,391A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-391A-6
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Query Match 90.9%; Score 50; DB 8; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.0063;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
Db 97 ARHNYGSFA 105
|||||

RESULT 5

US-08-677-599B-22
; Sequence 22, Application US/08677599B
; Patent No. US20020155117A1
; GENERAL INFORMATION:
; APPLICANT: Sucia-Foca, Nicole
; TITLE OF INVENTION: METHODS FOR DETECTING ORGAN ALLOGRAFT
; TITLE OF INVENTION: REJECTION AND USES THEREOF
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/677,599B
; FILING DATE: 08-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq. John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 50161-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212/278/0400
; TELEFAX: 212/391/0525
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-677-599B-22

Query Match 65.5%; Score 36; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYG 6
Db 9 ARHNYG 14
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RESULT 6

US-09-764-853-432
; Sequence 432, Application US/09764853
; Patent No. US20020090672A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJ206
; CURRENT APPLICATION NUMBER: US/09/764,853
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 939
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 432
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-853-432

Query Match 65.5%; Score 36; DB 10; Length 101;
Best Local Similarity 85.7%; Pred. No. 2.5;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 64 RHNYSSF 70
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RESULT 7

US-09-839-884-40
; Sequence 40, Application US/09839884
; Patent No. US20020076739A1
; GENERAL INFORMATION:
; APPLICANT: Aebersold, Rudolf H.
; APPLICANT: Gelb, Michael H.
; APPLICANT: Gygi, Steven
; APPLICANT: Scott, C R
; APPLICANT: Turesek, Frantisek
; APPLICANT: Gerber, Scott A
; APPLICANT: Rist, Beate
; TITLE OF INVENTION: Rapid Quantitative Analysis of Proteins or Protein
; TITLE OF INVENTION: Function in Complex Mixture
; FILE REFERENCE: 64-98A
; CURRENT APPLICATION NUMBER: US/09/839,884
; CURRENT FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: 09/383,062
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 60/097,788
; PRIOR FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40
; LENGTH: 30
; TYPE: PRT
; ORGANISM: yeast
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (2)
; OTHER INFORMATION: C at position 2 is ICAT-labeled cysteinyl residue.
US-09-839-884-40

Query Match 63.6%; Score 35; DB 10; Length 30;
Best Local Similarity 62.5%; Pred. No. 1.1;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFAE 10
Db 10 HNYGAFFQ 17
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RESULT 8

US-09-415-540-5
; Sequence 5, Application US/09415540
; Patent No. US20010010911A1
; GENERAL INFORMATION:
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: A NOVEL HUMAN PYROPHOSPHATASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/415,540
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/741,437
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0148 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 855-0555
TELEFAX: (415) 845-4166
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 287 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 4199
US-09-415-540-5

Query Match 63.6%; Score 35; DB 10; Length 287;
Best Local Similarity 62.5%; Pred. No. 12;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFAE 10
| | | | | :
DB 92 HNYGAPQ 99

RESULT 9
US-09-791-171-62
; Sequence 62, Application US/09791171
; Patent No. US2002094336A1
; GENERAL INFORMATION:
; APPLICANT: ANDERSEN, Peter
; APPLICANT: NIELSEN, Rikke
; APPLICANT: OETTINGER, Thomas
; APPLICANT: RASMUSSEN, Peter Birk
; APPLICANT: ROSENKRANDS, Ida
; APPLICANT: WELDRING, Karin
; APPLICANT: FLORIO, Walter
; TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
; FILE REFERENCE: 670001-2002.1
; CURRENT APPLICATION NUMBER: US/09/791,171
; CURRENT FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 09/050,739
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 0376/97
; PRIOR FILING DATE: 1997-04-02
; PRIOR APPLICATION NUMBER: 1277/97
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/044,624
; PRIOR FILING DATE: 1997-04-18
; PRIOR APPLICATION NUMBER: 60/070,488
; PRIOR FILING DATE: 1998-01-05
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 62
; LENGTH: 464
; TYPE: PNT
; ORGANISM: Mycobacterium tuberculosis
US-09-791-171-62

Query Match 61.8%; Score 34; DB 10; Length 464;
Best Local Similarity 62.5%; Pred. No. 31;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFAE 10
| | | | | :
DB 110 HGYGTAD 117

RESULT 10
US-08-677-599B-21
; Sequence 21, Application US/08677599B
; Patent No. US20020155117A1
; GENERAL INFORMATION:
; APPLICANT: Sucia-Foca, Nicole
; TITLE OF INVENTION: METHODS FOR DETECTING ORGAN ALLOGRAFT
; TITLE OF INVENTION: REJECTION AND USES THEREOF
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/677,599B
; FILING DATE: 08-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq., John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 50161-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212/278/0400
; TELEFAX: 212/391/0525
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-677-599B-21

Query Match 60.0%; Score 33; DB 1; Length 14;
Best Local Similarity 83.3%; Pred. No. 1.1;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYG 6
: | | | | |
DB 9 SRHNYG 14

RESULT 11
US-08-677-599B-11
; Sequence 11, Application US/08677599B
; Patent No. US20020155117A1
; GENERAL INFORMATION:
; APPLICANT: Sucia-Foca, Nicole
; TITLE OF INVENTION: METHODS FOR DETECTING ORGAN ALLOGRAFT
; TITLE OF INVENTION: REJECTION AND USES THEREOF
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York

STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/677,599B
FILING DATE: 08-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White Esq., John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 50161-A
TELEPHONE: 212/278/0400
TELEFAX: 212/391/0525
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-677-599B-11

Query Match 58.2%; Score 32; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHYNG 6
Db 10 RHYNG 14

RESULT 12
US-08-677-599B-12
Sequence 12, Application US/08677599B
Patent No. US2002015117A1
GENERAL INFORMATION:
APPLICANT: Sucia-Foca, Nicole
TITLE OF INVENTION: METHODS FOR DETECTING ORGAN ALLOGRAFT
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/677,599B
FILING DATE: 08-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White Esq., John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 50161-A
TELEPHONE: 212/278/0400
TELEFAX: 212/391/0525
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-677-599B-12

Query Match 58.2%; Score 32; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHYNG 6
Db 10 RHYNG 14

RESULT 13
US-08-677-599B-13
Sequence 13, Application US/08677599B
Patent No. US2002015117A1
GENERAL INFORMATION:
APPLICANT: Sucia-Foca, Nicole
TITLE OF INVENTION: METHODS FOR DETECTING ORGAN ALLOGRAFT
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/677,599B
FILING DATE: 08-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White Esq., John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 50161-A
TELEPHONE: 212/278/0400
TELEFAX: 212/391/0525
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-677-599B-13

Query Match 58.2%; Score 32; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHYNG 6
Db 10 RHYNG 14

RESULT 14
US-08-677-599B-14
Sequence 14, Application US/08677599B
Patent No. US2002015117A1
GENERAL INFORMATION:
APPLICANT: Sucia-Foca, Nicole
TITLE OF INVENTION: METHODS FOR DETECTING ORGAN ALLOGRAFT
NUMBER OF SEQUENCES: 23

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/677,599B
; FILING DATE: 08-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq., John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 50161-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212/278/0400
; TELEFAX: 212/391/0525
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: .peptide
; US-08-677-599B-14

Query Match 58.2%; Score 32; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHNYG 6
|||||
Db 10 RHNYG 14

RESULT 15
US-08-677-599B-15
; Sequence 15, Application US/08677599B
; Patent No. US20020155117A1
; GENERAL INFORMATION:
; APPLICANT: Sucia-Foca, Nicole
; TITLE OF INVENTION: METHODS FOR DETECTING ORGAN ALLOGRAFT
; TITLE OF INVENTION: REJECTION AND USES THEREOF
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/677,599B
; FILING DATE: 08-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq., John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 50161-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212/278/0400
; TELEFAX: 212/391/0525

; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-677-599B-15

Query Match 58.2%; Score 32; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHNYG 6
|||||
Db 10 RHNYG 14

Search completed: November 18, 2002, 18:45:17
Job time : 1.96078 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:01 ; Search time 4.2402 Seconds.
(without alignments)
69.390 Million cell updates/sec

Title: US-09-016-061-74

Perfect score: 55

Sequence: 1 ARHNYGSFAE 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	65.5	94	3	US-09-147-550-14
2	36	65.5	94	3	US-09-147-550-45
3	36	65.5	94	3	US-09-147-550-48
4	36	65.5	94	3	US-09-147-550-77
5	36	65.5	94	3	US-09-147-550-84
6	36	65.5	94	3	US-09-147-550-90
7	36	65.5	94	3	US-09-147-550-101
8	36	65.5	94	4	US-09-557-917-14
9	36	65.5	94	4	US-09-557-917-45
10	36	65.5	94	4	US-09-557-917-48
11	36	65.5	94	4	US-09-557-917-77
12	36	65.5	94	4	US-09-557-917-84
13	36	65.5	94	4	US-09-557-917-90
14	36	65.5	94	4	US-09-557-917-101
15	36	65.5	119	3	US-08-767-128-6
16	35	63.6	286	2	US-08-809-267-3
17	35	63.6	286	5	PCT-US95-13662A-3
18	35	63.6	287	2	US-08-741-437-5
19	35	63.6	287	2	US-09-134-593-5
20	34	61.8	191	4	US-09-443-041A-24
21	34	61.8	236	4	US-09-443-041A-30
22	34	61.8	260	4	US-09-443-041A-10
23	34	61.8	261	4	US-09-443-041A-26
24	34	61.8	269	4	US-09-443-041A-32
25	34	61.8	271	4	US-09-443-041A-38
26	34	61.8	271	4	US-09-443-041A-33
27	32	58.2	15	1	US-08-618-464-7

28	32	58.2	15	4	US-09-107-615-7	Sequence 7, Appli
29	32	58.2	16	4	US-09-181-896-2	Sequence 2, Appli
30	32	58.2	25	2	US-08-480-190-44	Sequence 44, Appli
31	32	58.2	25	2	US-08-488-379-44	Sequence 44, Appli
32	32	58.2	25	5	PCT-US93-07545-44	Sequence 44, Appli
33	32	58.2	36	1	US-08-053-131-84	Sequence 84, Appli
34	32	58.2	36	1	US-08-645-641-84	Sequence 84, Appli
35	32	58.2	36	1	US-07-853-4088-84	Sequence 84, Appli
36	32	58.2	36	2	US-08-096-762-84	Sequence 84, Appli
37	32	58.2	36	2	US-08-308-865-84	Sequence 84, Appli
38	32	58.2	36	4	US-09-042-353-281	Sequence 281, App
39	32	58.2	36	4	US-08-758-417A-129	Sequence 129, App
40	32	58.2	36	5	PCT-US92-10983-84	Sequence 84, Appli
41	32	58.2	80	1	US-08-264-250A-1	Sequence 1, Appli
42	32	58.2	89	1	US-08-025-038-30	Sequence 30, Appli
43	32	58.2	89	1	US-08-039-137-17	Sequence 17, Appli
44	32	58.2	90	2	US-08-485-133-23	Sequence 23, Appli
45	32	58.2	94	3	US-09-147-550-12	Sequence 12, Appli

ALIGNMENTS

RESULT 1
US-09-147-550-14
; Sequence 14, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 14
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-14

Query Match 65.5%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 80 RHNYGVF 86

RESULT 2
US-09-147-550-45
; Sequence 45, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979

; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-45

Query Match 65.5%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 2 RHNYGSF 8
Db 80 RHNYGVF 86

RESULT 3

US-09-147-550-48
; Sequence 48, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Alda, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-48

Query Match 65.5%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 2 RHNYGSF 8
Db 80 RHNYGVF 86

RESULT 4

US-09-147-550-77
; Sequence 77, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Alda, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 77
; LENGTH: 94

; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-77

Query Match 65.5%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 2 RHNYGSF 8
Db 80 RHNYGVF 86

RESULT 5

US-09-147-550-84
; Sequence 84, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Alda, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-84

Query Match 65.5%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 2 RHNYGSF 8
Db 80 RHNYGVF 86

RESULT 6

US-09-147-550-90
; Sequence 90, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Alda, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 90
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-90

Query Match 65.5%; Score 36; DB 3; Length 94;

Best Local Similarity 85.7%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
| | | | |
Db 80 RHNYGVF 86

RESULT 7
US-09-147-550-101
; Sequence 101, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-101

Query Match 65.5%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
| | | | |
Db 80 RHNYGVF 86

RESULT 8
US-09-557-917-14
; Sequence 14, Application US/09557917
; Patent No. 6284457
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-14

Query Match 65.5%; Score 36; DB 4; Length 94;
Best Local Similarity 85.7%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
| | | | |
Db 80 RHNYGVF 86

QY 2 RHNYGSF 8
| | | | |
Db 80 RHNYGVF 86

RESULT 9
US-09-557-917-45
; Sequence 45, Application US/09557917
; Patent No. 6284457
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-45

Query Match 65.5%; Score 36; DB 4; Length 94;
Best Local Similarity 85.7%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
| | | | |
Db 80 RHNYGVF 86

RESULT 10
US-09-557-917-48
; Sequence 48, Application US/09557917
; Patent No. 6284457
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-48

Query Match 65.5%; Score 36; DB 4; Length 94;
Best Local Similarity 85.7%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
| | | | |
Db 80 RHNYGVF 86

Db 80 RHNYGVF 86
|||||

RESULT 11

US-09-557-917-77
; Sequence 77, Application US/09557917
; Patent No. 6284457
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 77
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-77

Query Match 65.5%; Score 36; DB 4; Length 94;
Best Local Similarity 85.7%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

QY 2 RHNYGSF 8
|||||

Db 80 RHNYGVF 86

RESULT 12

US-09-557-917-84
; Sequence 84, Application US/09557917
; Patent No. 6284457
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-84

Query Match 65.5%; Score 36; DB 4; Length 94;
Best Local Similarity 85.7%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

QY 2 RHNYGSF 8
|||||

Db 80 RHNYGVF 86

RESULT 13

US-09-557-917-90
; Sequence 90, Application US/09557917
; Patent No. 6284457
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 90
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-90

Query Match 65.5%; Score 36; DB 4; Length 94;
Best Local Similarity 85.7%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
|||||

Db 80 RHNYGVF 86

RESULT 14

US-09-557-917-101
; Sequence 101, Application US/09557917
; Patent No. 6284457
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-101

Query Match 65.5%; Score 36; DB 4; Length 94;
Best Local Similarity 85.7%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
|||||

Db 80 RHNYGVF 86

Search completed: November 18, 2002, 17:43:38
Job time : 4.2402 secs

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RESULT 15
US-08-767-128-6
; Sequence 6, Application US/08767128
; Patent No. 6111079
; GENERAL INFORMATION:
; APPLICANT: WYLIE, DWANE E.
; APPLICANT: LOPEZ, OSVALDO
; APPLICANT: MURRAY, PETER JOSEPH
; APPLICANT: GOEBEL, PETER
; TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
; TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
; STREET: 3100 No. 6111079west Center, 90 South Seventh St
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/767,128
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE: 04-DEC-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/09258
; FILING DATE: 05-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/541,373
; FILING DATE: 10-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/462,798
; FILING DATE: 05-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G.
; REGISTRATION NUMBER: 35,093
; REFERENCE/DOCKET NUMBER: 8648.49USF1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/371-5278
; TELEFAX: 612/332-9081
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: Internal
; ORIGINAL SOURCE:
US-08-767-128-6
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Query Match 65.5%; Score 36; DB 3; Length 119;
Best Local Similarity 66.7%; Pred. No. 18;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 ARHNYGSFA 9
Db 97 ARHHGYGA 105
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:01 : Search time 4.90196 Seconds
(without alignments)
196.114 Million cell updates/sec

Title: US-09-016-061-76
Perfect score: 55
Sequence: 1 ARHNYGSFAM 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	70.9	446	2 T19625	hypothetical prote
2	39	70.9	1052	2 AF2959	conserved hypotet
3	39	70.9	1341	2 H98323	hypothetical prote
4	37	67.3	430	2 C81402	probable integral
5	36	65.5	82	2 I51106	Major Histocompati
6	36	65.5	89	2 S38688	MHC class II histo
7	36	65.5	89	2 S38683	MHC class II histo
8	36	65.5	89	2 S38684	MHC class II OVAR-
9	36	65.5	225	2 I47095	conserved hypotet
10	35	63.6	195	2 G86742	phosphatidylcholin
11	35	63.6	347	2 S43771	secreted glycoprot
12	35	63.6	383	2 S56179	glutamate-tRNA lig
13	35	63.6	473	2 D70405	Ig heavy chain V r
14	34	61.8	108	2 S26316	Ig heavy chain V r
15	34	61.8	110	2 S26317	conserved hypotet
16	34	61.8	210	1 B6265	hypothetical prote
17	34	61.8	220	2 T46055	translation initia
18	34	61.8	275	2 G75130	probable translati
19	34	61.8	275	2 D71087	inorganic diphosph
20	34	61.8	287	1 PWVKL	cytochrome c-type
21	34	61.8	287	1 S58614	cytochrome c-type
22	34	61.8	321	1 JQ0288	protein-tyrosine k
23	34	61.8	628	1 A56707	probable MPAL fami
24	34	61.8	662	2 H95934	gene 50 protein -
25	34	61.8	682	2 S30995	outer membrane pro
26	34	61.8	723	2 F83173	MHC HLA-DR-beta-1
27	34	61.8	80	2 I54469	MHC HLA-DR beta-1
28	33	60.0	80	2 I68777	
29	33	60.0	80	2 I68777	

30	33	60.0	81	2 I54550	HLA DRB1*1202 - hu
31	33	60.0	85	2 I59634	MHC class II DR-be
32	33	60.0	89	2 S38676	MHC class II histo
33	33	60.0	89	2 S38680	MHC class II histo
34	33	60.0	89	2 S57512	MHC class II histo
35	33	60.0	115	2 AD0414	probable exported
36	33	60.0	123	2 C25239	MHC class II histo
37	33	60.0	167	2 T16454	hypothetical prote
38	33	60.0	200	2 D32526	class II histocomp
39	33	60.0	203	2 H89768	hypothetical prote
40	33	60.0	237	2 C27060	class II histocomp
41	33	60.0	266	2 I54287	gene HLA-DRB1 prot
42	33	60.0	266	2 A27618	class II histocomp
43	33	60.0	266	2 I54295	lymphocyte antigen
44	33	60.0	279	2 T05421	hypothetical prote
45	33	60.0	362	2 B83963	hypothetical prote

ALIGNMENTS

RESULT 1

T19625
hypothetical protein C31H5.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
C:Accession: T19625
R:Kershaw, J.
submitted to the EMBL Data Library, April 1997
A:Reference number: Z19153
A:Accession: T19625
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-446 <WIL>
A:Cross-references: EMBL:Z93778; PIDN:CAB07846.1; GSPDB:GN00019; CESP:C31H5.6
A:Experimental source: clone C31H5
C:Genetics:
A:Gene: CESP:C31H5.6
A:Map position: 1
A:Introns: 49/2; 183/3; 218/3; 255/3; 285/2; 331/3; 360/3
C:Superfamily: Caenorhabditis elegans hypothetical protein W03D8.8

Query Match 70.9%; Score 39; DB 2; Length 446;
Best Local Similarity 87.5%; Pred. No. 9.6;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFA 9
Db 51 RHNYGSHA 58
|||||||

RESULT 2

AF2959
conserved hypothetical protein Atu3276 [Imported] - Agrobacterium tumefaciens (strain
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
C:Accession: AF2959
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McCl
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; PMID:11743193
A:Accession: AF2959
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1052 <KUR>
A:Cross-references: GB:AF008689; PIDN:AAL44092.1; PID:gl7741659; GSPDB:GN00187
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: Atu3276

A:Map position: linear chromosome

Query Match 70.9%; Score 39; DB 2; Length 1052;

Best Local Similarity 77.8%; Pred. No. 22;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAM 10

||||| ||

Db 979 RHNYGDTAM 987

RESULT 3

H98323

hypothetical protein AGR_L3085 [imported] - Agrobacterium tumefaciens (strain C58, Cere

C:Species: Agrobacterium tumefaciens

C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 11-Jan-2002

C:Accession: H98323

R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Ourullo, B.; Goldman,

A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;

Science 294, 2323-2328, 2001

A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum

A:Reference number: A97359; PMID:11743194

A:Accession: H98323

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1341 <KUR>

A:Cross-references: GB:AE007870; PIDN:AAK90114.1; PID:g15160106; GSPDB:GN00170

C:Genetics:

A:Gene: AGR_L3085

A:Map position: linear chromosome

Query Match

Best Local Similarity 70.9%; Score 39; DB 2; Length 1341;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAM 10

||||| ||

Db 1268 RHNYGDTAM 1276

RESULT 4

C81402

probable integral membrane protein Cj0555 [imported] - Campylobacter jejuni (strain NCIC

C:Species: Campylobacter jejuni

C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002

C:Accession: C81402

R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin

C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrell

Nature 403, 665-668, 2000

A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp

A:Reference number: A81250; MUID:20150912; PMID:10688204

A:Accession: C81402

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-430 <PAR>

A:Cross-references: GB:AL139075; GB:AL111168; NID:g6967817; PIDN:CAB75191.1; PID:g696802

A:Experimental source: serotype O2, strain NCIC 11168

C:Genetics:

A:Gene: Cj0555

Query Match

Best Local Similarity 67.3%; Score 37; DB 2; Length 430;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAM 10

||| | |||

Db 22 RHNVGIFAM 30

RESULT 5

I51106

Major Histocompatibility Complex class IIB - ring-necked pheasant (fragment)

C:Species: Phasianus colchicus (ring-necked pheasant)

C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 23-Jul-1999

C:Accession: I51106

R:Wittzell, H.; von Schantz, T.; Zoorob, R.; Auffray, C.

Immunogenetics 39, 395-403, 1994

A:Title: Molecular characterization of three Mhc class II B haplotypes in the ring-ne

A:Reference number: I51103; MUID:94245280; PMID:7910588

A:Accession: I51106

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-82 <WIT>

A:Cross-references: EMBL:X75406; NID:9496926; PIDN:CAA53160.1; PID:g496927

C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match

Best Local Similarity 65.5%; Score 36; DB 2; Length 82;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8

||||| |

Db 75 RHNYGVF 81

RESULT 6

S38688

MHC class II histocompatibility antigen HLA-DR-08 beta chain - northern lesser bushba

C:Species: Galago senegalensis (northern lesser bushbaby)

C:Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 19-May-2000

C:Accession: S38688

R:Figueroa, F.; O'Huigin, C.; Tichy, H.; Klein, J.

submitted to the EMBL Data Library, November 1993

A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduce

A:Reference number: S38676

A:Accession: S38688

A:Molecule type: DNA

A:Residues: 1-89 <FIG>

A:Cross-references: EMBL:Z27158

C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match

Best Local Similarity 65.5%; Score 36; DB 2; Length 89;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8

||||| |

Db 75 RHNYGVF 81

RESULT 7

S38683

MHC class II histocompatibility antigen HLA-DR-03 beta chain - northern lesser bushba

C:Species: Galago senegalensis (northern lesser bushbaby)

C:Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 19-May-2000

C:Accession: S38683

R:Figueroa, F.; O'Huigin, C.; Tichy, H.; Klein, J.

submitted to the EMBL Data Library, November 1993

A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduce

A:Reference number: S38676

A:Accession: S38683

A:Molecule type: DNA

A:Residues: 1-89 <FIG>

A:Cross-references: EMBL:Z27153

C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match

Best Local Similarity 65.5%; Score 36; DB 2; Length 89;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8

||||| |

Db 75 RHNYGVF 81

RESULT 8

S38684
MHC class II histocompatibility antigen HLA-DR-04 beta chain - northern lesser bushbaby
C:Species: Galago senegalensis (northern lesser bushbaby)
C:Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 19-May-2000
C:Accession: S38684
R:Figuerola, F.; O'Huigin, C.; Tichy, H.; Klein, J.
submitted to the EMBL Data Library, November 1993
A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduced from
A:Reference number: S38676
A:Accession: S38684
A:Molecule type: DNA
A:Residues: 1-89 <FIG>
A:Cross-references: EMBL:Z27154
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 65.5%; Score 36; DB 2; Length 89;
Best Local Similarity 85.7%; Pred. No. 7.4;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
|||||
Db 75 RHNYGVF 81

RESULT 9
I47095
MHC class II OVAR-DR-beta-3 - sheep (fragment)
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 15-Oct-1996 #sequence_revision 15-Oct-1996 #text_change 21-Jan-2000
C:Accession: I47095
R:Pabb, S.A.; Maddox, J.F.; Gogolin-Ewens, K.J.; Baker, L.; Wu, M.J.; Brandon, M.R.
Anim. Genet. 24, 249-255, 1993
A:Title: Isolation, characterization and evolution of ovine major histocompatibility complex
A:Reference number: I47075; MUID:94057592; PMID:7902039
A:Accession: I47095
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-225 <FAB>
A:Cross-references: GB:L04790; NID:g458880; PIDN:AAA16562.1; PID:g458881
C:Genetics:
A:Gene: OVAR-DRB3
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology
F:98-163/Domain: immunoglobulin homology <IMM>

Query Match 65.5%; Score 36; DB 2; Length 225;
Best Local Similarity 85.7%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
|||||
Db 68 RHNYGVF 74

RESULT 10
G86742
conserved hypothetical protein yj9f [imported] - Lactococcus lactis subsp. lactis (strain
C:Species: Lactococcus lactis subsp. lactis
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 17-May-2002
C:Accession: G86742
R:Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss
A:Reference number: A86625; MUID:21235186; PMID:11337471
A:Accession: G86742
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-195 <STO>
A:Cross-references: GB:AE005176; PID:g12723879; PIDN:AAK05041.1; GSPDB:GN00146
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: yj9f
C:Superfamily: hypothetical protein b1011

Query Match 63.6%; Score 35; DB 2; Length 195;
Best Local Similarity 62.5%; Pred. No. 25;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSF 8
|||||
Db 103 AKHNGAF 110

RESULT 11
S43771
phosphatidylcholine desaturase (EC 1.3.1.35) - *Synechococcus* sp. (strain PCC 7002)
N:Alternate names: Delta-12 desaturase; fatty acid desaturase (EC 1.14.99.-) (misiden
C:Species: *Synechococcus* sp.
A:Variety: PCC 7002
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-2000
C:Accession: S43771
R:Sakamoto, T.; Wada, H.; Nishida, I.; Ohmori, M.; Murata, N.
Plant Mol. Biol. 24, 643-650, 1994
A:Title: Identification of conserved domains in the Delta-12 desaturases of cyanobact
A:Reference number: S43770; MUID:94207189; PMID:8155883
A:Accession: S43771
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-347 <SAK>
A:Cross-references: GB:D13779; NID:g488510; PIDN:BA02922.1; PID:g488511
C:Superfamily: omega-3 fatty acid desaturase
C:Keywords: oxidoreductase

Query Match 63.6%; Score 35; DB 2; Length 347;
Best Local Similarity 77.8%; Pred. No. 44;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9
|||||
Db 334 AEHNVISFA 342

RESULT 12
S56179
secreted glycoprotein EP4, 47K, precursor - carrot (fragment)
C:Species: *Daucus carota* (carrot)
C:Date: 27-Oct-1995 #sequence_revision 26-Jul-1996 #text_change 21-Jul-2000
C:Accession: S56179; S56180
R:van Engelen, F.A.; de Jong, A.J.; Meijer, E.A.; Kuil, C.W.; Meyboom, J.K.; Dirkse,
Plant Mol. Biol. 27, 901-910, 1995
A:Title: Purification, immunological characterization and cDNA cloning of a 47 kDa gl
A:Reference number: S56179; MUID:95284347; PMID:7766880
A:Accession: S56179
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-383 <VAN>
A:Cross-references: EMBL:L36956; NID:g886222; PIDN:AAA98926.1; PID:g886223
A:Accession: S56180
A:Molecule type: protein
A:Residues: 121-133; 272-276; 281-284 <VAV>
C:Superfamily: myrosinase-associated protein MyAP
C:Keywords: glycoprotein
F:1-15/Domain: signal sequence (fragment) #status predicted <STG>
F:16-383/Product: secreted glycoprotein EP4, 47K #status predicted <MAT>

Query Match 63.6%; Score 35; DB 2; Length 383;
Best Local Similarity 55.6%; Pred. No. 48;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSFAM 10
|||||
Db 305 RYNYGEFSL 313

RESULT 13
D70405
glutamate-tRNA ligase (EC 6.1.1.17) - *Aquifex aeolicus*

C:Species: Aquifex aeolicus
 C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 03-Jun-2002
 C:Accession: D70405
 R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O'V.

Nature 392, 353-358, 1998
 A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
 A:Reference number: A70300; MUID:98196666; PMID:9537320
 A:Accession: D70405
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-473 <AOE>
 A:Cross-References: GB:AE000729; NID:g2983659; PIDN:RAC07230.1; PID:g2983664; GB:AE00065
 A:Experimental source: strain VF5
 C:Genetics:

A:Gene: gltX
 A:Superfamily: glutamate-tRNA ligase; glutamine-tRNA ligase homology
 C:Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis
 F:4-276/Domain: glutamine-tRNA ligase homology <EC1>

Query Match 63.6%; Score 35; DB 2; Length 473;
 Best Local Similarity 60.0%; Pred. No. 60;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARHNYGSFAM 10
 |||||
 Db 31 ARHNGGFVL 40

RESULT 14

S26316
 Ig heavy chain V region - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
 C:Accession: S26316
 R:Stark, S.E.; Caton, A.J.
 J. Exp. Med. 174, 613-624, 1991
 A:Title: Antibodies that are specific for a single amino acid interchange in a protein
 A:Reference number: S26309; MUID:91341421; PMID:1908510
 A:Accession: S26316
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-108 <STA>
 A:Cross-References: EMBL:X59190; NID:g52066; PIDN:CAA41900.1; PID:g1334035
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:2-85/Domain: immunoglobulin homology <IMM>

Query Match 61.8%; Score 34; DB 2; Length 108;
 Best Local Similarity 66.7%; Pred. No. 22;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
 |||||
 Db 84 ARGNYGNYA 92

RESULT 15

S26317
 Ig heavy chain V region - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 21-Jan-2000
 C:Accession: S26317
 R:Stark, S.E.; Caton, A.J.
 J. Exp. Med. 174, 613-624, 1991
 A:Title: Antibodies that are specific for a single amino acid interchange in a protein
 A:Reference number: S26309; MUID:91341421; PMID:1908510
 A:Accession: S26317
 A:Molecule type: mRNA
 A:Residues: 1-110 <STA>
 A:Cross-References: EMBL:X59186
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

F:4-87/Domain: immunoglobulin homology <IMM>

Query Match 61.8%; Score 34; DB 2; Length 110;
 Best Local Similarity 66.7%; Pred. No. 22;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
 |||||
 Db 86 ARGNYGNYA 94

Search completed: November 18, 2002, 17:47:07
 Job time : 4.90196 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:00 : Search time 2.45098 Seconds
(without alignments)
169.223 Million cell updates/sec

Title: US-09-016-061-76
Perfect score: 55
Sequence: 1 ARHNYGSFAM 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	67.3	323	1 CCSA_LOTJA	Q9bbp4 lotus japon
2	35	63.6	473	1 SVE_AQUAE	O67271 aquifex ae
3	34	61.8	275	1 IFZA_PIRAB	Q9v0e4 pyrococcus
4	34	61.8	275	1 IFZA_PIRHO	O58655 pyrococcus
5	34	61.8	284	1 IPYR_PICPA	O13505 pichia past
6	34	61.8	286	1 IPYR_KLULA	P13998 kluyveromyc
7	34	61.8	286	1 IPYR_YEAST	P00817 saccharomyc
8	34	61.8	321	1 CCSA_WAIZE	P46559 zea mays (m
9	34	61.8	321	1 CCSA_ORISA	P12215 oryza sativ
10	34	61.8	322	1 CCSA_WHEAT	P58266 triticum ae
11	34	61.8	323	1 CCSA_SPIOL	Q9m3j1 spinacia ol
12	34	61.8	629	1 KSVK_RAT	Q64725 rattus norv
13	34	61.8	682	1 VGS0_BPML5	Q05262 mycobacteri
14	33	60.0	448	1 NCAP_CVHOC	P33469 human coron
15	33	60.0	470	1 SYE2_RICPR	Q9zct8 rickettsia
16	33	60.0	583	1 NIR_BETVE	P38500 betula verr
17	33	60.0	594	1 NIR_SPIOL	P05314 spinacia ol
18	32	58.2	65	1 CCSA_OENBE	P31565 oenothera b
19	32	58.2	65	1 CCSA_PEA	P31172 pisum sativ
20	32	58.2	196	1 WBBJ_ECOLI	P37750 escherichia
21	32	58.2	197	1 Y61A_METJA	P81310 methanococc
22	32	58.2	198	1 HB2G_HUMAN	P01911 homo sapien
23	32	58.2	266	1 HB2A_HUMAN	P01913 homo sapien
24	32	58.2	266	1 HB2B_HUMAN	P01912 homo sapien
25	32	58.2	266	1 HB2C_HUMAN	P01914 homo sapien
26	32	58.2	266	1 HB2D_CANFA	P18470 canis fami
27	32	58.2	266	1 HB2E_HUMAN	P13759 homo sapien
28	32	58.2	266	1 HB2F_HUMAN	P04229 homo sapien
29	32	58.2	266	1 HB2G_HUMAN	P13758 homo sapien
30	32	58.2	266	1 HB2H_HUMAN	P13760 homo sapien
31	32	58.2	266	1 HB2I_HUMAN	P20039 homo sapien
32	32	58.2	266	1 HB2J_HUMAN	P13761 homo sapien
33	32	58.2	305	1 YN45_DEIRA	Q9rry7 deinococcus

ALIGNMENTS

RESULT 1

ID	CCSA_LOTJA	STANDARD;	PRT;	323 AA.
AC	Q9BBP4;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Cytochrome c biogenesis protein ccsa.			
GN	CCSA.			
OS	Lotus japonicus.			
OG	Chloroplast.			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;			
OC	eurosid 1; Fabales; Fabaceae; Papilionoideae; Lotaeae; Lotus.			
OX	NCBI_TaxID=34305;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Accession MG-20;			
RX	MEDLINE=21082929; PubMed=11214967;			
RA	Kato T., Kaneko T., Sato S., Nakamura Y., Tabata S.;			
RT	*Complete structure of the chloroplast genome of a legume, Lotus japonicus.*;			
RL	DNA Res. 7:323-330(2000).			
CC	- - FUNCTION: REQUIRED DURING CYTOCHROME BIOGENESIS AT THE STEP OF			
CC	HEME ATTACHMENT (BY SIMILARITY).			
CC	- - SIMILARITY: BELONGS TO THE CCMF/CYCK/CCL1/NRFE/CCSA FAMILY.			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
DR	EMBL; AP002983; BAB33244.1; -			
DR	InterPro; IPR002541; CytC_asm.			
DR	Pfam; PF01578; CytC_asm; 1.			
KW	Cytochrome c-type biogenesis; Chloroplast.			
SQ	SEQUENCE 323 AA; 37185 MW; 5A034E3E2829FE35 CRC64;			

Query Match 67.3%; Score 37; DB 1; Length 323;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 HNYGSF 8
| | | | |
Db 315 HNYGSF 320

RESULT 2

ID	SVE_AQUAE	STANDARD;	PRT;	473 AA.
AC	O67271;			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			

DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Glutamyl-tRNA synthetase (EC 6.1.1.17) (Glutamate--tRNA ligase)
DE (GluRS).
GN GLTX OR AQ_1221.
OS Aquifex aeolicus.
OC Bacteria; Aquificae; Aquificae (class); Aquificales; Aquificaceae;
OC Aquifex.
OX NCBI_TaxID=63363;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=VF5;
RC MEDLINE=98196666; PubMed=9537320;
RA Decker G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Sneed M.A., Keller M., Aubay M., Huber R.,
RA Feldman R.A., Olson G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus".
RL Nature 392:353-358(1998).
CC -1- CATALYTIC ACTIVITY: ATP + L-glutamate + tRNA(Glu) = AMP +
CC diphosphate + L-glutamyl-tRNA(Glu).
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
CC -----
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CC -----
CC EMBL: AJ248285; CAB49760.1; -.
CC HSSP: P05055; LSRO.
CC InterPro: IPR003029; S1.
CC Pfam: PF00575; S1; 1.
CC SMART: SM00316; S1; 1.
CC PROSITE: PS0126; S1; 1.
CC Initiation factor; Protein biosynthesis; RNA-binding;
CC Complete proteome.
CC DOMAIN 12 83 S1 MOTIF.
CC SEQUENCE 275 AA; 31912 MW; B2659F3A4987984F CRC64;
CC -----
CC Query Match 61.8%; Score 34; DB 1; Length 275;
CC Best Local Similarity 83.3%; Pred. No. 14;
CC Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
CC -----
CC QY 3 HNYGSF 8
CC |||||
CC Db 23 HNYGAF 28
CC -----
CC RESULT 4
CC IF2A_PYRHO STANDARD; PRT; 275 AA.
CC ID IF2A_PYRHO STANDARD; PRT; 275 AA.
CC AC 058655;
CC DT 15-DEC-1998 (Rel. 37, Created)
CC DT 15-DEC-1998 (Rel. 37, Last sequence update)
CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
CC DE Probable translation initiation factor 2 alpha subunit (eIF-2-alpha).
CC GN EIF2A OR PH0961.
CC OS Pyrococcus horikoshii.
CC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
CC Pyrococcus.
CC NCBI_TaxID=53953;
CC RN [1]
CC RN SEQUENCE FROM N.A.
CC RC STRAIN=OT3;
CC RC MEDLINE=98344137; PubMed=9679194;
CC RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
CC Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Negai Y.,
CC Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
CC Funahashi T., Tanaka T., Kudo Y., Yamazaki J., Kishida N., Oguchi A.,
CC Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
CC Masuchi Y., Shizuya H., Kikuchi H.;
CC "Complete sequence and gene organization of the genome of a hyper-
CC thermophilic archaeobacterium, Pyrococcus horikoshii OT3".
CC RNA Res. 5:55-76(1998).
CC -1- FUNCTION: EIF-2 FUNCTIONS IN THE EARLY STEPS OF PROTEIN SYNTHESIS
CC BY FORMING A TERNARY COMPLEX WITH GTP AND INITIATOR TRNA
CC (BY SIMILARITY).
CC -1- SUBUNIT: HETEROTRIMER COMPOSED OF AN ALPHA, A BETA, AND A GAMMA
CC CHAIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE EIF-2-ALPHA FAMILY.
CC -1- SIMILARITY: CONTAINS 1 S1 MOTIF DOMAIN.
CC -----
CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Glutamyl-tRNA synthetase (EC 6.1.1.17) (Glutamate--tRNA ligase)
DE (GluRS).
GN GLTX OR AQ_1221.
OS Aquifex aeolicus.
OC Bacteria; Aquificae; Aquificae (class); Aquificales; Aquificaceae;
OC Aquifex.
OX NCBI_TaxID=63363;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=VF5;
RC MEDLINE=98196666; PubMed=9537320;
RA Decker G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Sneed M.A., Keller M., Aubay M., Huber R.,
RA Feldman R.A., Olson G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus".
RL Nature 392:353-358(1998).
CC -1- CATALYTIC ACTIVITY: ATP + L-glutamate + tRNA(Glu) = AMP +
CC diphosphate + L-glutamyl-tRNA(Glu).
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
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CC -----
CC EMBL: AE000729; AAC07230.1; -.
CC HSSP: P27000; ICLN.
CC InterPro: IPR004527; GltX_bact.
CC InterPro: IPR000924; Glu-tRNA-synt_1c.
CC InterPro: IPR001412; tRNA-synt_1.
CC Pfam: PF00749; tRNA-synt_1c; 1.
CC PRINTS: PR00987; TRNASYNTHGLU.
CC TIGRFAMS: TIGR00464; gltX_bact; 1.
CC PROSITE: PS00178; AA_tRNA_Ligase_I; 1.
CC Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
CC Complete proteome.
CC SITE 10 20 "HIGH" REGION.
CC SITE 242 245 "KMSKS" REGION.
CC BINDING 245 245 ATP (BY SIMILARITY).
CC SEQUENCE 473 AA; 55121 MW; 5CB4D1590973E07A CRC64;
CC -----
CC Query Match 63.6%; Score 35; DB 1; Length 473;
CC Best Local Similarity 60.0%; Pred. No. 16;
CC Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
CC -----
CC QY 1 ARHNYGSFAM 10
CC |||||
CC Db 31 ARHNNGGFVL 40
CC -----
CC RESULT 3
CC IF2A_PYRAB STANDARD; PRT; 275 AA.
CC ID IF2A_PYRAB STANDARD; PRT; 275 AA.
CC AC Q9V084;
CC DT 16-OCT-2001 (Rel. 40, Created)
CC DT 16-OCT-2001 (Rel. 40, Last sequence update)
CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
CC DE Probable translation initiation factor 2 alpha subunit (eIF-2-alpha).
CC GN EIF2A OR PAB0568.
CC OS Pyrococcus abyssi.
CC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
CC Pyrococcus.
CC NCBI_TaxID=29292;
CC RN [1]
CC RN SEQUENCE FROM N.A.
CC RC STRAIN=GE5/ Orsav.
CC -1- SIMILARITY: BELONGS TO THE EIF-2-ALPHA FAMILY.
CC -1- SIMILARITY: CONTAINS 1 S1 MOTIF DOMAIN.

DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Glutamyl-tRNA synthetase (EC 6.1.1.17) (Glutamate--tRNA ligase)
DE (GluRS).
GN GLTX OR AQ_1221.
OS Aquifex aeolicus.
OC Bacteria; Aquificae; Aquificae (class); Aquificales; Aquificaceae;
OC Aquifex.
OX NCBI_TaxID=63363;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=VF5;
RC MEDLINE=98196666; PubMed=9537320;
RA Decker G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Sneed M.A., Keller M., Aubay M., Huber R.,
RA Feldman R.A., Olson G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus".
RL Nature 392:353-358(1998).
CC -1- CATALYTIC ACTIVITY: ATP + L-glutamate + tRNA(Glu) = AMP +
CC diphosphate + L-glutamyl-tRNA(Glu).
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
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CC -----
CC EMBL: AJ248285; CAB49760.1; -.
CC HSSP: P05055; LSRO.
CC InterPro: IPR003029; S1.
CC Pfam: PF00575; S1; 1.
CC SMART: SM00316; S1; 1.
CC PROSITE: PS0126; S1; 1.
CC Initiation factor; Protein biosynthesis; RNA-binding;
CC Complete proteome.
CC DOMAIN 12 83 S1 MOTIF.
CC SEQUENCE 275 AA; 31912 MW; B2659F3A4987984F CRC64;
CC -----
CC Query Match 61.8%; Score 34; DB 1; Length 275;
CC Best Local Similarity 83.3%; Pred. No. 14;
CC Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
CC -----
CC QY 3 HNYGSF 8
CC |||||
CC Db 23 HNYGAF 28
CC -----
CC RESULT 4
CC IF2A_PYRHO STANDARD; PRT; 275 AA.
CC ID IF2A_PYRHO STANDARD; PRT; 275 AA.
CC AC 058655;
CC DT 15-DEC-1998 (Rel. 37, Created)
CC DT 15-DEC-1998 (Rel. 37, Last sequence update)
CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
CC DE Probable translation initiation factor 2 alpha subunit (eIF-2-alpha).
CC GN EIF2A OR PH0961.
CC OS Pyrococcus horikoshii.
CC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
CC Pyrococcus
CC NCBI_TaxID=53953;
CC RN [1]
CC RN SEQUENCE FROM N.A.
CC RC STRAIN=OT3;
CC RC MEDLINE=98344137; PubMed=9679194;
CC RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
CC Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Negai Y.,
CC Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
CC Funahashi T., Tanaka T., Kudo Y., Yamazaki J., Kishida N., Oguchi A.,
CC Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
CC Masuchi Y., Shizuya H., Kikuchi H.;
CC "Complete sequence and gene organization of the genome of a hyper-
CC thermophilic archaeobacterium, Pyrococcus horikoshii OT3".
CC RNA Res. 5:55-76(1998).
CC -1- FUNCTION: EIF-2 FUNCTIONS IN THE EARLY STEPS OF PROTEIN SYNTHESIS
CC BY FORMING A TERNARY COMPLEX WITH GTP AND INITIATOR TRNA
CC (BY SIMILARITY).
CC -1- SUBUNIT: HETEROTRIMER COMPOSED OF AN ALPHA, A BETA, AND A GAMMA
CC CHAIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE EIF-2-ALPHA FAMILY.
CC -1- SIMILARITY: CONTAINS 1 S1 MOTIF DOMAIN.
CC -----
CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Glutamyl-tRNA synthetase (EC 6.1.1.17) (Glutamate--tRNA ligase)
DE (GluRS).
GN GLTX OR AQ_1221.
OS Aquifex aeolicus.
OC Bacteria; Aquificae; Aquificae (class); Aquificales; Aquificaceae;
OC Aquifex.
OX NCBI_TaxID=63363;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=VF5;
RC MEDLINE=98196666; PubMed=9537320;
RA Decker G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Sneed M.A., Keller M., Aubay M., Huber R.,
RA Feldman R.A., Olson G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus".
RL Nature 392:353-358(1998).
CC -1- CATALYTIC ACTIVITY: ATP + L-glutamate + tRNA(Glu) = AMP +
CC diphosphate + L-glutamyl-tRNA(Glu).
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
CC -----
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CC -----
CC EMBL: AE000729; AAC07230.1; -.
CC HSSP: P27000; ICLN.
CC InterPro: IPR004527; GltX_bact.
CC InterPro: IPR000924; Glu-tRNA-synt_1c.
CC InterPro: IPR001412; tRNA-synt_1.
CC Pfam: PF00749; tRNA-synt_1c; 1.
CC PRINTS: PR00987; TRNASYNTHGLU.
CC TIGRFAMS: TIGR00464; gltx_bact; 1.
CC PROSITE: PS00178; AA_tRNA_Ligase_I; 1.
CC Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
CC Complete proteome.
CC SITE 10 20 "HIGH" REGION.
CC FT SITE 242 245 "KMSKS" REGION.
CC FT BINDING 245 245 ATP (BY SIMILARITY).
CC SEQUENCE 473 AA; 55121 MW; 5CB4D1590973E07A CRC64;
CC -----
CC Query Match 63.6%; Score 35; DB 1; Length 473;
CC Best Local Similarity 60.0%; Pred. No. 16;
CC Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
CC -----
CC QY 1 ARHNYGSFAM 10
CC |||||
CC Db 31 ARHNNGGFVL 40
CC -----
CC RESULT 3
CC IF2A_PYRAB STANDARD; PRT; 275 AA.
CC ID IF2A_PYRAB STANDARD; PRT; 275 AA.
CC AC Q9V084;
CC DT 16-OCT-2001 (Rel. 40, Created)
CC DT 16-OCT-2001 (Rel. 40, Last sequence update)
CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
CC DE Probable translation initiation factor 2 alpha subunit (eIF-2-alpha).
CC GN EIF2A OR PAB0568.
CC OS Pyrococcus abyssi.
CC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
CC Pyrococcus.
CC NCBI_TaxID=29292;
CC RN [1]
CC RN SEQUENCE FROM N.A.
CC RC STRAIN=GE5/ Orsav.
CC SEQUENCE FROM N.A.
CC -1- SIMILARITY: BELONGS TO THE EIF-2-ALPHA FAMILY.
CC -1- SIMILARITY: CONTAINS 1 S1 MOTIF DOMAIN.

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 CC -----
 DR EMBL; AP000004; BAA30058.1; -;
 DR HSSP; P05055; ISRO.
 DR InterPro; IPR003029; S1.
 DR Pfam; PF00575; S1; 1.
 DR SMART; SM00316; S1; 1.
 DR PROSITE; PS50126; S1; 1.
 KW Initiation factor; Protein biosynthesis; RNA-binding;
 KW Complete proteome.
 FT DOMAIN 12 83 S1 MOTIF.
 SQ SEQUENCE 275 AA; 31980 MW; 6AAAD15F10FFB436 CRC64;

 Query Match 61.8%; Score 34; DB 1; Length 275;
 Best Local Similarity 83.3%; Pred. No. 14;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

 QY 3 HNYGSF 8
 Db 23 HNYGAF 28

 RESULT 5
 IPYR_PICPA
 ID IPYR_PICPA STANDARD; PRT; 284 AA.
 AC O13505;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Inorganic pyrophosphatase (EC 3.6.1.1) (Pyrophosphate phospho-
 DE hydrolase) (Pase).
 GN IPPI.
 OS Pichia pastoris (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Pichia.
 OX NCBI_TaxID=4922;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL Y-11430;
 RX MEDLINE=99034033; PubMed=9818724;
 RA Cosano I.C., Alvarez P., Molina M., Nombela C.;
 RT "Cloning and sequence analysis of the Pichia pastoris TRP1, IPPI and
 RT HIS3 genes.";
 RL Yeast 14:861-867(1998).
 CC -!- CATALYTIC ACTIVITY: Diphosphate + H(2)O = 2 phosphate.
 CC -!- COFACTOR: REQUIRES THE PRESENCE OF DIVALENT METAL CATION.
 CC MAGNESIUM CONFERS THE HIGHEST ACTIVITY.
 CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: BELONGS TO THE PPASE FAMILY.

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 CC -----
 DR EMBL; AJ001000; CAA04453.1; -;
 DR HSSP; P00817; IWGI.
 DR InterPro; IPR001596; Pyrophosphatase.
 DR Pfam; PF00719; Pyrophosphatase; 1.
 DR PROSITE; PS00387; PPASE; 1.
 KW Hydrolase; Magnesium.
 FT INIT_MET 0 0 BY SIMILARITY.
 SQ SEQUENCE 286 AA; 32034 MW; 11647F4ABD916A2F CRC64;

 Query Match 61.8%; Score 34; DB 1; Length 286;
 Best Local Similarity 83.3%; Pred. No. 15;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

FT ACT_SITE 56 56 PROBABLE.
 FT BINDING 78 78 INORGANIC PYROPHOSPHATE (BY SIMILARITY).
 SQ SEQUENCE 284 AA; 31937 MW; 3DAD27970D7775D6 CRC64;

 Query Match 61.8%; Score 34; DB 1; Length 284;
 Best Local Similarity 83.3%; Pred. No. 15;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

 QY 3 HNYGSF 8
 Db 91 HNYGAF 96

 RESULT 6
 IPYR_KLULA
 ID IPYR_KLULA STANDARD; PRT; 286 AA.
 AC P13998;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 01-OCT-1994 (Rel. 30, Last annotation update)
 DE Inorganic pyrophosphatase (EC 3.6.1.1) (Pyrophosphate phospho-
 DE hydrolase) (PPase).
 GN IPPI OR IPP.
 OS Kluyveromyces lactis (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
 OX NCBI_TaxID=28985;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89189093; PubMed=2538971;
 RA Stark M.J.R., Milner J.S.;
 RT "Cloning and analysis of the Kluyveromyces lactis TRP1 gene: a
 RT chromosomal locus flanked by genes encoding inorganic pyrophosphatase
 RT and histone H3.";
 RL Yeast 5:35-50(1989).
 RN [2]
 RP SIMILARITY TO E. COLI AND YEAST PPASES.
 RX MEDLINE=90254161; PubMed=2160278;
 RA Lahti R., Kolakowski L.F. Jr., Heinonen J., Vihinen M., Pohjanoksa K.,
 RA Cooperman B.S.;
 RT "Conservation of functional residues between yeast and E. coli
 RT inorganic pyrophosphatases.";
 RL Biochim. Biophys. Acta 1038:338-345(1990).
 CC -!- CATALYTIC ACTIVITY: Diphosphate + H(2)O = 2 phosphate.
 CC -!- COFACTOR: REQUIRES THE PRESENCE OF DIVALENT METAL CATION.
 CC MAGNESIUM CONFERS THE HIGHEST ACTIVITY.
 CC -!- SUBUNIT: HOMODIMER.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: BELONGS TO THE PPASE FAMILY.

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 CC -----
 DR EMBL; X14230; CAA32446.1; -;
 DR PIR; S07894; PWKL.
 DR HSSP; P00817; IWGI.
 DR InterPro; IPR001596; Pyrophosphatase.
 DR Pfam; PF00719; Pyrophosphatase; 1.
 DR PROSITE; PS00387; PPASE; 1.
 KW Hydrolase; Magnesium.
 FT INIT_MET 0 0 BY SIMILARITY.
 FT ACT_SITE 56 56 PROBABLE.
 FT BINDING 78 78 INORGANIC PYROPHOSPHATE (BY SIMILARITY).
 SQ SEQUENCE 286 AA; 32034 MW; 11647F4ABD916A2F CRC64;

 Query Match 61.8%; Score 34; DB 1; Length 286;
 Best Local Similarity 83.3%; Pred. No. 15;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
ID 1111:1
Db 91 HNYGAF 96

RESULT 7

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IPYR_YEAST
AC IPYR_YEAST STANDARD; PRT; 286 AA.
ID P00817;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Inorganic pyrophosphatase (EC 3.6.1.1) (Pyrophosphate phospho-
DE hydrolase) (Prase).
OS IPPI OR PPA1 OR PPA OR YBR011C OR YBR0202.
GN Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RN SEQUENCE FROM N.A.
RP STRAIN=X2180;
RX MEDLINE=89083474; PubMed=2849749;
RA Kolakowski L.F. Jr., Schloesser M., Cooperman B.S.;
RT "Cloning, molecular characterization and chromosome localization of
RT the inorganic pyrophosphatase (PPA) gene from S. cerevisiae.";
RL Nucleic Acids Res. 16:10441-10452(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c;
RA Entian K.-D., Koetter P., Rose M., Li Z., Thermann R., Brendel M.,
RA Baur A., Boles E., Miosga T., Schaaff-Gerstenschlaeger I.,
RA Zimmermann F.K.;
RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE.
RX MEDLINE=78087552; PubMed=340461;
RA Cohen S.A., Sterner R., Keim P.S., Heinrikson R.L.;
RT "Covalent structural analysis of yeast inorganic pyrophosphatase.";
RL J. Biol. Chem. 253:889-897(1978).
RN [4]
RP SEQUENCE OF 25-35 AND 239-251.
RC STRAIN=S288c;
RX MEDLINE=95203288; PubMed=7895733;
RA Gartsels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender B.,
RA Volpe T., Warner J.R., McLaughlin C.S.;
RT "Protein identifications for a Saccharomyces cerevisiae protein
RT database.";
RL Electrophoresis 15:1466-1486(1994).
RN [5]
RP SEQUENCE OF 239-249.
RC STRAIN=ATCC 38531 / Y41;
RX MEDLINE=97089742; PubMed=8935650;
RA Norbeck J., Blomberg A.;
RT "Protein expression during exponential growth in 0.7 M NaCl medium of
RT Saccharomyces cerevisiae.";
RL FEMS Microbiol. Lett. 137:1-8(1996).
RN [6]
RP ACTIVE SITE.
RX MEDLINE=80109718; PubMed=6101539;
RA Bond M.W., Chiu N.Y., Cooperman B.S.;
RT "Identification of an arginine important for enzymatic activity
RT within the covalent structure of yeast inorganic pyrophosphatase.";
RL Biochemistry 19:94-102(1980).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
RA Arutunian E.G., Terzian S.S., Voronova A.A., Kuranova I.P.,
RA Smirnova E.A., Vainstein B.K., Hohne W.E., Hansen G.;
RT "X-ray diffraction study of inorganic pyrophosphatase from baker's
RT yeast at the 3-A resolution.";
RL Dokl. Akad. Nauk SSSR 258:1481-1492(1981).
RN [8]

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RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE=97148342; PubMed=894974;
RA Heikinheimo P., Lehtonen J., Baykov A., Lahti R., Cooperman B.S.,
RA Goldman A.;
RT "The structural basis for pyrophosphatase catalysis.";
RL Structure 4:1491-1508(1996).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
RA Swaminathan K., Cooperman B.S., Lahti R., Voet D.;
RL Submitted (DEC-1997) to the PDB data bank.
RN [10]
RP X-RAY CRYSTALLOGRAPHY (2.15 ANGSTROMS) OF MUTANTS LYS-78 AND LYS-117.
RX MEDLINE=99036888; PubMed=9878371;
RA Tuomänen V., Heikinheimo P., Kajander T., Torkkel T., Hyytiä T.,
RA Kapyla J., Lahti R., Cooperman B.S., Goldman A.;
RT "The R78K and D117E active-site variants of Saccharomyces cerevisiae
RT soluble inorganic pyrophosphatase: structural studies and mechanistic
RT implications.";
RL J. Mol. Biol. 284:1565-1580(1998).
RN [11]
RN SIMILARITY TO E.COLI AND K.LACTIS PPASES.
RP MEDLINE=90254161; PubMed=2160278;
RX Lahti R., Kolakowski L.F. Jr., Heinonen J., Vihinen M., Pohjanoksa K.,
RA Cooperman B.S.;
RT "Conservation of functional residues between yeast and E. coli
RT inorganic pyrophosphatases.";
RL Biochim. Biophys. Acta 1038:338-345(1990).
CC -1- CATALYTIC ACTIVITY: Diphosphate + H(2)O = 2 phosphate.
CC -1- COFACTOR: REQUIRES THE PRESENCE OF DIVALENT METAL CATION.
CC MAGNESIUM CONFERS THE HIGHEST ACTIVITY. IT BINDS UP TO 4 DIVALENT
CC CATIONS PER SUBUNIT, WITH THREE REQUIRED FOR ACTIVITY.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE PPASE FAMILY.
CC -----
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CC -----
CC EMBL; X13253; CAA31629.1; -.
CC EMBL; Z35880; CAA84949.1; -.
CC PIR; S45864; PWBV.
CC PDB; 1PYP; 15-OCT-91.
CC PDB; 1YPP; 07-DEC-96.
CC PDB; 1WGI; 19-NOV-97.
CC PDB; 1WGI; 19-NOV-97.
CC PDB; 1H0J; 08-APR-98.
CC PDB; 1H0J; 08-APR-98.
CC PDB; 117E; 23-DEC-98.
CC PDB; 8PRK; 23-DEC-98.
CC PDB; 117E; 23-DEC-98.
CC SWISS-2DPAGE; P00817; YEAST.
CC COMPUYEAST-2DPAGE; P00817; -.
CC SGD; S0000215; IPPI.
CC InterPro; IPR001596; Pyrophosphatase.
CC Pfam; PF00719; Pyrophosphatase; 1.
CC PROSITE; PS00387; PPASE; 1.
CC KEGG; Hydrolyase; Magnesium; 3D-structure.
CC INIT_MET 0 0
CC ACT_SITE 56 56 PROBABLE.
CC BINDING 78 78 INORGANIC PYROPHOSPHATE.
CC CONFLICT 40 40 N -> D (IN REF. 3).
CC CONFLICT 71 71 D -> N (IN REF. 3).
CC CONFLICT 74 74 MISSING (IN REF. 3).
CC CONFLICT 123 123 E -> Q (IN REF. 3).
CC CONFLICT 136 136 Q -> E (IN REF. 3).
CC CONFLICT 186 186 N -> D (IN REF. 3).
CC CONFLICT 224 224 D -> N (IN REF. 3).
CC CONFLICT 266 266 L -> P (IN REF. 2).
CC STRAND 4 7

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FT STRAND 16 20
FT STRAND 25 25
FT TURN 28 30
FT TURN 38 41
FT STRAND 45 45
FT STRAND 55 55
FT STRAND 79 79
FT TURN 97 98
FT TURN 111 112
FT STRAND 121 123
FT TURN 131 132
FT STRAND 135 135
FT STRAND 138 146
FT STRAND 151 158
FT TURN 160 161
FT TURN 165 167
FT TURN 172 175
FT TURN 176 177
FT TURN 179 180
FT TURN 182 197
FT STRAND 203 203
FT TURN 205 207
FT STRAND 210 210
FT TURN 212 230
FT TURN 231 231
FT TURN 245 246
FT TURN 248 249
FT TURN 251 252
FT TURN 255 260
FT TURN 274 275
SQ SEQUENCE 286 AA; F29390260B60C8B2 CRC64;

Query Match 61.8%; Score 34; DB 1; Length 286;
Best Local Similarity 83.3%; Pred. No. 15;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
DB 91 HNYGAF 96

RESULT 8
CCSA_MAIZE STANDARD; PRT; 321 AA.
AC P46659;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Cytochrome c biogenesis protein ccsa.
GN CCSA.
OS Zea mays (Maize).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95395841; PubMed=7666415;
RA Maier R.M., Neckermann K., Igloi G.L., Koessel H.;
RT "Complete sequence of the maize chloroplast genome: gene content,
RT hotspots of divergence and fine tuning of genetic information by
RT transcript editing.";
RL J. Mol. Biol. 251:614-628(1995).
CC -!- FUNCTION: REQUIRED DURING CYTOCHROME BIOGENESIS AT THE STEP OF
CC HEME ATTACHMENT (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CCMP/CYCK/CCL1/NRFE/CCSA FAMILY.
CC -----
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CC -----
DR EMBL; X86563; CAA60348.1; -
DR PIR; JQ0288; JQ0288.
DR InterPro; IPR002541; CytC_asm.
DR Pfam; PF01578; CytC_asm; 1.
KW Cytochrome c-type biogenesis; Chloroplast.
SQ SEQUENCE 321 AA; 36093 MW; D959FE24A619B650 CRC64;

Query Match 61.8%; Score 34; DB 1; Length 321;
Best Local Similarity 62.5%; Pred. No. 17;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFAM 10
DB 311 HSYGSFTL 318

RESULT 9
CCSA_ORYSA STANDARD; PRT; 321 AA.
AC P12215;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cytochrome c biogenesis protein ccsa.
GN CCSA.
OS Oryza sativa (Rice).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=cv. Nipponbare;
RX MEDLINE=89364698; PubMed=2770692;
RA Hiratsuka J., Shimada H., Whittier R., Ishibashi T., Sakamoto M.,
RA Mori M., Kondo C., Honji Y., Sun C.-R., Meng B.-Y., Li Y.-Q.,
RA Kanno A., Nishizawa Y., Hirai A., Shinozaki K., Sugiyura M.;
RT "The complete sequence of the rice (Oryza sativa) chloroplast genome:
RT intermolecular recombination between distinct trna genes accounts for
RT a major plastid DNA inversion during the evolution of the cereals.";
RL Mol. Gen. Genet. 217:185-194(1989).
CC -!- FUNCTION: REQUIRED DURING CYTOCHROME BIOGENESIS AT THE STEP OF
CC HEME ATTACHMENT (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CCMP/CYCK/CCL1/NRFE/CCSA FAMILY.
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CC -----
DR EMBL; X15901; CAA33952.1; -
DR PIR; JQ0288; JQ0288.
DR InterPro; IPR002541; CytC_asm.
DR Pfam; PF01578; CytC_asm; 1.
KW Cytochrome c-type biogenesis; Chloroplast.
SQ SEQUENCE 321 AA; 36702 MW; D959FE24A619B650 CRC64;

Query Match 61.8%; Score 34; DB 1; Length 321;
Best Local Similarity 62.5%; Pred. No. 17;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFAM 10
DB 312 HSYGSFTL 319
```

```
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CC -----
DR EMBL; X86563; CAA60348.1; -
DR MaizDB; 118255; -
DR InterPro; IPR002541; CytC_asm.
DR Pfam; PF01578; CytC_asm; 1.
KW Cytochrome c-type biogenesis; Chloroplast.
SQ SEQUENCE 321 AA; 36093 MW; AF981BA461A5D1B CRC64;
```

```
Query Match 61.8%; Score 34; DB 1; Length 321;
Best Local Similarity 62.5%; Pred. No. 17;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 3 HNYGSFAM 10
DB 311 HSYGSFTL 318
```

```
RESULT 9
CCSA_ORYSA STANDARD; PRT; 321 AA.
AC P12215;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cytochrome c biogenesis protein ccsa.
GN CCSA.
OS Oryza sativa (Rice).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=cv. Nipponbare;
RX MEDLINE=89364698; PubMed=2770692;
RA Hiratsuka J., Shimada H., Whittier R., Ishibashi T., Sakamoto M.,
RA Mori M., Kondo C., Honji Y., Sun C.-R., Meng B.-Y., Li Y.-Q.,
RA Kanno A., Nishizawa Y., Hirai A., Shinozaki K., Sugiyura M.;
RT "The complete sequence of the rice (Oryza sativa) chloroplast genome:
RT intermolecular recombination between distinct trna genes accounts for
RT a major plastid DNA inversion during the evolution of the cereals.";
RL Mol. Gen. Genet. 217:185-194(1989).
```

```
CC -!- FUNCTION: REQUIRED DURING CYTOCHROME BIOGENESIS AT THE STEP OF
CC HEME ATTACHMENT (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CCMP/CYCK/CCL1/NRFE/CCSA FAMILY.
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CC -----
DR EMBL; X15901; CAA33952.1; -
DR PIR; JQ0288; JQ0288.
DR InterPro; IPR002541; CytC_asm.
DR Pfam; PF01578; CytC_asm; 1.
KW Cytochrome c-type biogenesis; Chloroplast.
SQ SEQUENCE 321 AA; 36702 MW; D959FE24A619B650 CRC64;
```

```
Query Match 61.8%; Score 34; DB 1; Length 321;
Best Local Similarity 62.5%; Pred. No. 17;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 3 HNYGSFAM 10
DB 312 HSYGSFTL 319
```

```
RESULT 8
CCSA_MAIZE STANDARD; PRT; 321 AA.
AC P46659;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Cytochrome c biogenesis protein ccsa.
GN CCSA.
OS Zea mays (Maize).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95395841; PubMed=7666415;
RA Maier R.M., Neckermann K., Igloi G.L., Koessel H.;
RT "Complete sequence of the maize chloroplast genome: gene content,
RT hotspots of divergence and fine tuning of genetic information by
RT transcript editing.";
RL J. Mol. Biol. 251:614-628(1995).
```

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CC -!- FUNCTION: REQUIRED DURING CYTOCHROME BIOGENESIS AT THE STEP OF
CC HEME ATTACHMENT (BY SIMILARITY).
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CC -----
DR EMBL; X86563; CAA60348.1; -
DR PIR; JQ0288; JQ0288.
DR InterPro; IPR002541; CytC_asm.
DR Pfam; PF01578; CytC_asm; 1.
KW Cytochrome c-type biogenesis; Chloroplast.
SQ SEQUENCE 321 AA; 36093 MW; D959FE24A619B650 CRC64;
```

```
Query Match 61.8%; Score 34; DB 1; Length 321;
Best Local Similarity 62.5%; Pred. No. 17;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 3 HNYGSFAM 10
DB 312 HSYGSFTL 319
```

```
Query Match 61.8%; Score 34; DB 1; Length 321;
Best Local Similarity 62.5%; Pred. No. 17;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 3 HNYGSFAM 10
DB 312 HSYGSFTL 319
```

```
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```

```
RESULT 10
CCSA_WHEAT
ID CCSA_WHEAT STANDARD; PRT; 322 AA.
AC P58266;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cytochrome c biogenesis protein ccsa.
GN CCSA.
OS Triticum aestivum (Wheat).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Chinese Spring;
RA Ogihara Y., Isono K., Kojima T., Endo A., Hanaoka M., Shiina T.,
RA Terachi T., Utsugi S., Murata M., Mori N., Takumi S., Ikeo K.,
RA Gojobori T., Murai R., Murai K., Matsuoka Y., Ohnishi Y., Tajiri H.,
RA Tsunewaki K.;
RT "Chinese spring wheat (Triticum aestivum L.) chloroplast genome:
RT complete sequence and contig clones.";
RT Plant Mol. Biol. Rep. 18:243-253(2000).
CC -!- FUNCTION: REQUIRED DURING CYTOCHROME BIOGENESIS AT THE STEP OF
CC HEME ATTACHMENT (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CCMF/CYCK/CCL1/NRFE/CCSA FAMILY.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AB042240; BAB47084.1; -.
DR InterPro; IPR002541; CytC_asm.
DR Pfam; PF01578; CytC_asm; 1.
KW Cytochrome c-type biogenesis; Chloroplast.
SQ SEQUENCE 322 AA; 36456 MW; F53F64214FC544D9 CRC64;

Query Match 61.8%; Score 34; DB 1; Length 322;
Best Local Similarity 62.5%; Pred. No. 17;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFAM 10
DB 312 HSYGSFTL 319

RESULT 11
CCSA_SPTOL
ID CCSA_SPTOL STANDARD; PRT; 323 AA.
AC Q9M3J1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cytochrome c biogenesis protein ccsa.
GN CCSA.
OS Spinacia oleracea (Spinach).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Geant d'hiver, and cv. Monatol;
RX MEDLINE=21187424; PubMed=11292076;
RA Schmitz-Linneberger C., Maier R.M., Alcaraz J.-P., Cottet A.,
RA Herrmann R.G., Mache R.;
```

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RT "The plastid chromosome of spinach (Spinacia oleracea): complete
RT nucleotide sequence and gene organization.";
RL Plant Mol. Biol. 45:307-315(2001).
CC -!- FUNCTION: REQUIRED DURING CYTOCHROME BIOGENESIS AT THE STEP OF
CC HEME ATTACHMENT (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CCMF/CYCK/CCL1/NRFE/CCSA FAMILY.
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CC -----
DR EMBL; AJ400848; CAB88783.1; -.
DR InterPro; IPR002541; CytC_asm.
DR Pfam; PF01578; CytC_asm; 1.
KW Cytochrome c-type biogenesis; Chloroplast.
SQ SEQUENCE 323 AA; 36994 MW; 55D28A1797D4A9F3 CRC64;

Query Match 61.8%; Score 34; DB 1; Length 323;
Best Local Similarity 62.5%; Pred. No. 17;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFAM 10
DB 313 HSYGSFTL 320

RESULT 12
KSYK_RAT
ID KSYK_RAT STANDARD; PRT; 629 AA.
AC Q64725;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tyrosine-protein kinase SYK (EC 2.7.1.112) (Spleen tyrosine kinase).
GN SYK.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95279402; PubMed=7759516;
RA Rowley R.B., Bolen J.B., Fargnoli J.;
RT "Molecular cloning of rodent p72syk. Evidence of alternative mRNA
RT splicing.";
RL J. Biol. Chem. 270:12659-12664(1995).
CC -!- FUNCTION: MAY PARTICIPATE IN SIGNALING PATHWAYS. PLAYS A ROLE IN
CC LYMPHOCYTE ACTIVATION.
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; SYKA AND SYKB (SHOWN HERE);
CC ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -!- PTM: AUTOPHOSPHORYLATED (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SYK/ZAP-
CC 70 SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 2 SH2 DOMAINS.
CC -----
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CC -----
DR EMBL; U21684; AAA75167.1; -.
DR EMBL; U21683; AAA75166.1; -.
DR HSSP; P43405; 1A81.
DR InterPro; IPR000719; Euk_pkinase.
```

DR InterPro: IPR000980; SH2.
DR InterPro: IPR001245; Tyr_kinase.
DR Pfam: PF00017; SH2_2
DR Pfam: PF00069; pkinase; 1.
DR PRINTS: PR00401; SH2DOMAIN.
DR ProDom: PD000001; Euk_pkinase; 1.
DR ProDom: PD000093; SH2; 2.
DR SMART: SM00252; SH2; 2.
DR SMART: SM00219; TyrKC; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00001; SH2; 2.
KW Transferrase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
KW SH2 domain; Repeat; Alternative splicing.
FT DOMAIN 14 106
FT DOMAIN 167 258 SH2 1.
FT DOMAIN 365 625 SH2 2.
FT NP_BIND 371 379 ATP (BY SIMILARITY).
FT BINDING 396 396 ATP (BY SIMILARITY).
FT ACT_SITE 488 488 BY SIMILARITY.
FT MOD_RES 519 519 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT VARSPPLIC 277 299 MISSING (IN ISOFORM SYKA).
SQ SEQUENCE 629 AA; 81169A643EC6A6FE CRC64;

Query Match 61.8%; Score 34; DB 1; Length 629;
Best Local Similarity 70.0%; Pred. No. 34;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSFAM 10
II I I I I I I
DB 195 ARDNGSFAL 204

RESULT 13
VG50_BPML5 STANDARD; PRT; 682 AA.
AC Q05282; (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Putative adenosylcobalamin-dependent ribonucleotide reductase
DE (EC 1.17.4.2) (GP50).
GN 50.
OS Mycobacteriophage L5.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
OC L5-like viruses.
OX NCBI_TaxID=31757;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93211282; PubMed=8459766;
RA Hatfull G.F., Sarkis G.J.;
RT "DNA sequence, structure and gene expression of mycobacteriophage L5:
a phage system for mycobacterial genetics.";
RL Mol. Microbiol. 7:395-403(1993).
CC -!- CATALYTIC ACTIVITY: 2'-deoxyribonucleoside triphosphate + oxidized
CC thioredoxin + H(2)O = ribonucleoside triphosphate + reduced
CC thioredoxin.
CC -----
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CC -----
CC EMBL: Z18946; CAA79426.1; -.
DR PIR: S30995; S30995.
DR InterPro: IPR001230; Prenyl_site.
DR InterPro: IPR000788; Ribonucleo_red.
DR Pfam: PF02867; ribonuc_red_lgc; 1.
KW Oxidoreductase; DNA replication.

SQ SEQUENCE 682 AA; 76331 MW; 8D2A71B873BC04A8 CRC64;

Query Match 61.8%; Score 34; DB 1; Length 682;
Best Local Similarity 60.0%; Pred. No. 37;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSFAM 10
I: I I I I I I
DB 311 AKEGYGSFAV 320

RESULT 14
NCAP_CVHOC STANDARD; PRT; 448 AA.
AC P33469;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE Nucleocapsid protein.
GN N.
OS Human coronavirus (strain OC43).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=31631;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89243809; PubMed=2541577;
RA Kanahora T., Soe L.H., Lai M.M.C.;
RT "Sequence analysis of nucleocapsid gene and leader RNA of human
coronavirus OC43";
RL Virus Res. 12:1-9(1989).
DR PIR: A60003; A60003.
DR InterPro: IPR001218; Corona_nucleocap.
DR Pfam: PF00937; Corona_nucleoca; 1.
KW Nucleocapsid.
SQ SEQUENCE 448 AA; 49316 MW; 5193AB1AE0D75626 CRC64;

Query Match 60.0%; Score 33; DB 1; Length 448;
Best Local Similarity 85.7%; Pred. No. 38;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
I I I I I I
DB 103 RHNRGSF 109

RESULT 15
SYE2_RICPR STANDARD; PRT; 470 AA.
AC Q92CT8;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE GlutamyI-tRNA synthetase 2 (EC 6.1.1.17) (Glutamate--tRNA ligase 2)
DE (GluRS 2).
GN GLTX2 OR RP623.
OS Rickettsia prowazekii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiidae; Rickettsia.
OX NCBI_TaxID=782;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Madrid E;
RX MEDLINE=95030499; PubMed=9823893;
RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,
RA Sicheritz-Ponten T., Alismark U.C.M., Podowski R.M., Naeslund A.K.,
RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
RT "The genome sequence of Rickettsia prowazekii and the origin of
mitochondria";
RL Nature 396:133-140(1998).
CC -!- CATALYTIC ACTIVITY: ATP + L-glutamate + tRNA(Glu) = AMP +
CC diphosphate + L-glutamyl-tRNA(Glu).
CC -!- SUBUNIT: MONOMER (BY SIMILARITY).

```
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
CC -----
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CC -----
CC EMBL; AJ235272; CAA15066.1; -.
CC HSSP; P27000; IGLN.
CC InterPro; IPR004527; GltX_bact.
CC InterPro; IPR000924; Glu_trna-synt_lc.
CC InterPro; IPR001412; trna-synt_I.
CC Pfam; PF00749; trna-synt_lc; 1.
CC PRINTS; PR00987; TRNASYNTHGLU.
CC TIGRFAMs; TIGR00464; gltX_bact; 1.
CC PROSITE; PS00178; AA_TRNA_LIGASE_I; FALSE_NEG.
KW Aminoacyl-trna synthetase; Protein biosynthesis; Ligase; ATP-binding;
KW Complete proteome.
FT SITE 10 20 "HIGH" REGION.
FT SITE 239 243 "KMSKS" REGION.
FT BINDING 242 242 ATP (BY SIMILARITY).
SQ SEQUENCE 470 AA; 53696 MW; DF1CE50A20B8A9FD CRC64;

Query Match 60.0%; Score 33; DB 1; Length 470;
Best Local Similarity 75.0%; Pred. No. 40;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSF 8
Db 31 ARHNGKF 38
|||||
|
```

Search completed: November 18, 2002, 17:33:29
Job time : 3.45098 secs

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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:01 : Search time 10.4412 Seconds
(without alignments)
197.341 Million cell updates/sec

Title: US-09-016-061-76
Perfect score: 55
Sequence: 1 ARHNYGSFAM 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL21.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_virus.*
16: sp_bacteriaph.*
17: sp_archaea.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	78.2	839	10 Q9LIE5	Q9LIE5 arabidopsis
2	40	72.7	276	7 Q9GJN0	Q9GJN0 caiman croc
3	39	70.9	446	5 O62086	O62086 caenorhabdi
4	39	70.9	1341	16 Q8UAU1	Q8UAU1 agrobacteri
5	38	69.1	89	7 O19495	O19495 gallus gall
6	37	67.3	478	16 O8XTH8	O8XTH8 raietonia s
7	37	67.3	5317	5 Q8TA74	Q8TA74 hemimentrot
8	36.5	66.4	89	7 Q30217	Q30217 homo sapien
9	36	65.5	39	7 P79474	P79474 cervus elap
10	36	65.5	39	7 P79477	P79477 cervus elap
11	36	65.5	39	7 P79478	P79478 cervus elap
12	36	65.5	39	7 P79479	P79479 cervus elap
13	36	65.5	67	7 Q8SP02	Q8SP02 hapalemur g
14	36	65.5	74	6 Q9TTM4	Q9TTM4 bos taurus
15	36	65.5	75	7 Q9GIJ5	Q9GIJ5 bos taurus
16	36	65.5	76	7 Q9TTPC2	Q9TTPC2 macaca mula

17	36	65.5	77	7 Q9GJ91	Q9GJ91 oviss aries
18	36	65.5	77	7 Q9GJ90	Q9GJ90 oviss aries
19	36	65.5	77	7 Q9GJ82	Q9GJ82 oviss aries
20	36	65.5	78	6 Q97968	Q97968 oviss aries
21	36	65.5	78	6 Q97835	Q97835 oviss aries
22	36	65.5	78	6 Q97839	Q97839 oviss aries
23	36	65.5	78	6 Q97844	Q97844 oviss aries
24	36	65.5	78	7 Q9MWT6	Q9MWT6 leopardus p
25	36	65.5	78	7 Q9MWT5	Q9MWT5 leopardus p
26	36	65.5	78	7 Q9MWT4	Q9MWT4 leopardus p
27	36	65.5	78	7 Q95HD1	Q95HD1 oviss aries
28	36	65.5	78	7 Q95HC6	Q95HC6 oviss aries
29	36	65.5	79	7 Q9MX19	Q9MX19 leopardus p
30	36	65.5	79	7 Q9MX13	Q9MX13 leopardus p
31	36	65.5	79	7 Q9MX03	Q9MX03 leopardus p
32	36	65.5	79	7 Q9MX00	Q9MX00 leopardus p
33	36	65.5	79	7 Q9MW29	Q9MW29 leopardus p
34	36	65.5	79	7 Q9MW28	Q9MW28 leopardus p
35	36	65.5	79	7 Q9MW27	Q9MW27 leopardus p
36	36	65.5	79	7 Q9MWY9	Q9MWY9 leopardus p
37	36	65.5	79	7 Q9MWY8	Q9MWY8 leopardus p
38	36	65.5	79	7 Q9MWY6	Q9MWY6 leopardus p
39	36	65.5	79	7 Q9MWY5	Q9MWY5 leopardus p
40	36	65.5	79	7 Q9MWY4	Q9MWY4 leopardus p
41	36	65.5	79	7 Q9MWY3	Q9MWY3 leopardus p
42	36	65.5	79	7 Q9MWX6	Q9MWX6 leopardus p
43	36	65.5	79	7 Q9MWX5	Q9MWX5 leopardus p
44	36	65.5	79	7 Q9MWX4	Q9MWX4 leopardus p
45	36	65.5	79	7 Q9MWX1	Q9MWX1 leopardus p

ALIGNMENTS

RESULT 1

Q9LIE5 PRELIMINARY: PRT; 839 AA.
AC Q9LIE5;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Far-red impaired response protein, mutator-like transposase-like
DE protein, phytochrome A signaling protein-like.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Magnoliophyta; Streptophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=20363099; PubMed=10907853;
RA Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.
RT Sequence features of the regions of 4,251,695 bp covered by ninety p1,
RT TAC and BAC clones."
RL DNA Res. 7:217-221(2000).
DR EMBL; AP001306; BAB03065.1;
DR InterPro; IPR004330; FARI.
DR InterPro; IPR001000; Glyco_hydro_10.
DR Pfam; PF03101; FARI. 1.
DR PROSITE; PS00591; GLYCOSYL_HYDROL_F10; UNKNOWN.1.
SQ SEQUENCE 839 AA; 95996 MW; CBBF60DF8B6797F8 CRC64;

Query Match 78.2%; Score 43; DB 10; Length 839;
Best Local Similarity 87.5%; Pred. No. 5.2;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;


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QY 1 ARHNGSF 8
DB 274 SRHNGSF 281
    :|||||
RESULT 2
ID Q9GJNO PRELIMINARY; PRT; 276 AA.
AC Q9GJNO;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II beta chain.
GN HCTIBETA.
OS Caiman crocodilus (Spectacled caiman) (Caiman sclerops).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Crocodylidae; Alligatorinae; Caiman.
OX NCBI_TaxID=8499;
[1]
RN SEQUENCE FROM N.A.
RA Voldby J., Vitved L., Due M., Gronlund J., Holmskov U., Teisner B.,
RA Salomonsen J., Brusgaard K., Skjold K.;
RT "Cloning, sequence and genomic structure of MHC class II antigens from
RT the spectacled caiman, Caiman crocodilus."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF256651; AAF9283.1; -.
DR HSSP; P13760; 2SER.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC..
DR InterPro; IPR000353; MHC_II_beta.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00969; MHC_II_beta; 1.
DR ProDom; PD000328; MHC_II_beta; 1.
DR SMART; SM00407; IGcl; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR Glycoprotein; MHC II; Transmembrane.
SQ SEQUENCE 276 AA; 30366 MW; EA8A4684986AEA6A CRC64;

    Query Match 72.7%; Score 40; DB 7; Length 276;
    Best Local Similarity 87.5%; Pred. No. 5.8;
    Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFA 9
DB 108 RHNYGVFA 115
    :|||||
RESULT 3
ID O62086 PRELIMINARY; PRT; 446 AA.
AC O62086;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE C31H5.6 protein.
GN C31H5.6
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
[1]
RN SEQUENCE FROM N.A.
RA Kershaw J.K.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RX SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology."
RL Science 282:2012-2018(1998).
DR EMBL; Z93778; CAB07846.1; -.
DR InterPro; IPR000379; Ser_estrs_site.

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SQ SEQUENCE 446 AA; 50763 MW; 82AD969CDAD753DE CRC64;

    Query Match 70.9%; Score 39; DB 5; Length 446;
    Best Local Similarity 87.5%; Pred. No. 16;
    Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFA 9
DB 51 RHNYGSHA 58
    :|||||
RESULT 4
ID Q8UAU1 PRELIMINARY; PRT; 1341 AA.
AC Q8UAU1;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical protein Atu3276.
GN ATU3276 OR AGR_L3085.
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=176299;
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE=21608550; PubMed=11743193;
RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. S.,
RA Chapman P., Clendinning J., Deatherage G., Gillet W., Grant C.,
RA Kutayavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA Nester E.W.;
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
RT C58."
RL Science 294:2317-2323(2001).
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=21608551; PubMed=11743194;
RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
RA Quorillo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
RA Houmlet K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
RA Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
RA Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
RA Cielo C., Slater S.;
RT "Genome sequence of the plant pathogen and biotechnology agent
RT Agrobacterium tumefaciens C58."
RL Science 294:2323-2328(2001).
DR EMBL; AE009257; AAL44092.1; ALT_INIT.
DR EMBL; AE008356; AAK90114.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 1341 AA; 132309 MW; BB0BC2A8290206FA CRC64;

    Query Match 70.9%; Score 39; DB 16; Length 1341;
    Best Local Similarity 77.8%; Pred. No. 55;
    Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAM 10
DB 1368 RHNYGDTAM 1276
    :|||||
RESULT 5
ID O19495 PRELIMINARY; PRT; 89 AA.
AC O19495;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

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DE MHC class II beta 1 domain (Fragment).

GN B-LBI.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=15.151-5; TISSUE=BURSA;
RX MEDLINE=98179131; PubMed=9510552;
RA Pharr G.T., Dodgson J.B., Hunt H.D., Bacon L.D.;
RT "Class II MHC cDNAs in 1515 B-congenic chickens.";
RL Immunogenetics 47:350-354(1998).
DR EMBL: U91532; AAC15813.1; -;
DR InterPro: IPR000353; MHC_II_beta.
DR Pfam: PF00969; MHC_II_beta; 1.
DR ProbDom: PD000328; MHC_II_beta; 1.
KW Glycoprotein; MHC II; Transmembrane.
FT NON_TER 1
FT NON_TER 89
SQ SEQUENCE 89 AA; 10724 MW; BC7D558B6ABE1379 CRC64;

Query Match 69.1%; Score 38; DB 7; Length 89;
Best Local Similarity 85.7%; Pred. No. 4.1;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
DB 75 RHNYGDF 81

RESULT 6

Q8XTH8 PRELIMINARY; PRT; 478 AA.
ID Q8XTH8
AC Q8XTH8
DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Probable transmembrane protein.
DR RSP0132 OR RS02988.
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Plasmid megaplasmid.
OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
OC Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GM11000;
RX MEDLINE=21681879; PubMed=11823852;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Ariat M., Billault A., Brottier P., Camus J.C., Catolico L.,
RA Chandler M., Choisme N., Claudel-Renard C., Cunnac S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,
RA Siguer P., Thebaud P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502(2002).
DR EMBL: AL646076; CAD17283.1; -;
DR InterPro: IPR000160; GDEF.
DR Pfam: PF00990; GDEF; 1.
DR SMART: SM00267; DUF1; 1.
DR TIGRFAMs: TIGR00254; GDEF; 1.
KW Plasmid; Complete proteome.
SQ SEQUENCE 478 AA; 51177 MW; 0AC648F05A11D6A6 CRC64;

Query Match 67.3%; Score 37; DB 16; Length 478;
Best Local Similarity 70.0%; Pred. No. 43;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSFAM 10
DB 377 ARHNGSTFAM 386

RESULT 7

Q8TA74 PRELIMINARY; PRT; 5317 AA.
ID Q8TA74
AC Q8TA74;
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Ryanodine receptor.
OS Hemitecnrotus pulcherrimus (Sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
OC Hemitecnrotus.
OX NCBI_TaxID=7650;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21821894; PubMed=11832393;
RA Shima M., Murayama T., Ogawa Y.;
RT "Molecular cloning and characterization of ryanodine receptor from
unfertilized sea urchin eggs";
RL Am. J. Physiol. Regul. Integr. Comp. Physiol. 282:R727-R737(2002).
DR EMBL: AB051576; BAB84714.1; -;
KW Receptor.
SQ SEQUENCE 5317 AA; 597209 MW; 2FA8A1D8CBE28A78 CRC64;

Query Match 67.3%; Score 37; DB 5; Length 5317;
Best Local Similarity 85.7%; Pred. No. 6.6e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGS 7
DB 3329 ARHNYGA 3335

RESULT 8

Q30217 PRELIMINARY; PRT; 89 AA.
ID Q30217
AC Q30217;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
DE MHC class II HLA-DRB9 (Fragment).
GN DRB9.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95279172; PubMed=7759314;
RA Arvidsson A.K., Svensson A.C., Widmark E., Andersson G., Rask L.,
RA Larhammar D.;
RT "Characterization of three separated exons in the HLA class II DR
region of the human major histocompatibility complex.";
RL Hum. Immunol. 42:254-264(1995).
DR EMBL: S78510; AAD14284.1; -;
DR InterPro: IPR000353; MHC_II_beta.
DR Pfam: PF00969; MHC_II_beta; 1.
KW Glycoprotein; MHC II; Transmembrane.
FT NON_TER 1
FT NON_TER 89
SQ SEQUENCE 89 AA; 10489 MW; 10027003DC27E99E CRC64;

Query Match 66.4%; Score 36.5; DB 7; Length 89;
Best Local Similarity 66.7%; Pred. No. 8.1;
Matches 8; Conservative 1; Mismatches 0; Indels 3; Gaps 1;

QY 2 RHNYG---SFAM.10
DB 75 RHNYGVFEFSFM 86

RESULT 9

P79474 ID P79474 PRELIMINARY: PRT: 39 AA.
 AC P79474;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE MHC class II DRB (Fragment).
 OS Cervus elaphus (Red deer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervioidea;
 OC Cervidae; Cervinae; Cervus.
 OX NCBI_TaxID=9860;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Swarbrick P.A., Crawford A.M.;
 RT "The MHC class II DRB intron 2 microsatellite of red deer.";
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U63077; AAB37777.1; -.
 DR InterPro; IPR000353; MHC_II_beta.
 DR Pfam; PF00969; MHC_II_beta; 1.
 DR ProDom; PD000328; MHC_II_beta; 1.
 KW Glycoprotein; MHC II; Transmembrane.
 FT NON_TER 1
 FT NON_TER 39
 SQ SEQUENCE 39 AA; 4767 MW; CAF3680999733DID CRC64;

Query Match 65.5%; Score 36; DB 7; Length 39;
 Best Local Similarity 85.7%; Pred. No. 4;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
 |||||
 DB 25 RHNYGVF 31

RESULT 10

P79477 ID P79477 PRELIMINARY: PRT: 39 AA.
 AC P79477;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE MHC class II DRB (Fragment).
 OS Cervus elaphus (Red deer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervioidea;
 OC Cervidae; Cervinae; Cervus.
 OX NCBI_TaxID=9860;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Swarbrick P.A., Crawford A.M.;
 RT "The MHC class II DRB intron 2 microsatellite of red deer.";
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U63080; AAB37780.1; -.
 DR InterPro; IPR000353; MHC_II_beta.
 DR Pfam; PF00969; MHC_II_beta; 1.
 DR ProDom; PD000328; MHC_II_beta; 1.
 KW Glycoprotein; MHC II; Transmembrane.
 FT NON_TER 1
 FT NON_TER 39
 SQ SEQUENCE 39 AA; 4806 MW; C2188A16752A3C1D CRC64;

Query Match 65.5%; Score 36; DB 7; Length 39;
 Best Local Similarity 85.7%; Pred. No. 4;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
 |||||
 DB 25 RHNYGVF 31

RESULT 11

Q8SP02 ID P79478 PRELIMINARY: PRT: 39 AA.
 AC P79478;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE MHC class II DRB (Fragment).
 OS Cervus elaphus (Red deer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervioidea;
 OC Cervidae; Cervinae; Cervus.
 OX NCBI_TaxID=9860;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Swarbrick P.A., Crawford A.M.;
 RT "The MHC class II DRB intron 2 microsatellite of red deer.";
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U63081; AAB37781.1; -.
 DR InterPro; IPR000353; MHC_II_beta.
 DR Pfam; PF00969; MHC_II_beta; 1.
 DR ProDom; PD000328; MHC_II_beta; 1.
 KW Glycoprotein; MHC II; Transmembrane.
 FT NON_TER 1
 FT NON_TER 39
 SQ SEQUENCE 39 AA; 4806 MW; C2188A16752A3C1D CRC64;

Query Match 65.5%; Score 36; DB 7; Length 39;
 Best Local Similarity 85.7%; Pred. No. 4;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
 |||||
 DB 25 RHNYGVF 31

RESULT 13
 Q8SP02

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ID Q8SP02* PRELIMINARY; PRT; 67 AA.
AC Q8SP02;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE MHC class II antigen (Fragment).
DE HAGG-DRB.
GN Hapalemur griseus griseus.
OS Hapalemur griseus griseus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Strepsirhini; Lemnidae; Hapalemur.
OX NCBI_TaxID=122219;
RN [1]
RP SEQUENCE FROM N.A.
RA Go Y., Satta Y., Kawamoto Y., Rakotoarisoa G., Randrianjafy A.,
RA Koyama N., Hirai H.;
RT "MHC-DRB genes evolution in lemurs.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB078220; BAB88434.1; -.
FT NON_TER 1
FT NON_TER 1
FT NON_TER 67
SQ SEQUENCE 67 AA; 8083 MW; 559300839F0EFA52 CRC64;

Query Match 65.5%; Score 36; DB 7; Length 67;
Best Local Similarity 85.7%; Pred. No. 7.4;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 59 RHNYGVF 65

RESULT 14
Q9TTM4
ID Q9TTM4 PRELIMINARY; PRT; 74 AA.
AC Q9TTM4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC(BOLA) class II DR-beta chain (Fragment).
GN BOLA-DRB3.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-JAPANESE BLACK;
RA Takeshima S., Ikegami M., Morita M., Nakai Y., Aida Y.;
RT "Identification of BOLA-DRB3 exon 2 of Japanese black cattle.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB033388; BAA85470.1; -.
DR InterPro; IPR000353; MHC_II_beta.
DR Pfam; PF00969; MHC_II_beta.1.
DR ProDom; PD000328; MHC_II_beta.1.
KW Glycoprotein; MHC II; Transmembrane.
FT NON_TER 1
FT NON_TER 74
SQ SEQUENCE 74 AA; 9132 MW; C5834842F0E38BA6 CRC64;

Query Match 65.5%; Score 36; DB 6; Length 74;
Best Local Similarity 85.7%; Pred. No. 8.3;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 68 RHNYGVF 74

RESULT 15
Q9GIJ5
ID Q9GIJ5 PRELIMINARY; PRT; 75 AA.
AC Q9GIJ5;

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DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC(BOLA) class II DR-beta chain (Fragment).
GN BOLA-DRB3.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-JAPANESE BLACK; TISSUE=PERIPHERAL BLOOD LYMPHOCYTE;
RA Takeshima S., Ikegami M., Saitou N., Morita M., Inoko T., Aida Y.;
RT "Nature and origin of polymorphism in BOLA-DRB3 gene.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB053167; BAB20423.1; -.
DR InterPro; IPR000353; MHC_II_beta.
DR Pfam; PF00969; MHC_II_beta.1.
DR ProDom; PD000328; MHC_II_beta.1.
KW Glycoprotein; MHC II; Transmembrane.
FT NON_TER 1
FT NON_TER 75
SQ SEQUENCE 75 AA; 9260 MW; C58310BD57BB7401 CRC64;

Query Match 65.5%; Score 36; DB 7; Length 75;
Best Local Similarity 85.7%; Pred. No. 8.4;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 69 RHNYGVF 75

Search completed: November 18, 2002, 17:40:49
Job time : 11.4912 secs

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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:21:57 ; Search time 13.8235 Seconds
(without alignments)
96.394 Million cell updates/sec

Title: US-09-016-061-76
Perfect score: 55
Sequence: 1 ARHNGSFAM 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	55	100.0	10	19 AAW76028	LM609 grafted anti
2	55	100.0	10	22 AAB61386	Mutant VH CDR3 pep
3	50	90.9	10	19 AAW76024	LM609 grafted anti
4	50	90.9	10	19 AAW76025	LM609 grafted anti
5	50	90.9	10	19 AAW76026	LM609 grafted anti
6	50	90.9	10	19 AAW76027	LM609 grafted anti
7	50	90.9	10	19 AAW76029	LM609 grafted anti
8	50	90.9	10	19 AAW76030	LM609 grafted anti
9	50	90.9	10	19 AAW76010	LM609 grafted anti
10	50	90.9	10	22 AAB61368	LM609 VH CDR3 pept

11	50	90.9	10	22 AAB61382	Mutant VH CDR3 pep
12	50	90.9	10	22 AAB61383	Mutant VH CDR3 pep
13	50	90.9	10	22 AAB61384	Mutant VH CDR3 pep
14	50	90.9	10	22 AAB61385	Mutant VH CDR3 pep
15	50	90.9	10	22 AAB61387	Mutant VH CDR3 pep
16	50	90.9	10	22 AAB61388	Mutant VH CDR3 pep
17	50	90.9	117	19 AAW76001	Vitaxin antibody h
18	50	90.9	117	19 AAW76003	LM609 antibody hea
19	50	90.9	117	20 AAY06381	Murine monoclonal
20	50	90.9	117	20 AAY06387	Humanised LM609 an
21	50	90.9	117	22 AAG63587	A heavy chain vari
22	50	90.9	117	22 AAG63589	A heavy chain vari
23	50	90.9	117	22 AAB61359	Vitaxin heavy chai
24	50	90.9	117	22 AAB61361	Antibody LM609 hea
25	50	90.9	118	20 AAY06384	Humanised LM609 an
26	50	90.9	118	20 AAY06385	Humanised LM609 an
27	50	90.9	118	20 AAY06386	Humanised LM609 an
28	50	90.9	118	20 AAY06383	Humanised LM609 an
29	50	90.9	130	20 AAY06379	Murine monoclonal
30	47	85.5	10	19 AAW76021	LM609 grafted anti
31	47	85.5	10	22 AAB61379	Mutant VH CDR3 pep
32	46	83.6	10	19 AAW76039	LM609 grafted anti
33	46	83.6	10	19 AAW76040	LM609 grafted anti
34	46	83.6	10	19 AAW76022	LM609 grafted anti
35	46	83.6	10	19 AAW76023	LM609 grafted anti
36	46	83.6	10	22 AAB61380	Mutant VH CDR3 pep
37	46	83.6	10	22 AAB61381	Mutant VH CDR3 pep
38	46	83.6	10	22 AAB61397	Multiple mutant VH
39	46	83.6	10	22 AAB61398	Multiple mutant VH
40	45	81.8	10	19 AAW76037	LM609 grafted anti
41	45	81.8	10	19 AAW76020	LM609 grafted anti
42	45	81.8	10	22 AAB61378	Mutant VH CDR3 pep
43	45	81.8	10	22 AAB61395	Multiple mutant VH
44	42	76.4	110	20 AAW84099	Vitronectin alpha-
45	42	76.4	117	20 AAW84093	Murine vitronectin

ALIGNMENTS

RESULT 1
AAW76028
ID AAW76028 standard; Protein: 10 AA.
XX AAW76028;
AC AAW76028;
DT 02-NOV-1998 (first entry)
XX LM609 grafted antibody V-H region CDR3 protein fragment #10.
DE Vitaxin; antibody; variable region; heavy chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
XX WO9833919-A2.
XX 06-AUG-1998.
XX 30-JAN-1998; 98WO-US01826.
XX 30-JAN-1997; 97US-0791391.
XX (IXSY-) IXSYS INC.
XX Glaser SM, Huse WD;
XX WPI; 1998-437472/37.
XX N-PSDB; AAW49865.

XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
XX Claim 62; Page 41; 129pp; English.
XX
XX AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
CC antibodies contain non-murine framework regions so are suitable for use
CC in humans. Enhanced types of LM609 have affinity more than 90 times
CC greater than that of parent the parent antibody.
XX
XX Sequence 10 AA;
XX
XX Query Match 100.0%; Score 55; DB 19; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 0.0033;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 1 ARHNYGSFAM 10
XX |
XX Db 1 ARHNYGSFAM 10
XX |

XX RESULT 2
XX AAB61386
XX ID AAB61386 standard; peptide; 10 AA.
XX AC AAB61386;
XX
XX 03-APR-2001 (first entry)
XX
XX DE Mutant VH CDR3 peptide #9.
XX
XX LM609; grafted antibody; alphaVbeta_3 integrin; angiogenesis;
XX inflammatory; cancer; retina; restenosis; osteoporosis.
XX
XX OS Unidentified.
XX
XX PN WO200078815-A1.
XX
XX PD 28-DEC-2000.
XX
XX PF 23-JUN-2000; 2000WO-US17454.
XX
XX PR 24-JUN-1999; 99US-0339922.
XX
XX PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX
XX PI Huse WD, Wu H;
XX
XX WPI; 2001-050110/06.
XX
XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
PT osteoporosis -
XX
XX Disclosure; Page 41; 132pp; English.
XX
XX The present invention relates to enhanced LM609 grafted antibodies
CC exhibiting selective binding affinity to alphaVbeta_3 integrin or
CC their functional fragments. The antibodies or their functional
CC fragments can be used in the diagnosis and treatment of
CC alphaVbeta_3-mediated diseases such as angiogenesis, inflammatory

CC diseases (such as psoriasis and chronic articular rheumatism),
CC disorders associated with inappropriate or inopportune invasion of
CC vessels (such as diabetic retinopathy, neovascular glaucoma and
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
CC diseases (such as macular degeneration), restenosis and
CC osteoporosis.
XX
XX Sequence 10 AA;
XX
XX Query Match 100.0%; Score 55; DB 22; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 0.0033;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 1 ARHNYGSFAM 10
XX |
XX Db 1 ARHNYGSFAM 10
XX |

XX RESULT 3
XX AAW76024
XX ID AAW76024 standard; Protein; 10 AA.
XX AC AAW76024;
XX
XX 02-NOV-1998 (first entry)
XX
XX DE LM609 grafted antibody V-H region CDR3 protein fragment #6.
XX
XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
XX LM609; inhibitor; integrin-mediated signal transduction; treatment;
XX diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
XX neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
XX macular degeneration; osteoporosis; primer; V-H region; CDR;
XX complementarity determining region.
XX
XX OS Mus sp.
XX
XX PN WO9833919-A2.
XX
XX PD 06-AUG-1998.
XX
XX PF 30-JAN-1998; 98WO-US01826.
XX
XX PR 30-JAN-1997; 97US-0791391.
XX
XX PA (IXSY-) IXSYS INC.
XX
XX PI Glaser SM, Huse WD;
XX
XX WPI; 1998-437472/37.
XX
XX DR N-PSDB; AAV49861.
XX
XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
XX Claim 62; Page 41; 129pp; English.
XX
XX AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
CC antibodies contain non-murine framework regions so are suitable for use
CC in humans. Enhanced types of LM609 have affinity more than 90 times
CC greater than that of parent the parent antibody.
XX
XX Sequence 10 AA;
XX

Query Match 90.9%; Score 50; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.024;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
 DB 1 ARHNYGSFA 9
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RESULT 4
 AAW76025
 ID AAW76025 standard; Protein; 10 AA.

XX

AC AAW76025;

XX

DT 02-NOV-1998 (first entry)

XX

DE LM609 grafted antibody V-H region CDR3 protein fragment #7.

XX

KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.

XX

OS Mus sp.

XX

PN WO9833919-A2.

XX

PD 06-AUG-1998.

XX

PF 30-JAN-1998; 98WO-US01826.

XX

PR 30-JAN-1997; 97US-0791391.

XX

PA (IXSY-) IXSYS INC.

XX

PI Glaser SM, Huse WD;

XX

DR WPI; 1998-437472/37.

XX

DR N-PSDB; AAV49862.

XX

PS Claim 62; Page 41; 129pp; English.

XX

CC AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
 CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
 CC antibodies contain non-murine framework regions so are suitable for use
 CC in humans. Enhanced types of LM609 have affinity more than 90 times
 CC greater than that of parent the parent antibody.

XX

SQ Sequence 10 AA;

XX

Query Match 90.9%; Score 50; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.024;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9

DB 1 ARHNYGSFA 9

|||||

XX

AC AAW76027;

XX

RESULT 5
 AAW76026
 ID AAW76026 standard; Protein; 10 AA.

XX

AC AAW76026;

XX

DT 02-NOV-1998 (first entry)

XX

DE LM609 grafted antibody V-H region CDR3 protein fragment #8.

XX

KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.

XX

OS Mus sp.

XX

PN WO9833919-A2.

XX

PD 06-AUG-1998.

XX

PF 30-JAN-1998; 98WO-US01826.

XX

PR 30-JAN-1997; 97US-0791391.

XX

PA (IXSY-) IXSYS INC.

XX

PI Glaser SM, Huse WD;

XX

DR WPI; 1998-437472/37.

XX

DR N-PSDB; AAV49863.

XX

PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

XX

PS Claim 62; Page 41; 129pp; English.

XX

CC AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
 CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
 CC antibodies contain non-murine framework regions so are suitable for use
 CC in humans. Enhanced types of LM609 have affinity more than 90 times
 CC greater than that of parent the parent antibody.

SQ Sequence 10 AA;

XX

Query Match 90.9%; Score 50; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.024;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9

DB 1 ARHNYGSFA 9

|||||

XX

AC AAW76027;

XX

AC AAW76027 standard; Protein; 10 AA.

XX

AC AAW76027;

XX

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DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #9.
XX
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
XX
OS Mus sp.
XX
PN WO9833919-A2.
XX
PD 06-AUG-1998.
XX
PF 30-JAN-1998; 98WO-US01826.
XX
PR 30-JAN-1997; 97US-0791391.
XX
PA (IXSY-) IXSYS INC.
XX
PI Glaser SM, Huse WD;
XX
DR N-PSDB; AAV49864.
XX
XX
Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
integrin - and related grafted antibodies based on murine monoclonal
LM609, also related nucleic acid, used to treat, prevent or diagnose
angiogenesis or restenosis
XX
PS Claim 62; Page 41; 129pp; English.
XX
AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
LM609 heavy and light chain variable region. LM609 and the antibody
vitaxin bind selectively to integrin alphaVbeta3 and can be used to
inhibit binding of alphaVbeta3 to a ligand and thus block
integrin-mediated signal transduction. This is useful in the treatment,
prevention and diagnosis of alphaVbeta3-mediated disease, specifically
angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
antibodies contain non-murine framework regions so are suitable for use
in humans. Enhanced types of LM609 have affinity more than 90 times
greater than that of parent the parent antibody.
XX
SQ Sequence 10 AA;
Query Match 90.9%; Score 50; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ARHNYGSFA 9
Db 1 ARHNYGSFA 9
|||||||
RESULT 7
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ID AAW76029 standard; Protein; 10 AA.
XX
AC AAW76029;
XX
XX 02-NOV-1998 (first entry)
XX
DE LM609 grafted antibody V-H region CDR3 protein fragment #11.
XX
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW complementarity determining region.
XX
OS Mus sp.
XX
PN WO9833919-A2.
XX
PD 06-AUG-1998.
XX
PF 30-JAN-1998; 98WO-US01826.
XX
PR 30-JAN-1997; 97US-0791391.
XX
PA (IXSY-) IXSYS INC.
XX
PI Glaser SM, Huse WD;
XX
DR N-PSDB; AAV49866.
XX
XX
Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
integrin - and related grafted antibodies based on murine monoclonal
LM609, also related nucleic acid, used to treat, prevent or diagnose
angiogenesis or restenosis
XX
PS Claim 62; Page 41; 129pp; English.
XX
AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
LM609 heavy and light chain variable region. LM609 and the antibody
vitaxin bind selectively to integrin alphaVbeta3 and can be used to
inhibit binding of alphaVbeta3 to a ligand and thus block
integrin-mediated signal transduction. This is useful in the treatment,
prevention and diagnosis of alphaVbeta3-mediated disease, specifically
angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
antibodies contain non-murine framework regions so are suitable for use
in humans. Enhanced types of LM609 have affinity more than 90 times
greater than that of parent the parent antibody.
XX
SQ Sequence 10 AA;
Query Match 90.9%; Score 50; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ARHNYGSFA 9
Db 1 ARHNYGSFA 9
|||||||
RESULT 8
AAW76030
ID AAW76030 standard; Protein; 10 AA.
XX
AC AAW76030;
XX
XX 02-NOV-1998 (first entry)
XX
DE LM609 grafted antibody V-H region CDR3 protein fragment #12.
XX
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
XX
OS Mus sp.
XX
PN WO9833919-A2.
XX
PD 06-AUG-1998.

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XX PF 30-JAN-1998; 98WO-US01826.
XX PR 30-JAN-1997; 97US-0791391.
XX XX (IXSY-) IXSYS INC.
XX PA Glaser SM, Huse WD;
XX PI WPI: 1998-437472/37.
XX DR N-PSDB; AAV49867.
XX DR Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
XX PT integrin - and related grafted antibodies based on murine monoclonal
XX PT LM609, also related nucleic acid, used to treat, prevent or diagnose
XX PT angiogenesis or restenosis
XX PS Claim 62; Page 41; 129pp; English.
XX CC AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
XX CC LM609 heavy and light chain variable region. LM609 and the antibody
XX CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
XX CC inhibit binding of alphavbeta3 to a ligand and thus block
XX CC integrin-mediated signal transduction. This is useful in the treatment,
XX CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
XX CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
XX CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
XX CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
XX CC antibodies contain non-murine framework regions so are suitable for use
XX CC in humans. Enhanced types of LM609 have affinity more than 90 times
XX CC greater than that of parent the parent antibody.
XX SQ Sequence 10 AA;
XX Query Match 90.9%; Score 50; DB 19; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 0.024;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
Db 1 ARHNYGSFA 9
|||||||

RESULT 9
AAW76010
ID AAW76010 standard; Protein; 10 AA.
XX AC AAW76010;
XX DT 02-NOV-1998 (first entry)
XX DE LM609 grafted antibody V-H region CDR3 protein fragment #1.
XX KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
XX KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
XX KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
XX KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
XX KW macular degeneration; osteoporosis; primer; V-H region; CDR;
XX KW complementarity determining region.
XX OS Mus sp.
XX PN WO9833919-A2.
XX PD 06-AUG-1998.
XX PF 30-JAN-1998; 98WO-US01826.
XX PR 30-JAN-1997; 97US-0791391.
XX PA (IXSY-) IXSYS INC.
XX PI Glaser SM, Huse WD;

Query Match 90.9%; Score 50; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
Db 1 ARHNYGSFA 9
|||||||

RESULT 10
AAB61368
ID AAB61368 standard; peptide; 10 AA.
XX AC AAB61368;
XX DT 03-APR-2001 (first entry)
XX DE LM609 VH CDR3 peptide.
XX KW LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
XX KW inflammatory; cancer; retina; restenosis; osteoporosis.
XX OS Unidentified.
XX PN WO200078815-A1.
XX PD 28-DEC-2000.
XX PF 23-JUN-2000; 2000WO-US17454.
XX PR 24-JUN-1999; 99US-0339922.
XX PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX PI Huse WD, Wu H;
XX DR WPI: 2001-050110/06.
XX PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity
XX PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
XX PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
XX PT osteoporosis.
XX PS Disclosure; Page 39; 132pp; English.
XX CC The present invention relates to enhanced LM609 grafted antibodies
XX CC exhibiting selective binding affinity to alphavbeta_3 integrin or

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XX DE Mutant VH CDR3 peptide #7.
 XX KW LM609; grafted antibody; alphaVbeta_3 integrin; angiogenesis;
 XX KW inflammatory; cancer; retina; restenosis; osteoporosis.
 XX OS Unidentified.
 XX PN WO200078815-A1.
 XX PD 28-DEC-2000.
 XX PF 23-JUN-2000; 2000WO-US17454.
 XX PR 24-JUN-1999; 99US-0339922.
 XX PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
 XX PI Huse WD, Wu H;
 XX DR WPI; 2001-050110/06.
 XX XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -
 XX XX Disclosure; Page 41; 132pp; English.
 XX XX The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphaVbeta_3 integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphaVbeta_3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.
 XX XX Sequence 10 AA;
 PS Query Match 90.9%; Score 50; DB 22; Length 10;
 PS Best Local Similarity 100.0%; Pred. No. 0.024;
 PS Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ARHNYGSFA 9
 Db | | | | | | | | | |
 1 ARHNYGSFA 9
 RESULT 14
 AAB61385
 ID AAB61385 standard; peptide; 10 AA.
 AC AAB61385;
 XX 03-APR-2001 (first entry)
 DT Mutant VH CDR3 peptide #8.
 DE LM609; grafted antibody; alphaVbeta_3 integrin; angiogenesis;
 XX inflammatory; cancer; retina; restenosis; osteoporosis.
 KW Unidentified.
 XX WO200078815-A1.
 XX PD 28-DEC-2000.
 XX PF 23-JUN-2000; 2000WO-US17454.
 XX PR 24-JUN-1999; 99US-0339922.
 XX PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
 XX PI Huse WD, Wu H;
 XX DR WPI; 2001-050110/06.
 XX XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -
 XX XX Disclosure; Page 41; 132pp; English.

XX PR 24-JUN-1999; 99US-0339922.
 XX PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
 XX PI Huse WD, Wu H;
 XX DR WPI; 2001-050110/06.
 XX XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -
 XX XX Disclosure; Page 41; 132pp; English.
 XX XX The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphaVbeta_3 integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphaVbeta_3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.
 XX XX Sequence 10 AA;
 PS Query Match 90.9%; Score 50; DB 22; Length 10;
 PS Best Local Similarity 100.0%; Pred. No. 0.024;
 PS Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ARHNYGSFA 9
 Db | | | | | | | | | |
 1 ARHNYGSFA 9
 RESULT 15
 AAB61387
 ID AAB61387 standard; peptide; 10 AA.
 AC AAB61387;
 XX 03-APR-2001 (first entry)
 DT Mutant VH CDR3 peptide #10.
 DE LM609; grafted antibody; alphaVbeta_3 integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis.
 XX Unidentified.
 XX WO200078815-A1.
 XX PD 28-DEC-2000.
 XX PF 23-JUN-2000; 2000WO-US17454.
 XX PR 24-JUN-1999; 99US-0339922.
 XX PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
 XX PI Huse WD, Wu H;
 XX DR WPI; 2001-050110/06.
 XX XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -
 XX XX Disclosure; Page 41; 132pp; English.

XX The present invention relates to enhanced LM609 grafted antibodies
CC exhibiting selective binding affinity to alphaVbeta₃ integrin or
CC their functional fragments. The antibodies or their functional
CC fragments can be used in the diagnosis and treatment of
CC alphaVbeta₃-mediated diseases such as angiogenesis, inflammatory
CC diseases (such as psoriasis and chronic articular rheumatism),
CC disorders associated with inappropriate or inopportune invasion of
CC vessels (such as diabetic retinopathy, neovascular glaucoma and
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
CC diseases (such as macular degeneration), restenosis and
CC osteoporosis.

XX SQ Sequence 10 AA;

Query Match 90.9%; Score 50; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.024; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
Db 1 ARHNYGSFA 9
|||||||

Search completed: November 18, 2002, 17:31:39
Job time : 14.8235 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:54:45 ; Search time 1.96078 Seconds
(without alignments)
76.811 Million cell updates/sec

Title: US-09-016-061-76

Perfect score: 55

Sequence: 1 ARHNYGSPAM 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 97044 seqs, 15060890 residues

Total number of hits satisfying chosen parameters: 97044

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_AA:*
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9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
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11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
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14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	90.9	117	8	US-08-790-540A-2
2	50	90.9	117	8	US-08-790-540A-6
3	50	90.9	117	8	US-08-791-391A-2
4	50	90.9	117	8	US-08-791-391A-6
5	36	65.5	14	1	US-08-677-599B-22
6	36	65.5	101	10	US-09-764-853-432
7	34	61.8	30	10	US-09-839-884-40
8	34	61.8	287	10	US-09-415-540-5
9	33	60.0	14	1	US-08-677-599B-21
10	32	58.2	14	1	US-08-677-599B-11
11	32	58.2	14	1	US-08-677-599B-12
12	32	58.2	14	1	US-08-677-599B-13
13	32	58.2	14	1	US-08-677-599B-14
14	32	58.2	14	1	US-08-677-599B-15
15	32	58.2	14	1	US-08-677-599B-16
16	32	58.2	14	1	US-08-677-599B-17
17	32	58.2	14	1	US-08-677-599B-18
18	32	58.2	14	1	US-08-677-599B-19
19	32	58.2	14	1	US-08-677-599B-20

20	32	58.2	14	1	US-08-677-599B-23
21	32	58.2	15	10	US-09-756-983-11
22	32	58.2	25	1	US-08-677-599B-8
23	32	58.2	93	12	US-10-081-281-121
24	32	58.2	94	10	US-09-766-378A-37
25	32	58.2	181	10	US-09-815-837-103
26	32	58.2	183	10	US-09-815-837-16
27	32	58.2	184	10	US-09-815-837-15
28	32	58.2	185	10	US-09-815-837-13
29	32	58.2	185	10	US-09-815-837-14
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31	32	58.2	186	10	US-09-815-837-19
32	32	58.2	186	10	US-09-815-837-20
33	32	58.2	187	10	US-09-815-837-18
34	32	58.2	189	10	US-09-815-837-21
35	32	58.2	189	10	US-09-815-837-22
36	32	58.2	193	10	US-09-815-837-23
37	32	58.2	193	10	US-09-815-837-24
38	32	58.2	196	10	US-09-741-669-368
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42	32	58.2	207	12	US-10-081-281-93
43	32	58.2	208	10	US-09-815-837-102
44	32	58.2	209	10	US-09-815-837-58
45	32	58.2	210	10	US-09-815-837-40

ALIGNMENTS

RESULT 1

US-08-790-540A-2

; Sequence 2, Application US/08790540A

; Patent No. US20010011125A1

; GENERAL INFORMATION:

; APPLICANT: Huse, William D.

; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human

; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use

; NUMBER OF SEQUENCES: 24

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Campbell & Flores LLP

; STREET: 4370 La Jolla Village Drive, Suite 700

; CITY: San Diego

; STATE: California

; COUNTRY: United States

; ZIP: 92122

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/790,540A

; FILING DATE: 30-JAN-1997

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: Campbell, Cathryn A.

; REGISTRATION NUMBER: 31,815

; REFERENCE/DOCKET NUMBER: P-IX 2405

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (619) 535-9001

; TELEFAX: (619) 535-8949

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 117 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-790-540A-2

Query Match 90.9%; Score 50; DB 8; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.0054;

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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
   |||||
Db 97 ARHNYGSFA 105

RESULT 2
US-08-790-540A-6
; Sequence 6, Application US/08790540A
; Patent No. US2001001125A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-790-540A-6

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/790,540A
FILING DATE: 30-JAN-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX 2405
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-790-540A-6

Query Match 90.9%; Score 50; DB 8; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
   |||||
Db 97 ARHNYGSFA 105

RESULT 3
US-08-791-391A-2
; Sequence 2, Application US/08791391A
; Patent No. US20010016645A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-791-391A-2

Query Match 90.9%; Score 50; DB 8; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
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Db 97 ARHNYGSFA 105

RESULT 4
US-08-791-391A-6
; Sequence 6, Application US/08791391A
; Patent No. US20010016645A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-791-391A-6

Query Match 90.9%; Score 50; DB 8; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/791,391A
FILING DATE: 30-JAN-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX 1482
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-791-391A-2

Query Match 90.9%; Score 50; DB 8; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
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Db 97 ARHNYGSFA 105

RESULT 4
US-08-791-391A-6
; Sequence 6, Application US/08791391A
; Patent No. US20010016645A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-791-391A-6

Query Match 90.9%; Score 50; DB 8; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
   |||||
Db 97 ARHNYGSFA 105

RESULT 4
US-08-791-391A-6
; Sequence 6, Application US/08791391A
; Patent No. US20010016645A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-791-391A-6

Query Match 90.9%; Score 50; DB 8; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Query Match 90.9%; Score 50; DB 8; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
Db 97 ARHNYGSFA 105
|||||

RESULT 5

US-08-677-599B-22
; Sequence 22, Application US/08677599B
; Patent No. US2002015117A1
; GENERAL INFORMATION:
; APPLICANT: Sucia-Foca, Nicole
; TITLE OF INVENTION: METHODS FOR DETECTING ORGAN ALLOGRAFT
; TITLE OF INVENTION: REJECTION AND USES THEREOF
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/677,599B
; FILING DATE: 08-JUL-1996
; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq., John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 50161-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212/278/0400
; TELEFAX: 212/391/0525

; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-677-599B-22

Query Match 65.5%; Score 36; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYG 6
Db 9 ARHNYG 14
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RESULT 6

US-09-764-853-432
; Sequence 432, Application US/09764853
; Patent No. US20020090672A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJ206
; CURRENT APPLICATION NUMBER: US/09/764,853
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 939
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 432
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-853-432

Query Match 65.5%; Score 36; DB 10; Length 101;
Best Local Similarity 85.7%; Pred. No. 2.2;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 64 RHNYSSF 70
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RESULT 7

US-09-839-884-40
; Sequence 40, Application US/09839884
; Patent No. US20020076739A1
; GENERAL INFORMATION:
; APPLICANT: Aebersold, Rudolf H.
; APPLICANT: Gelb, Michael H.
; APPLICANT: Gygi, Steven
; APPLICANT: Scott, C R
; APPLICANT: Turecek, Frantisek
; APPLICANT: Gerber, Scott A
; APPLICANT: Rist, Beate
; TITLE OF INVENTION: Rapid Quantitative Analysis of Proteins or Protein
; TITLE OF INVENTION: Function in Complex Mixture
; FILE REFERENCE: 64-98A
; CURRENT APPLICATION NUMBER: US/09/839,884
; CURRENT FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: 09/383,062
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 60/097,788
; PRIOR FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40
; LENGTH: 30
; TYPE: PRT
; ORGANISM: yeast
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (2)
; OTHER INFORMATION: C at position 2 is ICAT-labeled cysteinyl residue.
US-09-839-884-40

Query Match 61.8%; Score 34; DB 10; Length 30;
Best Local Similarity 83.3%; Pred. No. 1.5;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
Db 10 HNYGAF 15
|||||

RESULT 8

US-09-415-540-5
; Sequence 5, Application US/09415540
; Patent No. US20010010911A1
; GENERAL INFORMATION:
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: A NOVEL HUMAN PYROPHOSPHATASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/415,540
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/741,437
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0148 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 855-0555
TELEFAX: (415) 845-4166
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 287 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 4199
US-09-415-540-5

Query Match 61.8%; Score 34; DB 10; Length 287;
Best Local Similarity 83.3%; Pred. No. 16;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
DB 92 HNYGAF 97

RESULT 9
US-08-677-599B-21
Sequence 21, Application US/08677599B
Patent No. US20020155117A1
GENERAL INFORMATION:
APPLICANT: Sucia-Foca, Nicole
TITLE OF INVENTION: METHODS FOR DETECTING ORGAN ALLOGRAFT
TITLE OF INVENTION: REJECTION AND USES THEREOF
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/677,599B
FILING DATE: 08-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White Esq., John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 50161-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212/278/0400
TELEFAX: 212/391/0525
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:

LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-677-599B-21

Query Match 60.0%; Score 33; DB 1; Length 14;
Best Local Similarity 83.3%; Pred. No. 1;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYG 6
DB 9 SRHNYG 14

RESULT 10
US-08-677-599B-11
Sequence 11, Application US/08677599B
Patent No. US20020155117A1
GENERAL INFORMATION:
APPLICANT: Sucia-Foca, Nicole
TITLE OF INVENTION: METHODS FOR DETECTING ORGAN ALLOGRAFT
TITLE OF INVENTION: REJECTION AND USES THEREOF
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/677,599B
FILING DATE: 08-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White Esq., John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 50161-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212/278/0400
TELEFAX: 212/391/0525
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-677-599B-11

Query Match 58.2%; Score 32; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHNYG 6
DB 10 RHNYG 14

RESULT 11
US-08-677-599B-12
Sequence 12, Application US/08677599B
Patent No. US20020155117A1
GENERAL INFORMATION:
APPLICANT: Sucia-Foca, Nicole
TITLE OF INVENTION: METHODS FOR DETECTING ORGAN ALLOGRAFT


```

; TITLE OF INVENTION: REJECTION AND USES THEREOF
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/677,599B
; FILING DATE: 08-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq., John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 50161-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212/278/0400
; TELEFAX: 212/391/0525
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-677-599B-12

Query Match 58.2%; Score 32; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHYNG 6
DB 10 RHYNG 14

RESULT 12
US-08-677-599B-13
; Sequence 13, Application US/08677599B
; Patent No. US2002015117A1
; GENERAL INFORMATION:
; APPLICANT: Sucia-Foca, Nicole
; TITLE OF INVENTION: METHODS FOR DETECTING ORGAN ALLOGRAFT
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/677,599B
; FILING DATE: 08-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq., John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 50161-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212/278/0400
; TELEFAX: 212/391/0525
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-677-599B-14

Query Match 58.2%; Score 32; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHYNG 6
DB 10 RHYNG 14

RESULT 13
US-08-677-599B-14
; Sequence 14, Application US/08677599B
; Patent No. US2002015117A1
; GENERAL INFORMATION:
; APPLICANT: Sucia-Foca, Nicole
; TITLE OF INVENTION: METHODS FOR DETECTING ORGAN ALLOGRAFT
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/677,599B
; FILING DATE: 08-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq., John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 50161-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212/278/0400
; TELEFAX: 212/391/0525
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-677-599B-14

Query Match 58.2%; Score 32; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHYNG 6
DB 10 RHYNG 14

RESULT 14
US-08-677-599B-15
; Sequence 15, Application US/08677599B

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; TELEPHONE: 212/278/0400
; TELEFAX: 212/391/0525
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-677-599B-13

Query Match 58.2%; Score 32; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHYNG 6
DB 10 RHYNG 14

RESULT 13
US-08-677-599B-14
; Sequence 14, Application US/08677599B
; Patent No. US2002015117A1
; GENERAL INFORMATION:
; APPLICANT: Sucia-Foca, Nicole
; TITLE OF INVENTION: METHODS FOR DETECTING ORGAN ALLOGRAFT
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/677,599B
; FILING DATE: 08-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq., John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 50161-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212/278/0400
; TELEFAX: 212/391/0525
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-677-599B-14

Query Match 58.2%; Score 32; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHYNG 6
DB 10 RHYNG 14

RESULT 14
US-08-677-599B-15
; Sequence 15, Application US/08677599B

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Patent No. US20020155117A1
GENERAL INFORMATION:
APPLICANT: Sucia-Foca, Nicole
TITLE OF INVENTION: METHODS FOR DETECTING ORGAN ALLOGRAFT
REJECTION AND USES THEREOF
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/677,599B
FILING DATE: 08-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White Esq., John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 50161-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212/278/0400
TELEFAX: 212/391/0525
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-677-599B-15

Query Match 58.2%; Score 32; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHNYG 6
|||||
Db 10 RHNYG 14

RESULT 15
US-08-677-599B-16
Sequence 16, Application US/08677599B
Patent No. US20020155117A1
GENERAL INFORMATION:
APPLICANT: Sucia-Foca, Nicole
TITLE OF INVENTION: METHODS FOR DETECTING ORGAN ALLOGRAFT
REJECTION AND USES THEREOF
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/677,599B
FILING DATE: 08-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: White Esq., John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 50161-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212/278/0400
TELEFAX: 212/391/0525
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-677-599B-16

Query Match 58.2%; Score 32; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHNYG 6
|||||
Db 10 RHNYG 14

Search completed: November 18, 2002, 18:45:17
Job time : 1.96078 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:01 ; Search time 4.2402 Seconds
(without alignments)
69.390 Million cell updates/sec

Title: US-09-016-061-76
Perfect score: 55
Sequence: 1 ARHNYGSPAM 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	41	74.5	119	3	US-08-767-128-6
2	36	65.5	94	3	US-09-147-550-14
3	36	65.5	94	3	US-09-147-550-45
4	36	65.5	94	3	US-09-147-550-48
5	36	65.5	94	3	US-09-147-550-77
6	36	65.5	94	3	US-09-147-550-84
7	36	65.5	94	3	US-09-147-550-90
8	36	65.5	94	3	US-09-147-550-101
9	36	65.5	94	4	US-09-557-917-14
10	36	65.5	94	4	US-09-557-917-45
11	36	65.5	94	4	US-09-557-917-48
12	36	65.5	94	4	US-09-557-917-77
13	36	65.5	94	4	US-09-557-917-84
14	36	65.5	94	4	US-09-557-917-90
15	36	65.5	94	4	US-09-557-917-101
16	35	63.6	191	4	US-09-443-041A-24
17	35	63.6	236	4	US-09-443-041A-30
18	35	63.6	260	4	US-09-443-041A-10
19	35	63.6	261	4	US-09-443-041A-26
20	35	63.6	269	4	US-09-443-041A-28
21	35	63.6	271	4	US-09-443-041A-32
22	35	63.6	271	4	US-09-443-041A-33
23	34	61.8	286	2	US-08-809-267-3
24	34	61.8	286	5	PCT-US95-13662A-3
25	34	61.8	287	2	US-08-741-437-5
26	34	61.8	287	2	US-09-134-593-5
27	32	58.2	15	1	US-08-618-464-7

28	32	58.2	15	4	US-09-107-615-7	Sequence 7, Appl
29	32	58.2	16	4	US-09-181-896-2	Sequence 2, Appl
30	32	58.2	25	2	US-08-480-150-44	Sequence 44, Appl
31	32	58.2	25	2	US-08-488-379-44	Sequence 44, Appl
32	32	58.2	25	5	PCT-US93-07545-44	Sequence 44, Appl
33	32	58.2	36	1	US-08-053-131-84	Sequence 84, Appl
34	32	58.2	36	1	US-08-645-641-84	Sequence 84, Appl
35	32	58.2	36	1	US-07-853-408B-84	Sequence 84, Appl
36	32	58.2	36	2	US-08-096-762-84	Sequence 84, Appl
37	32	58.2	36	2	US-08-308-865-84	Sequence 84, Appl
38	32	58.2	36	4	US-09-042-353-281	Sequence 281, App
39	32	58.2	36	4	US-08-758-417A-129	Sequence 129, App
40	32	58.2	36	5	PCT-US92-10983-84	Sequence 84, Appl
41	32	58.2	80	1	US-08-264-250A-1	Sequence 1, Appl
42	32	58.2	89	1	US-08-025-038-30	Sequence 30, Appl
43	32	58.2	89	1	US-08-039-137-17	Sequence 17, Appl
44	32	58.2	90	2	US-08-485-133-23	Sequence 23, Appl
45	32	58.2	94	3	US-09-147-550-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-08-767-128-6
; Sequence 6, Application US/08767128
; Patent No. 6111079
; GENERAL INFORMATION:
; APPLICANT: WYLIE, DWANE E.
; APPLICANT: LOPEZ, OSVALDO
; APPLICANT: MURRAY, PETER JOSEPH
; APPLICANT: GOEBEL, PETER
; TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
; TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
; STREET: 3100 No. 6111079west Center, 90 South Seventh St
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/767,128
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE: 04-DEC-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/09258
; FILING DATE: 05-JUN-1996
; APPLICATION DATA:
; APPLICATION NUMBER: 08/541,373
; FILING DATE: 10-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/462,798
; FILING DATE: 05-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G.
; REGISTRATION NUMBER: 35,093
; REFERENCE/DOCKET NUMBER: 8648.49USF1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/371-5278
; TELEFAX: 612/332-9081
; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: Internal
; ORIGINAL SOURCE:
US-08-767-128-6

Query Match 74.5%; Score 41; DB 3; Length 119;
Best Local Similarity 70.0%; Pred. No. 2.1;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNGSFAM 10
|||:|:|
Db 97 ARHGYGYAM 106

RESULT 2

US-09-147-550-14
; Sequence 14, Application US/09147550
; Patent No. 6090540

; GENERAL INFORMATION:

; APPLICANT: Aida, Yoko

; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550

; CURRENT FILING DATE: 1999-04-23

; EARLIER FILING DATE: 1997-07-17

; EARLIER APPLICATION NUMBER: JP 8-190933

; EARLIER FILING DATE: 1996-07-19

; EARLIER FILING DATE: 1997-03-28

; NUMBER OF SEQ ID NOS: 115

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 14

; LENGTH: 94

; TYPE: PRT

; ORGANISM: BOVINE

US-09-147-550-14

Query Match 65.5%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
|||||
Db 80 RHNYGVF 86

RESULT 3

US-09-147-550-45

; Sequence 45, Application US/09147550
; Patent No. 6090540

; GENERAL INFORMATION:

; APPLICANT: Aida, Yoko

; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550

; CURRENT FILING DATE: 1999-04-23

; EARLIER FILING DATE: 1997-07-17

; EARLIER APPLICATION NUMBER: JP 8-190933

; EARLIER FILING DATE: 1996-07-19

; EARLIER FILING DATE: 1997-03-28

; NUMBER OF SEQ ID NOS: 115

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-45

Query Match 65.5%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
|||||
Db 80 RHNYGVF 86

RESULT 4

US-09-147-550-48

; Sequence 48, Application US/09147550
; Patent No. 6090540

; GENERAL INFORMATION:

; APPLICANT: Aida, Yoko

; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550

; CURRENT FILING DATE: 1999-04-23

; EARLIER FILING DATE: 1997-07-17

; EARLIER APPLICATION NUMBER: JP 8-190933

; EARLIER FILING DATE: 1996-07-19

; EARLIER FILING DATE: 1997-03-28

; NUMBER OF SEQ ID NOS: 115

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 48

; LENGTH: 94

; TYPE: PRT

; ORGANISM: BOVINE

US-09-147-550-48

Query Match 65.5%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
|||||
Db 80 RHNYGVF 86

RESULT 5

US-09-147-550-77

; Sequence 77, Application US/09147550
; Patent No. 6090540

; GENERAL INFORMATION:

; APPLICANT: Aida, Yoko

; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550

; CURRENT FILING DATE: 1999-04-23

; EARLIER FILING DATE: 1997-07-17

; EARLIER APPLICATION NUMBER: JP 8-190933

; EARLIER FILING DATE: 1996-07-19

; EARLIER FILING DATE: 1997-03-28

; NUMBER OF SEQ ID NOS: 115

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 77

; LENGTH: 94

; TYPE: PRT

; ORGANISM: BOVINE

US-09-147-550-77

Query Match 65.5%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
| | | | |
DB 80 RHNYGVF 86

RESULT 6

US-09-147-550-84
; Sequence 84, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; EARLIER FILING DATE: 1999-04-23
; EARLIER FILING DATE: 1997-07-17
; EARLIER FILING DATE: 1997-07-17
; EARLIER FILING DATE: 1996-07-19
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-84

Query Match 65.5%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
| | | | |
DB 80 RHNYGVF 86

RESULT 7

US-09-147-550-90
; Sequence 90, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; EARLIER FILING DATE: 1999-04-23
; EARLIER FILING DATE: 1997-07-17
; EARLIER FILING DATE: 1997-07-17
; EARLIER FILING DATE: 1996-07-19
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 90
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-90

Query Match 65.5%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
| | | | |
DB 80 RHNYGVF 86

RESULT 8
US-09-147-550-101

; Sequence 101, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; EARLIER FILING DATE: 1999-04-23
; EARLIER FILING DATE: 1997-07-17
; EARLIER FILING DATE: 1996-07-19
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-101

Query Match 65.5%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
| | | | |
DB 80 RHNYGVF 86

RESULT 9

US-09-557-917-14
; Sequence 14, Application US/09557917
; Patent No. 6284457
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR FILING DATE: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR FILING DATE: 1996-07-19
; PRIOR FILING DATE: 1996-07-19
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-14

Query Match 65.5%; Score 36; DB 4; Length 94;
Best Local Similarity 85.7%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
| | | | |

Db 80 RHNYGVF 86

```
RESULT 10
US-09-557-917-45
; Sequence 45, Application US/09557917
; Patent No. 6284457
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-45
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Query Match 65.5%; Score 36; DB 4; Length 94;
Best Local Similarity 85.7%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
| | | | |
Db 80 RHNYGVF 86

```
RESULT 11
US-09-557-917-48
; Sequence 48, Application US/09557917
; Patent No. 6284457
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-48
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Query Match 65.5%; Score 36; DB 4; Length 94;
Best Local Similarity 85.7%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
| | | | |
Db 80 RHNYGVF 86

```
RESULT 12
US-09-557-917-77
; Sequence 77, Application US/09557917
; Patent No. 6284457
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 77
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-77
```

Query Match 65.5%; Score 36; DB 4; Length 94;
Best Local Similarity 85.7%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
| | | | |
Db 80 RHNYGVF 86

```
RESULT 13
US-09-557-917-84
; Sequence 84, Application US/09557917
; Patent No. 6284457
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-84
```

Query Match 65.5%; Score 36; DB 4; Length 94;
Best Local Similarity 85.7%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
| | | | |
Db 80 RHNYGVF 86

Search completed: November 18, 2002, 17:43:38
Job time : 4.2402 secs

RESULT 14
US-09-557-917-90
; Sequence 90, Application US/09557917
; Patent No. 6284457
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 90
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-90

Query Match 65.5%; Score 36; DB 4; Length 94;
Best Local Similarity 85.7%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
| | | | |
Db 80 RHNYGVF 86

RESULT 15
US-09-557-917-101
; Sequence 101, Application US/09557917
; Patent No. 6284457
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-101

Query Match 65.5%; Score 36; DB 4; Length 94;
Best Local Similarity 85.7%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
| | | | |
Db 80 RHNYGVF 86

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:01 ; Search time 4.90196 Seconds
(without alignments)
196.114 Million cell updates/sec

Title: US-09-016-061-80
Perfect score: 54
Sequence: 1 ARHNYGSFAA 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR.73:**
1: piri:**
2: pir2:**
3: pir3:**
4: pir4:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	79.6	446	2	hypothetical prote
2	36	66.7	82	2	Major Histocompati
3	36	66.7	89	2	MHC class II histo
4	36	66.7	89	2	MHC class II histo
5	36	66.7	89	2	MHC class II histo
6	36	66.7	225	2	MHC class II OVAR-
7	35	64.8	195	2	conserved hypothet
8	35	64.8	347	2	phosphatidylcholin
9	34	63.0	108	2	Ig heavy chain v r
10	34	63.0	110	2	Ig heavy chain v r
11	34	63.0	113	2	Ig heavy chain v r
12	34	63.0	210	1	conserved hypothet
13	34	63.0	275	2	translation initia
14	34	63.0	275	2	probable translati
15	34	63.0	287	1	inorganic diphosph
16	34	63.0	287	1	inorganic diphosph
17	34	63.0	638	2	conserved hypothet
18	34	63.0	723	2	outer membrane pro
19	34	63.0	1052	2	conserved hypothet
20	34	63.0	1341	2	hypothetical prote
21	33	61.1	65	2	hypothetical prote
22	33	61.1	80	2	MHC class II DR-be
23	33	61.1	80	2	MHC HLA-DR beta-1
24	33	61.1	81	2	HLA DRB1*1202 - hu
25	33	61.1	85	2	MHC class II DR-be
26	33	61.1	89	2	MHC class II DR-be
27	33	61.1	89	2	MHC class II histo
28	33	61.1	89	2	MHC class II histo
29	33	61.1	123	2	MHC class II histo

30	33	61.1	167	2	T16454
31	33	61.1	200	2	D32526
32	33	61.1	220	2	T46055
33	33	61.1	237	2	C27060
34	33	61.1	266	2	I54287
35	33	61.1	266	2	A27618
36	33	61.1	266	2	I54295
37	33	61.1	279	2	T05421
38	33	61.1	360	2	S48566
39	33	61.1	362	2	B83963
40	33	61.1	383	2	S56179
41	33	61.1	448	1	A60003
42	33	61.1	470	2	H71667
43	33	61.1	473	2	D70405
44	33	61.1	479	2	E87135
45	33	61.1	662	2	H95934

hypothetical prote
class II histocomp
hypothetical prote
class II histocomp
gene HLA-DRB1 prot
class II histocomp
lymphocyte antigen
hypothetical prote
hypothetical prote
secreted glycoprot
nucleocapsid prote
glutamate-ERNA lig
glutamate-ERNA lig
probable-exported
probable MPAl faml

ALIGNMENTS

RESULT 1

T19625
hypothetical protein C31H5.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
C:Accession: T19625
R:Kershaw, J.
submitted to the EMBL Data Library, April 1997
A:Reference number: Z19153
A:Accession: T19625
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-446 <WIL>
A:Cross-references: EMBL:Z93778; PIDN:CAB07846.1; GSPDB:GN00019; CESP:C31H5.6
A:Experimental source: clone C31H5
C:Genetics:
A:Gene: CESP:C31H5.6
A:Map position: 1
A:Introns: 49/2; 85/1; 120/2; 183/3; 218/3; 255/3; 285/2; 331/3; 360/3
C:Superfamily: Caenorhabditis elegans hypothetical protein W03D8.8

Query Match 79.6%; Score 43; DB 2; Length 446;
Best Local Similarity 88.9%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHYNGSFAA 10
Db 51 RHYNGSHAA 59

RESULT 2

I51106
Major Histocompatibility Complex class IIB - ring-necked pheasant (fragment)
C:Species: Phasianus colchicus (ring-necked pheasant)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 23-Jul-1999
C:Accession: I51106
R:Witzell, H.; von Schantz, T.; Zoorob, R.; Auffray, C.
Immunogenetics 39, 395-403, 1994
A:Title: Molecular characterization of three Mhc class II B haplotypes in the ring-ne
A:Reference number: I51103; MUID:94245280; PMID:7910588
A:Accession: I51106
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-82 <WIT>
A:Cross-references: EMBL:X75406; NID:g496926; PIDN:CAA53160.1; PID:g496927
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 66.7%; Score 36; DB 2; Length 82;
Best Local Similarity 85.7%; Pred. No. 7.1;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHYNGSF 8

Db 75 RHNYGVF 81
|||||

RESULT 3

S38688
MHC class II histocompatibility antigen HLA-DR-08 beta chain - northern lesser bushbaby
C:Species: Galago senegalensis (northern lesser bushbaby)
C:Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 19-May-2000
C:Accession: S38688
R:Figueroa, F.; O'Huigin, C.; Tichy, H.; Klein, J.
submitted to the EMBL Data Library, November 1993
A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduced from
A:Reference number: S38676
A:Accession: S38688
A:Molecule type: DNA
A:Residues: 1-89 <FIG>
A:Cross-references: EMBL:Z27158
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 66.7%; Score 36; DB 2; Length 89;
Best Local Similarity 85.7%; Pred. No. 7.7;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
|||||

Db 75 RHNYGVF 81

RESULT 4

S38683
MHC class II histocompatibility antigen HLA-DR-03 beta chain - northern lesser bushbaby
C:Species: Galago senegalensis (northern lesser bushbaby)
C:Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 19-May-2000
C:Accession: S38683
R:Figueroa, F.; O'Huigin, C.; Tichy, H.; Klein, J.
submitted to the EMBL Data Library, November 1993
A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduced from
A:Reference number: S38676
A:Accession: S38683
A:Molecule type: DNA
A:Residues: 1-89 <FIG>
A:Cross-references: EMBL:Z27153
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 66.7%; Score 36; DB 2; Length 89;
Best Local Similarity 85.7%; Pred. No. 7.7;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
|||||

Db 75 RHNYGVF 81

RESULT 5

S38684
MHC class II histocompatibility antigen HLA-DR-04 beta chain - northern lesser bushbaby
C:Species: Galago senegalensis (northern lesser bushbaby)
C:Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 19-May-2000
C:Accession: S38684
R:Figueroa, F.; O'Huigin, C.; Tichy, H.; Klein, J.
submitted to the EMBL Data Library, November 1993
A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduced from
A:Reference number: S38676
A:Accession: S38684
A:Molecule type: DNA
A:Residues: 1-89 <FIG>
A:Cross-references: EMBL:Z27154
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 66.7%; Score 36; DB 2; Length 89;
Best Local Similarity 85.7%; Pred. No. 7.7;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
|||||

Db 75 RHNYGVF 81

RESULT 6

I47095
MHC class II OVAR-DR-beta-3 - sheep (fragment)
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 15-Oct-1996 #sequence_revision 15-Oct-1996 #text_change 21-Jan-2000
C:Accession: I47095
R:Fabbs, S.A.; Maddox, J.F.; Gogolin-Evans, K.J.; Baker, L.; Wu, M.J.; Brandon, M.R.
Anim. Genet. 24, 249-255, 1993
A:Title: Isolation, characterization and evolution of ovine major histocompatibility
A:Reference number: I47075; MUID:94057592; PMID:7902039
A:Accession: I47095
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-225 <FAB>
A:Cross-references: GB:L04790; NID:g458880; PIDN:AAAI6562.1; PID:g458881
C:Genetics:
C:Gene: OVAR-DRB3
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology
F:98-163/Domain: immunoglobulin homology <IMM>

Query Match 66.7%; Score 36; DB 2; Length 225;
Best Local Similarity 85.7%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
|||||

Db 68 RHNYGVF 74

RESULT 7

G86742
conserved hypothetical protein yjgF [Imported] - Lactococcus lactis subsp. lactis (st
C:Species: Lactococcus lactis subsp. lactis
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 17-May-2002
C:Accession: G86742
R:Boletín, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Eh
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis
A:Reference number: A86625; MUID:21235186; PMID:11337471
A:Accession: G86742
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-195 <STO>
A:Cross-references: GB:AE005176; PID:g12723879; PIDN:AAK05041.1; GSPDB:GN00146
A:Experimental source: strain IL1403
C:Genetics:
C:Gene: yjgF
C:Superfamily: hypothetical protein b1011

Query Match 64.8%; Score 35; DB 2; Length 195;
Best Local Similarity 62.5%; Pred. No. 26;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSF 8
|:|:|:|

Db 103 AKHNGAF 110

RESULT 8

S43771
phosphatidylcholine desaturase (EC 1.3.1.35) - Synechococcus sp. (strain PCC 7002)
N:Alternate names: Delta-12 desaturase; fatty acid desaturase (EC 1.14.99.-) [misiden
C:Species: Synechococcus sp.
A:Variety: PCC 7002
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-2000
C:Accession: S43771
R:Sakamoto, T.; Wada, H.; Nishida, I.; Ohmori, M.; Murata, N.

Plant Mol. Biol. 24, 643-650, 1994
A:Title: Identification of conserved domains in the Delta-12 desaturases of cyanobacteria
A:Reference number: S43770; MUID:94207189; PMID:8155883
A:Accession: S43771

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-347 <SAK>
A:Cross-references: GB:D13779; NID:g488510; PIDN:BAA02922.1; PID:g488511
C:Superfamily: omega-3 fatty acid desaturase
C:Keywords: oxidoreductase

Query Match 64.8%; Score 35; DB 2; Length 347;
Best Local Similarity 77.8%; Pred. No. 45;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSA 9
I I I I I I I

Db 334 AEHNYISFA 342

RESULT 9

S26316

Ig heavy chain V region - mouse

C:Species: Mus musculus (house mouse)

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000

C:Accession: S26316

R:Stark, S.E.; Caton, A.J.

J. Exp. Med. 174, 613-624, 1991

A:Title: Antibodies that are specific for a single amino acid interchange in a protein e

A:Reference number: S26309; MUID:91341421; PMID:1908510

A:Accession: S26316

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-108 <STA>

A:Cross-references: EMBL:X59190; NID:g52066; PIDN:CAAA1900.1; PID:g1334035

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:2-85/Domain: immunoglobulin homology <IMM>

Query Match 63.0%; Score 34; DB 2; Length 108;

Best Local Similarity 66.7%; Pred. No. 23;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSA 9

I I I I I I I

Db 84 ARGNYGNYA 92

RESULT 10

S26317

Ig heavy chain V region - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 21-Jan-2000

C:Accession: S26317

R:Stark, S.E.; Caton, A.J.

J. Exp. Med. 174, 613-624, 1991

A:Title: Antibodies that are specific for a single amino acid interchange in a protein e

A:Reference number: S26309; MUID:91341421; PMID:1908510

A:Accession: S26317

A:Molecule type: mRNA

A:Residues: 1-110 <STA>

A:Cross-references: EMBL:X59186

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:4-87/Domain: immunoglobulin homology <IMM>

Query Match 63.0%; Score 34; DB 2; Length 110;

Best Local Similarity 66.7%; Pred. No. 23;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSA 9

I I I I I I I

Db 86 ARGNYGNYA 94

RESULT 11

S26468

Ig heavy chain V region - mouse

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C:Accession: S26468

R:Kavaler, J.

submitted to the EMBL Data Library, April 1991

A:Reference number: S26459

A:Accession: S26468

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-113 <KAV>

A:Cross-references: EMBL:X59107; NID:g51944; PIDN:CAA41833.1; PID:g51945

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:11-94/Domain: immunoglobulin homology <IMM>

Query Match 63.0%; Score 34; DB 2; Length 113;

Best Local Similarity 60.0%; Pred. No. 24;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSFAA 10

I I I I I I I

Db 93 ARHPYGNYYA 102

RESULT 12

B69265

conserved hypothetical protein AF0122 - Archaeoglobus fulgidus

C:Species: Archaeoglobus fulgidus

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000

C:Accession: B69265

R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod

.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E

Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.

Nature 390, 364-370, 1997

A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes,

Smith, H.O.; Woese, C.R.; Venter, J.C.

A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch

A:Reference number: A69250; MUID:98049343; PMID:9389475

A:Accession: B69265

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-210 <KLE>

A:Cross-references: GB:AE001098; GB:AE000782; NID:g2689421; PIDN:AAB91117.1; PID:g265

C:Superfamily: conserved hypothetical protein AF0119

Query Match 63.0%; Score 34; DB 1; Length 210;

Best Local Similarity 85.7%; Pred. No. 43;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8

I I I I I I I

Db 128 RHAYGSF 134

RESULT 13

G75130

translation initiation factor aif-2, subunit alpha (aif2a) PAB0568 - Pyrococcus aby

C:Species: Pyrococcus abyssi

C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000

C:Accession: G75130

R:anonymous, Genoscope

submitted to the EMBL Data Library, July 1999

A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome s

A:Reference number: A75001

A:Accession: G75130

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-275 <KAW>

A:Cross-references: GB:AJ248285; GB:AL096836; NID:g5458067; PIDN:CAB49760.1; PID:g545827
 A:Experimental source: strain Orsay
 C:Genetics:
 A:Gene: alf2A; PAB0568
 C:Superfamily: translation initiation factor eIF-2 alpha chain

Query Match 63.0%; Score 34; DB 2; Length 275;
 Best Local Similarity 83.3%; Pred. No. 56;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 HNYGSF 8
 Db 23 HNYGAF 28
 |||||

RESULT 14
 D71087
 probable translation initiation factor eIF-2 alpha chain - Pyrococcus horikoshii
 C:Species: Pyrococcus horikoshii
 C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000
 C:Accession: D71087
 R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin
 M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kishida, N.; Oguchi
 DNA Res. 5, 55-76, 1998
 A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
 A:Reference number: A71000; MUID:98344137; PMID:9679194
 C:Accession: D71087
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-275 <RAW>
 A:Cross-references: GB:AP000004; NID:g3236131; PIDN:BAA30058.1; PID:g3257375
 A:Experimental source: strain OT3
 A:Note: this accession replaces an interim accession for a sequence replaced by GenBank
 C:Genetics:
 A:Gene: PR0961
 C:Superfamily: translation initiation factor eIF-2 alpha chain

Query Match 63.0%; Score 34; DB 2; Length 275;
 Best Local Similarity 83.3%; Pred. No. 56;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 HNYGSF 8
 Db 23 HNYGAF 28
 |||||

RESULT 15
 FWBY
 inorganic diphosphatase (EC 3.6.1.1) - yeast (Saccharomyces cerevisiae)
 N:Alternate names: protein YBR011c; protein YBR0202; pyrophosphate phosphohydrolase
 C:Species: Saccharomyces cerevisiae
 C:Date: 30-Nov-1980 #sequence_revision 09-Sep-1994 #text_change 03-Jun-2002
 C:Accession: S45864; S07679; A01014; S29189
 R:Entian, K.D.; Koetter, P.; Rose, M.; Li, Z.; Thermann, R.; Brendel, M.; Baur, A.; Bole
 submitted to the Protein Sequence Database, August 1994
 A:Reference number: S45862
 A:Accession: S45864
 A:Molecule type: DNA
 A:Residues: 1-287 <ENT>
 A:Cross-references: EMBL:235880; NID:g536205; PIDN:CAA84949.1; PID:g536206; GSPDB:GN000
 A:Experimental source: strain S288C
 R:Kolakowski Jr., L.F.; Schloesser, M.; Cooperman, B.S.
 Nucleic Acids Res. 16, 10441-10452, 1988
 A:Title: Cloning, molecular characterization and chromosome localization of the inorganic
 A:Reference number: S07679; MUID:89083474; PMID:2849749
 A:Accession: S07679
 A:Molecule type: DNA
 A:Residues: 1-266, 'L', 268-287 <KOL>
 A:Cross-references: EMBL:X13253; NID:g4198; PIDN:CAA31629.1; PID:g4199
 R:Cohen, S.A.; Sterner, R.; Keim, P.S.; Heintz, R.L.
 J. Biol. Chem. 253, 889-897, 1978
 A:Title: Covalent structural analysis of yeast inorganic pyrophosphatase.
 A:Reference number: A92241; MUID:78087552; PMID:340461

A:Accession: A01014
 A:Molecule type: protein
 A:Residues: 2-40, 'D', 42-71, 'N', 73, 75-117, 'N', 119-123, 'Q', 125-136, 'E', 138-186, 'D', 188-
 A:Note: this is the final paper in a series
 A:Note: no disulfide bonds are present
 R:Raznikov, A.V.; Sklyankina, V.A.; Avaeva, S.M.
 FEBS Lett. 308, 62-64, 1992
 A:Title: Tyrosine-89 is important for enzymatic activity of S. cerevisiae inorganic p
 A:Reference number: S29189; MUID:92354770; PMID:1322842
 A:Accession: S29189
 A:Molecule type: protein
 A:Residues: 83-105, 'E', 107-112 <RAZ>
 R:Bond, M.W.; Chiu, N.Y.; Cooperman, B.S.
 Biochemistry 19, 94-102, 1980
 A:Title: Identification of an arginine important for enzymatic activity within the co
 A:Reference number: A90443
 A:Contents: annotation; active site
 C:Genetics:
 A:Gene: SGD:IPPL; PPA; MIPS:YBR011c
 A:Cross-references: SGD:S0000215; MIPS:YBR011c
 A:Map position: 2R
 C:Function:
 A:Description: catalyzes hydrolysis of pyrophosphate to orthophosphate
 A:Note: requires divalent metal cation
 C:Superfamily: inorganic pyrophosphatase
 C:Keywords: homodimer; hydrolase
 F:2-287/Product: inorganic pyrophosphate #status experimental <MAT>
 F:79/Binding site: pyrophosphate (Arg) #status experimental

Query Match 63.0%; Score 34; DB 1; Length 287;
 Best Local Similarity 83.3%; Pred. No. 58;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 HNYGSF 8
 Db 92 HNYGAF 97
 |||||

Search completed: November 18, 2002, 17:47:08
 Job time : 5.90196 secs

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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:00 ; Search time 2.45098 Seconds
(without alignments)
169.223 Million cell updates/sec

Title: US-09-016-061-80
Perfect score: 54
Sequence: 1 ARHNYGSPAA 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	70.4	323	1	CCSA_LOTJA
2	34	63.0	275	1	IF2A_PVRAB
3	34	63.0	275	1	IF2A_PVRHO
4	34	63.0	284	1	IPYR_PICPA
5	34	63.0	286	1	IPYR_KIULA
6	34	63.0	286	1	IPYR_YEAST
7	34	63.0	606	1	Y475_ARATH
8	33	61.1	65	1	CCSA_PEA
9	33	61.1	328	1	CCSA_ARATH
10	33	61.1	448	1	NCAP_CVHOC
11	33	61.1	470	1	SYE2_RICPR
12	33	61.1	473	1	SYE2_AQUAE
13	33	61.1	682	1	VG50_BPML5
14	33	61.1	789	1	ACOX_YEAST
15	33	61.1	1386	1	RPOD_MARPO
16	32	59.3	65	1	CCSA_OENBE
17	32	59.3	98	1	VG7_BPPH2
18	32	59.3	98	1	VG7_BPPZA
19	32	59.3	196	1	WBBJ_EGOLI
20	32	59.3	198	1	HB2G_HUMAN
21	32	59.3	266	1	HB2A_HUMAN
22	32	59.3	266	1	HB2B_HUMAN
23	32	59.3	266	1	HB2C_HUMAN
24	32	59.3	266	1	HB2D_CANFA
25	32	59.3	266	1	HB2D_HUMAN
26	32	59.3	266	1	HB2E_HUMAN
27	32	59.3	266	1	HB2F_HUMAN
28	32	59.3	266	1	HB2H_HUMAN
29	32	59.3	266	1	HB2I_HUMAN
30	32	59.3	266	1	HB2J_HUMAN
31	32	59.3	305	1	YN45_DEIRA
32	32	59.3	313	1	CCSA_TOBAC
33	32	59.3	319	1	CCSA_OENHO

34	32	59.3	321	1	CCSA_MAIZE	P46659	zea mays	(m
35	32	59.3	321	1	CCSA_ORYSA	P12215	oryza sativ	
36	32	59.3	322	1	CCSA_WHEAT	P58266	triticum ae	
37	32	59.3	323	1	CCSA_SPIOL	Q9mj11	spinacia ol	
38	32	59.3	349	1	PTEL_YEAST	P41903	saccharomyc	
39	32	59.3	385	1	O65B_DROME	P82983	drosophila	
40	32	59.3	464	1	DLDH_MYCTU	O53747	mycobacteri	
41	32	59.3	491	1	SYE_LISIN	Q92f38	listeria in	
42	32	59.3	491	1	SYE_LISMO	Q8vab3	listeria mo	
43	32	59.3	528	1	PR12_YEAST	P20457	saccharomyc	
44	32	59.3	560	1	THS1_HALVO	O30561	halobacteri	
45	32	59.3	597	1	GAN_HUMAN	Q9h2c0	homo sapien	

ALIGNMENTS

RESULT 1
CCSA_LOTJA STANDARD; PRT; 323 AA.
AC Q9BBP4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Cytochrome c biogenesis protein ccsc.
GN CCSA.
OS Lotus japonicus.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae; Lotus.
OX NCBI_TaxID=34305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Accession MG-20;
RX MEDLINE=21082929; PubMed=11214967;
RA Kato T., Kaneko T., Sato S., Nakamura Y., Tabata S.;
RT "Complete structure of the chloroplast genome of a legume, Lotus japonicus.";
RL DNA Res. 7:323-330(2000).
CC -!- FUNCTION: REQUIRED DURING CYTOCHROME BIOGENESIS AT THE STEP OF HEME ATTACHMENT (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CCNF/CYCK/CCL1/NRFE/CCSA FAMILY.
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CC -----
CC EMBL: AP002983; BAB33244.1; -.
DR InterPro: IPR002541; CytC_asm.
DR Pfam: PF01578; CytC_asm; 1.
KW Cytochrome c-type biogenesis; Chloroplast.
SQ SEQUENCE 323 AA; 37185 MW; 5A034E3E2829FE35 CRC64;
Query Match 70.4%; Score 38; DB 1; Length 323;
Best Local Similarity 75.0%; Pred. No. 2.6;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Oy 3 HNYGSPAA 10
|||||
Db 315 HNYGSFTS 322
RESULT 2
ID IF2A_PVRAB STANDARD; PRT; 275 AA.
AC Q9V0E4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Probable translation initiation factor 2 alpha subunit (eIF-2-alpha).
 GN EIF2A OR PAB0568.
 OS Pyrococcus abyssi.
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 OC Pyrococcus.
 OX NCBI_TaxID=29292;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GE5 / Orsay;
 RA Heilig R.;
 RT "Pyrococcus abyssi genome sequence: insights into archaeal chromosome
 structure and evolution.";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: EIF-2 FUNCTIONS IN THE EARLY STEPS OF PROTEIN SYNTHESIS
 CC BY FORMING A TERNARY COMPLEX WITH GTP AND INITIATOR TRNA
 CC (BY SIMILARITY).
 CC -1- SUBUNIT: HETEROTRIMER COMPOSED OF AN ALPHA, A BETA, AND A GAMMA
 CC CHAIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE EIF-2-ALPHA FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 S1 MOTIF DOMAIN.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AJ248285; CAB49760.1; -
 DR HSSP; P05055; LSRO.
 DR InterPro: IPR003029; S1.
 DR Pfam; PF00575; S1; 1.
 DR SMART; SM00316; S1; 1.
 DR PROSITE; PS0126; S1; 1.
 KW Initiation factor; Protein biosynthesis; RNA-binding;
 KW Complete proteome.
 FT DOMAIN 12 83 S1 MOTIF.
 SQ SEQUENCE 275 AA; 31912 MW; B2659F3A49879B4F CRC64;
 Query Match 63.0%; Score 34; DB 1; Length 275;
 Best Local Similarity 83.3%; Pred. No. 14;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 3 HNYGSF 8
 | | | | |
 DB 23 HNYGAF 28
 RESULT 3
 IF2A_PYRHO STANDARD; PRT; 275 AA.
 ID IF2A_PYRHO
 AC 058655;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Probable translation initiation factor 2 alpha subunit (eIF-2-alpha).
 GN EIF2A OR PH0961.
 OS Pyrococcus horikoshii.
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 OC Pyrococcus.
 OX NCBI_TaxID=53953;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=OT3;
 RX MEDLINE=98344137; PubMed=9679194;
 RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
 RA Yamanoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
 RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
 RA Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
 RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
 RA Masuchi Y., Shizuya H., Kikuchi H.;

RT "Complete sequence and gene organization of the genome of a hyper-
 thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
 RL DNA Res. 5:55-76(1998).
 CC -1- FUNCTION: EIF-2 FUNCTIONS IN THE EARLY STEPS OF PROTEIN SYNTHESIS
 CC BY FORMING A TERNARY COMPLEX WITH GTP AND INITIATOR TRNA
 CC (BY SIMILARITY).
 CC -1- SUBUNIT: HETEROTRIMER COMPOSED OF AN ALPHA, A BETA, AND A GAMMA
 CC CHAIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE EIF-2-ALPHA FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 S1 MOTIF DOMAIN.
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 CC -----
 CC EMBL; AP000004; BAA30058.1; -
 DR HSSP; P05055; LSRO.
 DR InterPro: IPR003029; S1.
 DR Pfam; PF00575; S1; 1.
 DR SMART; SM00316; S1; 1.
 DR PROSITE; PS0126; S1; 1.
 KW Initiation factor; Protein biosynthesis; RNA-binding;
 KW Complete proteome.
 FT DOMAIN 12 83 S1 MOTIF.
 SQ SEQUENCE 275 AA; 31980 MW; 6AAAD15F10FFB436 CRC64;
 Query Match 63.0%; Score 34; DB 1; Length 275;
 Best Local Similarity 83.3%; Pred. No. 14;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 3 HNYGSF 8
 | | | | |
 DB 23 HNYGAF 28
 RESULT 4
 IPYR_PICPA STANDARD; PRT; 284 AA.
 ID IPYR_PICPA
 AC 013505;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Inorganic pyrophosphatase (EC 3.6.1.1) (pyrophosphate phospho-
 DE hydrolase) (Ppase).
 GN IPPI.
 OS Pichia pastoris (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Pichia.
 OX NCBI_TaxID=4922;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NREL Y-11430;
 RX MEDLINE=99034033; PubMed=9818724;
 RA Cosano I.C., Alvarez P., Molina M., Nombela C.;
 RT "Cloning and sequence analysis of the Pichia pastoris TRP1, IPPI and
 RT HIS3 genes.";
 RL Yeast 14:861-867(1998).
 CC -1- CATALYTIC ACTIVITY: Diphosphate + H(2)O = 2 phosphate.
 CC -1- COFACTOR: REQUIRES THE PRESENCE OF DIVALENT METAL CATION.
 CC MAGNESIUM CONFERS THE HIGHEST ACTIVITY.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: BELONGS TO THE PPASE FAMILY.
 CC -----
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CC -----
 CC EMBL: AJ001000; CAA04453.1; -
 CC HSSP: P00817; IWGI.
 DR InterPro: IPR001596; Pyrophosphatase.
 DR Pfam: PF00719; Pyrophosphatase; 1.
 DR PROSITE: PS00387; PPASE; 1.
 KW Hydrolase; Magnesium.
 FT INIT_MET 0 BY SIMILARITY.
 FT ACT_SITE 56 PROBABLE.
 FT BINDING 78 INORGANIC PYROPHOSPHATE (BY SIMILARITY).
 SQ SEQUENCE 284 AA; 31937 MW; 3DAD27970D7775D6 CRC64;

Query Match 63.0%; Score 34; DB 1; Length 284;

Best Local Similarity 83.3%; Pred. No. 14;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 HNYGSF 8

Db 91 HNYGAF 96

RESULT 5

ID IPYR_KLUJA STANDARD; PRT; 286 AA.
 AC P13996;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 01-OCT-1994 (Rel. 30, Last annotation update)
 DE Inorganic pyrophosphatase (EC 3.6.1.1) (Pyrophosphate phospho-
 DE hydrolase) (PPase).
 GN IPPI OR IPP.
 OS Kluveromyces lactis (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Kluveromyces.
 OX NCBI_TaxID=28995;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89189093; PubMed=2538971;
 RA Stark M.J.R., Milner J.S.;
 RT "Cloning and analysis of the Kluveromyces lactis TRP1 gene: a
 RT chromosomal locus flanked by genes encoding inorganic pyrophosphatase
 RT and histone H3.";
 RL Yeast 5:35-50(1989).
 RN [2]

RP SIMILARITY TO E.COLI AND YEAST PPASES.

RX MEDLINE=90254161; PubMed=2160278;
 RA Lahti R., Kolakowski L.F. Jr., Heinonen J., Vihinen M., Pohjanoksa K.,
 RA Cooperman B.S.;
 RT "Conservation of functional residues between yeast and E. coli
 RT inorganic pyrophosphatases.";
 RL Biochim. Biophys. Acta 1038:338-345(1990).
 CC -!- CATALYTIC ACTIVITY: Diphosphate + H(2)O = 2 phosphate.
 CC -!- COFACTOR: REQUIRES THE PRESENCE OF DIVALENT METAL CATION.
 CC MAGNESIUM CONFERS THE HIGHEST ACTIVITY.
 CC -!- SUBUNIT: HOMODIMER.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: BELONGS TO THE PPASE FAMILY.

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CC EMBL: X14230; CAA32446.1; -

DR PIR: S07894; PWVKL.

DR HSSP: P00817; IWGI.

DR InterPro: IPR001596; Pyrophosphatase.

DR Pfam: PF00719; Pyrophosphatase; 1.

DR PROSITE: PS00387; PPASE; 1.
 KW Hydrolase; Magnesium.
 FT INIT_MET 0 BY SIMILARITY.
 FT ACT_SITE 56 PROBABLE.
 FT BINDING 78 INORGANIC PYROPHOSPHATE (BY SIMILARITY).
 SQ SEQUENCE 286 AA; 32034 MW; 11647F4ABD916A2F CRC64;

Query Match 63.0%; Score 34; DB 1; Length 286;

Best Local Similarity 83.3%; Pred. No. 15;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 HNYGSF 8

Db 91 HNYGAF 96

RESULT 6

ID IPYR_YEAST STANDARD; PRT; 286 AA.
 AC P00817;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Inorganic pyrophosphatase (EC 3.6.1.1) (Pyrophosphate phospho-
 DE hydrolase) (PPase).
 GN IPPI OR PPAL OR PPA OR YBR011C OR YBR0202.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=X2180;
 RX MEDLINE=89083474; PubMed=2849749;
 RA Kolakowski L.F. Jr., Schloesser M., Cooperman B.S.;
 RT "Cloning, molecular characterization and chromosome localization of
 RT the inorganic pyrophosphatase (PPA) gene from S. cerevisiae.";
 RL Nucleic Acids Res. 16:10441-10452(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C;
 RX Entian K.-D., Koetter P., Rose M., Li Z., Thermann R., Brendel M.,
 RA Baur A., Boles E., Miosga T., Schaeff-Gerstenschlaeger I.,
 RA Zimmermann F.K.;
 RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE.

RX MEDLINE=78087552; PubMed=340461;

RA Cohen S.A., Sterner R., Keim P.S., Heinrikson R.L.;

RT "Covalent structural analysis of yeast inorganic pyrophosphatase.";
 RL J. Biol. Chem. 253:889-897(1978).
 RN [4]

RP SEQUENCE OF 25-35 AND 239-251.

RX STRAIN=S288C;

RX MEDLINE=95203288; PubMed=7895733;

RA Garrels J.I., Fitcher B., Kobayashi R., Latter G.I., Schwender B.,
 RA Volpe T., Warner J.R., McLaughlin C.S.;

RT "Protein identifications for a Saccharomyces cerevisiae protein
 RT database";
 RL Electrophoresis 15:1466-1486(1994).
 RN [5]

RP SEQUENCE OF 239-249.

RC STRAIN=ATCC 38531 / Y41;

RX MEDLINE=97089742; PubMed=8935650;

RA Norbeck J., Blomberg A.;

RT "Protein expression during exponential growth in 0.7 M NaCl medium of
 RT Saccharomyces cerevisiae.";
 RL FEMS Microbiol. Lett. 137:1-8(1996).
 RN [6]

RP ACTIVE SITE.

RX MEDLINE=80109718; PubMed=6101539;

RA Bond M.W., Chiu N.Y., Cooperman B.S.;

RT "Identification of an arginine important for enzymatic activity

RT within the covalent structure of yeast inorganic pyrophosphatase.";
 RL Biochemistry 19:94-102(1980).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
 RA Arutunian E.G., Terzian S.S., Voronova A.A., Kuranova I.P.,
 RA Smirnova E.A., Vainstein B.K., Hohne W.E., Hansen G.;
 RT "X-ray diffraction study of inorganic pyrophosphatase from baker's
 RT yeast at the 3-A resolution.";
 RL Dokl. Akad. Nauk SSSR 258:1481-1492(1981).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RX MEDLINE=97148342; PubMed=8994974;
 RA Heikinheimo P., Lehtonen J., Baykov A., Lahti R., Cooperman B.S.,
 RA Goldman A.;
 RT "The structural basis for pyrophosphatase catalysis.";
 RL Structure 4:1491-1508(1996).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
 RA Swaminathan K., Cooperman B.S., Lahti R., Voet D.;
 RL Submitted (DEC-1997) to the PDB data bank.
 RN [10]
 RP X-RAY CRYSTALLOGRAPHY (2.15 ANGSTROMS) OF MUTANTS LYS-78 AND LYS-117.
 RX MEDLINE=99096888; PubMed=9878371;
 RA Tuominen V., Heikinheimo P., Kajander T., Torkkel T., Hyttia T.,
 RA Kapyla J., Lahti R., Cooperman B.S., Goldman A.;
 RT "The R78K and D117E active-site variants of Saccharomyces cerevisiae
 RT soluble inorganic pyrophosphatase: structural studies and mechanistic
 RT implications.";
 RL J. Mol. Biol. 284:1565-1580(1998).
 RN [11]
 RP SIMILARITY TO E.COLI AND K.LACTIS PPASES.
 RX MEDLINE=90254161; PubMed=2160278;
 RA Lahti R., Kolakowski L.F. Jr., Heinonen J., Vihinen M., Pohjanoksa K.,
 RA Cooperman B.S.;
 RT "Conservation of functional residues between yeast and E. coli
 RT inorganic pyrophosphatases.";
 RL Biochim. Biophys. Acta 1038:338-345(1990).
 CC -|- CATALYTIC ACTIVITY: Diphosphate + H(2)O = 2 phosphate.
 CC -|- COFACTOR: REQUIRES THE PRESENCE OF DIVALENT METAL CATION.
 CC MAGNESIUM CONFERS THE HIGHEST ACTIVITY. IT BINDS UP TO 4 DIVALENT
 CC CATIONS PER SUBUNIT, WITH THREE REQUIRED FOR ACTIVITY.
 CC -|- SUBUNIT: HOMODIMER.
 CC -|- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -|- SIMILARITY: BELONGS TO THE PPASE FAMILY.
 CC -----
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 CC -----
 DR EMBL; X13253; CAA31629.1; -;
 DR EMBL; Z35880; CAA84949.1; -;
 DR PIR; S45864; PMBY.
 DR PDB; 1YPP; 15-OCT-91.
 DR PDB; 1YPP; 07-DEC-96.
 DR PDB; 1WGI; 19-NOV-97.
 DR PDB; 1WGI; 19-NOV-97.
 DR PDB; 1HUJ; 08-APR-98.
 DR PDB; 1HUK; 08-APR-98.
 DR PDB; 117E; 23-DEC-98.
 DR PDB; 8PRK; 23-DEC-98.
 DR SWISS-2DPAGE; P00817; YEAST.
 DR COMPUYEAST-2DPAGE; P00817; -;
 DR SGD; S0000215; IPPL.
 DR InterPro; IPR001596; Pyrophosphatase.
 DR Pfam; PF00719; Pyrophosphatase; 1.
 DR PROSITE; PS00387; PPASE; 1.
 KW Hydrolase; Magnesium; 3D-structure.
 FT INIT_MET 0 0
 FT ACT_SITE 56 56 PROBABLE.

FT BINDING 78 78 INORGANIC PYROPHOSPHATE.
 FT CONFLICT 40 40 N -> D (IN REF. 3).
 FT CONFLICT 71 71 D -> N (IN REF. 3).
 FT CONFLICT 74 74 MISSING (IN REF. 3).
 FT CONFLICT 123 123 E -> Q (IN REF. 3).
 FT CONFLICT 136 136 Q -> E (IN REF. 3).
 FT CONFLICT 186 186 N -> D (IN REF. 3).
 FT CONFLICT 224 224 D -> N (IN REF. 3).
 FT CONFLICT 266 266 L -> P (IN REF. 2).
 FT STRAND 4 7
 FT STRAND 16 20
 FT STRAND 25 25
 FT STRAND 28 30
 FT TURN 38 41
 FT STRAND 45 45
 FT STRAND 55 55
 FT STRAND 79 79
 FT TURN 97 98
 FT TURN 111 112
 FT STRAND 121 123
 FT TURN 131 132
 FT STRAND 135 135
 FT STRAND 138 146
 FT STRAND 151 158
 FT TURN 160 161
 FT TURN 165 167
 FT HELIX 172 175
 FT TURN 176 177
 FT TURN 179 180
 FT HELIX 182 197
 FT STRAND 203 203
 FT HELIX 205 207
 FT STRAND 210 210
 FT HELIX 212 230
 FT TURN 231 231
 FT TURN 245 246
 FT TURN 248 249
 FT TURN 251 252
 FT TURN 255 260
 FT TURN 274 275
 SQ SEQUENCE 286 AA; 32184 MW; F29390260B0C8B2 CRC64;
 Query Match 63.0%; Score 34; DB 1; Length 286;
 Best Local Similarity 83.3%; Pred. No. 15;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 3 HNYGSF 8
 DB 91 HNYGAF 96
 |||||
 RESULT 7
 Y475_ARATH STANDARD; PRT; 606 AA.
 ID Y475_ARATH STANDARD; PRT; 606 AA.
 AC P58223; O49507;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Putative nucleic acid binding protein At4g18375.
 GN AT4G18375 OR F28J12.30.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=20083488; PubMed=10617198;
 RA Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,
 RA Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terryn N.,
 RA Harris B., Ansoorge W., Brandt P., Grivell L., Rieger M.,
 RA Weichselgartner M., de Simone V., Obermaier B., Mache R., Mueller M.,

RA Kreis M., Delsen M., Puigdomenech P., Watson M., Schmidhelmi T., Reichert B., Portetelle D., Perez-Alonso M., Bouter M., Bancroft I., Vos P., Hoheisel J., Zimmermann W., Wedler H., Ridley P., Langham S.-A., McCullagh B., Wilham L., Robben J., Vandenbussche F., Van der Schueren J., Grynmpraz B., Chuang Y.-J., Vandenbussche F., Braeken M., Weitzinger T., Bothe G., Ramsperger U., Hilbert H., Braun M., Holzner E., Brandt A., Peters S., van Staveren M., Dirkse W., Moolijman P., Klein Lanckhorst R., Rose M., Hauf J., Koetter P., Berner S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H., De Keyser A., Buyschaert C., Giesen J., Villarroel R., De Clercq R., Van Montagu M., Rogers J., Cronin A., Quail A., Bray-Allen S., Clark L., Doggett J., Hall S., Kay M., Lennard N., McLaughlin K., Pettitt A., Rajandream M.A., Lyne M., Benes V., Rechmann S., Borkova D., Bloeker H., Scharfe M., Grimm M., Loehner T.-H., Dose S., de Haan M., Maarse A., Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Fartmann B., Grandrath K., Dauner D., Herzl A., Neumann S., Argirou A., Vitale D., Liguori R., Piravandi E., Massenet O., Quigley F., Clabaud G., Muendlein A., Felber R., Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S., Cheford F., Cooke R., Berger C., Monfort A., Casasuberta E., Gibbons T., Weber N., Vandenbol M., Barques M., Terol J., Torres A., Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T., Heijnen L., Schwarz S., Scholler P., Heber S., Francis P., Bielke C., Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S., Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K., Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L., Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J., Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J., LaTrille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D., Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K., Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L., Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D., Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshi C., Antonoli B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C., Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R., Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Tili S., Granat S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A., Chen E., Marra M., Martienssen R., McCombie W.R.; 'thaliana.'; RT Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.; RL Nature 402:769-777(1999). [2] RP CONCEPTUAL TRANSLATION. RA Kieselbach T.; RL Unpublished observations (JUL-2001). CC -!- SUBCELLULAR LOCATION: Nuclear (potential). CC -!- SIMILARITY: CONTAINS 5 KH DOMAINS. CC -!- CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A GENE PREDICTION ERROR AND THE FUSION OF THE CDS FOR THIS PROTEIN WITH THE CDS FOR CHLOROPLAST PROTEASE HHOA. CC ----- CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch). CC ----- CC EMBL; AL021710; CAA16717.1; ALT-SEQ. DR EMBL; AL161548; CAB78839.1; ALT-SEQ. DR InterPro; IPR004087; KH_dom. DR InterPro; IPR004088; KH_type_1. DR Pfam; PF00013; KH-domain; 5. DR SMART; SM00322; KH; 5. DR PROSITE; PS00084; KH_TYPE_1; 5. DR Hypothetical protein; Nuclear protein; RNA-binding; Repeat. KW DOMAIN 35 99 KH 1. FT DOMAIN 138 210 KH 2. FT DOMAIN 311 380 KH 3. FT DOMAIN 394 455 KH 4. FT DOMAIN 535 599 KH 5.

SQ SEQUENCE 606 AA; 65760 MW; 61F135BB8647C0C CRC64; Query Match 63.0%; Score 34; DB 1; Length 606; Best Local Similarity 75.0%; Pred. No. 32; Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0; Qy 3 HNYGSFAA 10 | | | | | Db 509 HYGGSFPA 516 | | | | | RESULT 8 CCSA_PEA STANDARD; PRT; 65 AA. ID CCSA_PEA AC P31172; DT 01-JUL-1993 (Rel. 26, Created) DT 01-JUL-1993 (Rel. 26, Last sequence update) DT 01-NOV-1997 (Rel. 35, Last annotation update) DE Cytochrome c biogenesis protein ccsa (Fragment). GN CCSA. OS Pisum sativum (Garden pea). OG Chloroplast. OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum. OX NCBI_TaxID=3888; RN [1] SEQUENCE FROM N.A. RP STRAIN=cv. Alaska; RX MEDLINE=91355950; PubMed=1884007; RA Nagano Y., Ishikawa H., Matsuno R., Sasaki Y.; RT "Nucleotide sequence and expression of the ribosomal protein L2 gene in pea chloroplasts." RL Plant Mol. Biol. 17:541-545(1991). CC -!- FUNCTION: REQUIRED DURING CYTOCHROME BIOGENESIS AT THE STEP OF HEME ATTACHMENT (BY SIMILARITY). CC -!- SIMILARITY: BELONGS TO THE CCNF/CYCK/CCL1/NRFE/CCSA FAMILY. CC ----- CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch). CC ----- CC EMBL; X59015; CAA1754.1; -. DR PIR; S17441; S17441. DR InterPro; IPR002541; CytC_asm. DR Pfam; PF01578; CytC_asm; 1. KW Cytochrome c-type biogenesis; Chloroplast. FT NON_TER 1 SQ SEQUENCE 65 AA; 7396 MW; 9E523E0C70B102AA CRC64; Query Match 61.1%; Score 33; DB 1; Length 65; Best Local Similarity 62.5%; Pred. No. 49; Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0; Qy 3 HNYGSFAA 10 | | | | | Db 57 HSYGSFST 64 | | | | | RESULT 9 CCSA_ARATH STANDARD; PRT; 328 AA. ID CCSA_ARATH AC P56770; DT 30-MAY-2000 (Rel. 39, Created) DT 30-MAY-2000 (Rel. 39, Last sequence update) DT 16-OCT-2001 (Rel. 40, Last annotation update) DE Cytochrome c biogenesis protein ccsa. GN CCSA. OS Arabidopsis thaliana (Mouse-ear cress).


```

OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20039611; PubMed=10574454;
RA Sato S., Nakamura Y., Kaneko T., Asamizu E., Tabata S.;
RT "Complete structure of the chloroplast genome of Arabidopsis
thaliana.";
RL DNA Res. 6:283-290(1999).
CC -1- FUNCTION: REQUIRED DURING CYTOCHROME BIOGENESIS AT THE STEP OF
CC HEME ATTACHMENT (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CCMF/CYCK/CCL1/NRFE/CCSA FAMILY.
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CC -----
DR EMBL; AF000423; BAA84436.1; -.
DR InterPro; IPR002541; CytC.asn.
DR Pfam; PF01578; CytC.asn; 1.
SQ Cytochrome c-type biogenesis; Chloroplast.
KW SEQUENCE 328 AA; 37732 MW; C88D1508B2924D6F CRC64;

Query Match 61.1%; Score 33; DB 1; Length 328;
Best Local Similarity 62.5%; Pred. No. 27;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFAA 10
Db 320 HSYGSFTS 327

RESULT 10
NCAP_CVHOC STANDARD; PRT; 448 AA.
AC P33469;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE Nucleocapsid protein.
GN N.
OS Human coronavirus (strain OC43).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=31631;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89243809; PubMed=2541577;
RA Kamahora T., See L.H., Lai M.M.C.;
RT "Sequence analysis of nucleocapsid gene and leader RNA of human
coronavirus OC43.";
RL Virus Res. 12:1-9(1989).
DR PIR; A60003; A60003.
DR InterPro; IPR001218; Corona_nucleocap.
DR Pfam; PF00937; Corona_nucleoca; 1.
KW Nucleocapsid.
SQ SEQUENCE 448 AA; 49316 MW; 5193AB1AE0D75626 CRC64;

Query Match 61.1%; Score 33; DB 1; Length 448;
Best Local Similarity 85.7%; Pred. No. 37;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 103 RHNNGSF 109

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RESULT 11
SYE2_RICPR STANDARD; PRT; 470 AA.
AC Q9ZCT8; 2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Glutamyl-tRNA synthetase 2 (EC 6.1.1.17) (Glutamate--tRNA ligase 2)
DE (GLURS 2).
DE
GN GLYX2 OR RP623.
OS Rickettsia prowazekii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=782;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Madrid E;
RX MEDLINE=99039499; PubMed=9823893;
RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,
RA Sicheritz-Ponten T., Alismark U.C.M., Podowski R.M., Naeslund A.K.,
RA Eriksson A.S., Winkler H.H., Kurland C.G.;
RT "The genome sequence of Rickettsia prowazekii and the origin of
mitochondria.";
RL Nature 396:133-140(1998).
CC -1- CATALYTIC ACTIVITY: ATP + L-glutamate + tRNA(Glu) = AMP +
CC diphosphate + L-glutamyl-tRNA(Glu).
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
CC -----
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CC -----
DR EMBL; AJ235272; CAAL5066.1; -.
DR HSPF; P27000; IGLN.
DR InterPro; IPR004527; GltX_bact.
DR InterPro; IPR000924; Glu_tRNA-synt_1c.
DR InterPro; IPR001412; tRNA-synt_1.
DR Pfam; PF00749; tRNA-synt_1c; 1.
DR PRINTS; PR00987; TRNASYNTHGLU.
DR TIGRFAMS; TIGR00464; gltX_bact; 1.
DR PROSITE; PS00178; AA_TRNA_LIGASE_I; FALSE_NEG.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
KW Complete proteome.
FT SITE 10 20 "HIGH" REGION.
FT SITE 239 243 "KMSKS" REGION.
FT BINDING 242 242 ATP (BY SIMILARITY).
SQ SEQUENCE 470 AA; 53696 MW; DFICE50A20B9A9FD CRC64;

Query Match 61.1%; Score 33; DB 1; Length 470;
Best Local Similarity 75.0%; Pred. No. 39;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNGVSF 8
Db 31 ARHNGKF 38

RESULT 12
SYE_AQUAE STANDARD; PRT; 473 AA.
AC Q67271;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Glutamyl-tRNA synthetase (EC 6.1.1.17) (Glutamate--tRNA ligase)

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DE (Glurs).
GN GLTX OR AQ_1221.
OS Aquifex aeolicus.
OC Bacteria; Aquificae; Aquificae (class); Aquificales; Aquificaceae;
OC Aquifex.
OX NCBI_TaxID=63363;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VF5;
RX MEDLINE=98196666; PubMed=9537320;
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Snead M.A., Keller M., AuJay M., Huber R.,
RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus.";
RL Nature 392:353-358(1998).
CC -1- CATALYTIC ACTIVITY: ATP + L-glutamate + tRNA(Glu) = AMP +
CC diphosphate + L-glutamyl-tRNA(Glu).
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
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CC -----
CC EMBL; AF000729; AAC07230.1; -.
CC HSSP; P27000; IGLN.
CC InterPro; IPR004527; Gltx_bact.
CC InterPro; IPR000924; Glu_trna-synt_lc.
CC InterPro; IPR001412; trna-synt_1.
CC Pfam; PF00749; trna-synt_lc; 1.
CC PRINTS; PR00987; TRNASYNTHGLU.
CC TIGRFS; TIGR00464; gltx_bact; 1.
CC PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
CC Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
CC Complete proteome.
CC SITE 10 20 "HIGH" REGION.
CC SITE 242 246 "KMSKS" REGION.
CC BINDING 245 245 ATP (BY SIMILARITY).
CC SEQUENCE 473 AA; 55121 MW; 5CB4D1590973E07A CRC64;
Query Match 61.1%; Score 33; DB 1; Length 473;
Best Local Similarity 75.0%; Pred. No. 39;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 ARHNYGSF 8
Db 31 ARHNGGF 38
RESULT 13
VG50_BPML5 STANDARD; PRT; 682 AA.
AC Q05262;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Putative adenosylcobalamin-dependent ribonucleotide reductase
DE (EC 1.17.4.2) (GP50).
GN 50.
OS Mycobacteriophage L5.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
OC L5-like viruses.
OX NCBI_TaxID=31757;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93211282; PubMed=8459766;
RA Hatfull G.F., Sarkis G.J.;

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```

RT "DNA sequence, structure and gene expression of mycobacteriophage L5:
RT a phage system for mycobacterial genetics.";
RL Mol. Microbiol. 7:395-405(1993).
CC -1- CATALYTIC ACTIVITY: 2'-deoxyribonucleoside triphosphate + oxidized
CC thioredoxin + H(2)O = ribonucleoside triphosphate + reduced
CC thioredoxin.
CC -----
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CC -----
CC EMBL; Z18946; CAA79426.1; -.
CC PIR; S30995; S30995.
CC InterPro; IPR001230; Prenyl_site.
CC InterPro; IPR000788; Ribonucleo_red.
CC Pfam; PF02867; ribonuc_red_lgc; 1.
CC Oxidoreductase; DNA replication.
CC SEQUENCE 682 AA; 76331 MW; 8D2A71B873BC04A8 CRC64;
Query Match 61.1%; Score 33; DB 1; Length 682;
Best Local Similarity 66.7%; Pred. No. 58;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 1 ARHNYGSFA 9
Db 311 AKEGVGSFA 319
RESULT 14
ACOX_YEAST STANDARD; PRT; 789 AA.
AC P39533;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative aconitase in PRP21-USP12 intergenic region (EC 4.2.1.3).
GN YJL200C OR J0327.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=95274326; PubMed=7754713;
RA Purnelle B., Coster F., Goffeau A.;
RT "The sequence of a 36 kb segment on the left arm of yeast chromosome
RT X identifies 24 open reading frames including NUC1, PRP21 (SPP91),
RT CDC6, CRV2, the gene for S24, a homologue to the aconitase gene ACO1
RT and two homologues to chromosome III genes.";
RL yeast 10:1235-1249(1994).
CC -1- CATALYTIC ACTIVITY: Citrate = cis-aconitate + H(2)O.
CC -1- SIMILARITY: BELONGS TO THE ACONITASE/IPM ISOMERASE FAMILY.
CC -----
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CC -----
CC EMBL; X77688; CAA54757.1; -.
CC EMBL; Z49475; CAA89495.1; -.
CC PIR; S46631; S46631.
CC HSSP; P20004; 1AMJ.
CC SGB; S0003736; YJL200C.
CC InterPro; IPR000573; Aconitase_C.
CC InterPro; IPR001030; Aconitase_N.

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DR Pfam; PF00330; aconitase; 1.
 DR Pfam; PF00694; Aconitase_C; 1.
 DR PRINTS; PR00415; ACONITASE.
 DR PRODOM; PD000511; Aconitase.N; 1.
 DR PROSITE; PS00450; ACONITASE_1; 1.
 DR PROSITE; PS01244; ACONITASE_2; 1.
 KW Hypothetical protein; Lyase; Tricarboxylic acid cycle; Iron-sulfur;
 4Fe-4S.
 FT METAL 385 385 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
 FT METAL 448 448 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
 FT METAL 451 451 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
 SQ SEQUENCE 789 AA; 86583 MW; FABA4FE482D3F993 CRC64;

Query Match 61.1%; Score 33; DB 1; Length 789;
 Best Local Similarity 60.0%; Pred. No. 67;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARHNYGSFAA 10
 | | | | | : |
 Db 663 AEHNYGEGSA 672

RESULT 15
 RPOD_MARPO STANDARD; PRT; 1386 AA.
 AC P06274;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE DNA-directed RNA polymerase beta" chain (EC 2.7.7.6).
 GN RPOC2.
 OS Marchantia polymorpha (Liverwort).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Marchantiophyta;
 OC Marchantiopsida; Marchantiidae; Marchantiales; Marchantiaceae;
 OC Marchantiaceae; Marchantia.
 OX NCBI_TaxID=3197;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ohyama K., Fukuzawa H., Kohchi T., Shirai H., Sano T., Sano S.,
 RA Umesono K., Shiki Y., Takeuchi M., Chang Z., Aota S., Inokuchi H.,
 RA Ozeki H.;
 RT "Chloroplast gene organization deduced from complete sequence of
 RT liverwort Marchantia polymorpha chloroplast DNA.";
 RL Nature 322:572-574(1986).
 CC -!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
 CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
 CC SUBSTRATES.
 CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
 CC {RNA}(N).
 CC -!- SUBUNIT: IN CHLOROPLAST THE RNA POLYMERASE IS COMPOSED OF FOUR
 CC SUBUNITS: ALPHA, BETA, BETA', AND BETA".
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 CC -----
 CC EMBL; X04465; CAA28063.1; -.
 DR PIR; A00698; RNLVC2.
 DR PIR; S01575; S01575.
 DR HSSP; Q9KWU6; LHQM.
 DR InterPro; IPR000722; RNA_pol_A.
 DR InterPro; IPR002879; RNA_pol_A2.
 DR Pfam; PF00623; RNA_pol_A; 1.
 DR Pfam; PF01854; RNA_pol_A2; 2.
 KW Transferase; Transcription; DNA-directed RNA polymerase; Chloroplast.
 SQ SEQUENCE 1386 AA; 160155 MW; 18BE458FC1A5C3F9 CRC64;

Query Match¹.
 61.1%; Score 33; DB 1; Length 1386;

Best Local Similarity 75.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 HNYGSFAA 10
 | | | | | |
 Db 86 HNYGSLHA 93

Search completed: November 18, 2002, 17:33:29
 Job time : 2.45098 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:01 ; Search time 10.4412 Seconds
(without alignments)
197.341 Million cell updates/sec

Title: US-09-016-061-80
Perfect score: 54
Sequence: 1 ARHNYGSFAA 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	79.6	446	5	O62086 caenorhabdi
2	43	79.6	839	10	O9LIE5 arabidopsis
3	40	74.1	276	7	O9GJN0 caiman croc
4	38	70.4	89	7	O19495 gallus garl
5	37	68.5	469	13	O8UV27 claritas gar
6	37	68.5	479	13	O8UV26 claritas gar
7	37	68.5	5317	5	O8TA74 hamacentrot
8	36	66.7	39	7	P79474 cervus elap
9	36	66.7	39	7	P79477 cervus elap
10	36	66.7	39	7	P79478 cervus elap
11	36	66.7	39	7	P79479 cervus elap
12	36	66.7	67	7	O8SP02 hapalemur g
13	36	66.7	74	6	O9TTM4 bos taurus
14	36	66.7	75	7	O9GIJ5 bos taurus
15	36	66.7	76	7	O9TPC2 macaca mula
16	36	66.7	77	7	O9GJ91 ovnis arles

17	36	66.7	77	7	O9GJ90	O9GJ90 ovnis arles
18	36	66.7	77	7	O9GJ82	O9GJ82 ovnis arles
19	36	66.7	78	6	O97968	O97968 ovnis arles
20	36	66.7	78	6	O97835	O97835 ovnis arles
21	36	66.7	78	6	O97839	O97839 ovnis arles
22	36	66.7	78	6	O97844	O97844 ovnis arles
23	36	66.7	78	7	O9MWT6	O9MWT6 leopardus p
24	36	66.7	78	7	O9MWT5	O9MWT5 leopardus p
25	36	66.7	78	7	O9MWT4	O9MWT4 leopardus p
26	36	66.7	78	7	O95HDI	O95HDI ovnis arles
27	36	66.7	78	7	O95HC6	O95HC6 ovnis arles
28	36	66.7	79	7	O9MX19	O9MX19 leopardus p
29	36	66.7	79	7	O9MX13	O9MX13 leopardus p
30	36	66.7	79	7	O9MX03	O9MX03 leopardus p
31	36	66.7	79	7	O9MX00	O9MX00 leopardus p
32	36	66.7	79	7	O9MWZ9	O9MWZ9 leopardus p
33	36	66.7	79	7	O9MWZ8	O9MWZ8 leopardus p
34	36	66.7	79	7	O9MWZ7	O9MWZ7 leopardus p
35	36	66.7	79	7	O9MWY9	O9MWY9 leopardus p
36	36	66.7	79	7	O9MWY8	O9MWY8 leopardus p
37	36	66.7	79	7	O9MWY6	O9MWY6 leopardus p
38	36	66.7	79	7	O9MWY5	O9MWY5 leopardus p
39	36	66.7	79	7	O9MWY4	O9MWY4 leopardus p
40	36	66.7	79	7	O9MWY3	O9MWY3 leopardus p
41	36	66.7	79	7	O9MWX6	O9MWX6 leopardus p
42	36	66.7	79	7	O9MWX5	O9MWX5 leopardus p
43	36	66.7	79	7	O9MWX4	O9MWX4 leopardus p
44	36	66.7	79	7	O9MWX1	O9MWX1 leopardus p
45	36	66.7	79	7	O9MWX0	O9MWX0 leopardus p

ALIGNMENTS

RESULT 1

O62086 PRELIMINARY; PRT; 446 AA.
ID O62086
AC O62086;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE C3IH5.6 protein.
GN C3IH5.6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Kershaw J.K.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for investigating biology."
RL Science 282:2012-2018(1998).
DR EMBL: Z93778; CAB07846.1; .
DR InterPro: IPR000379; SeI_estrs_site.
SQ SEQUENCE 446 AA; 50763 MW; 82AD969CDAD753DE CRC64;

Query Match 79.6%; Score 43; DB 5; Length 446;
Best Local Similarity 88.9%; Pred. No. 2.7;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 RHNYGSFAA 10
|||||
Db 51 RHNYGSFAA 59

RESULT 2

O9LIE5

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ID Q9LIES PRELIMINARY; PRT; 839 AA.
AC Q9LIES;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Far-red impaired response protein, mutator-like transposase-like
DE protein, phytochrome A signaling protein-like.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Nakamura Y.;
RL MEDLINE=20363099; PubMed=10907853;
RX "Structural analysis of Arabidopsis thaliana chromosome 3. II.
RT Sequence features of the regions of 4,251,695 bp covered by ninety P1,
RT TAC and BAC clones.";
RL DNA Res. 7:217-221(2000).
DR EMBL; AP001306; BAB03065.1; -.
DR InterPro; IPR004330; FARI.
DR InterPro; IPR001000; Glyco_hydro_10.
DR Pfam; PF03101; FARI; 1.
DR PROSITE; PS00591; GLYCOSYL_HYDROL_F10; UNKNOWN_1.
SQ SEQUENCE 839 AA; 95996 MW; CBBF60DF8B6797F8 CRC64;

Query Match 79.6%; Score 43; DB 10; Length 839;
Best Local Similarity 87.5%; Pred. No. 5.5;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNGSFF 8
:|||||
DB 274 SRHNGSFF 281

RESULT 3
Q9GJNO PRELIMINARY; PRT; 276 AA.
AC Q9GJNO;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MHC class II beta chain.
GN HClIBETA.
OS Caiman crocodilus (Spectacled caiman) (Caiman sclerops).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Crocodyliidae; Alligatorinae; Caiman.
OX NCBI_TaxID=8499;
RN [1]
RP SEQUENCE FROM N.A.
RA Voldby J., Vitved L., Due M., Gronlund J., Holmskov U., Teisner B.,
RA Salomonson J., Brusgaard K., Skjold K.;
RT "Cloning, sequence and genomic structure of MHC class II antigens from
RT the spectacled caiman, Caiman crocodilus.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF256651; AAF9283.1; -.
DR HSSP; P13760; ZSEB.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR000353; MHC_II_beta.
DR Pfam; PF00047; ig; 1.
DR Pfam; PF00969; MHC_II_beta; 1.
DR ProDom; PD000328; MHC_II_beta; 1.
DR SMART; SM00407; IGCL; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR Glycoprotein; MHC II; Transmembrane.
KW
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SQ SEQUENCE 276 AA; 30366 MW; EA8A4684986AEA6A CRC64;

Query Match 74.1%; Score 40; DB 7; Length 276;
Best Local Similarity 87.5%; Pred. No. 6.3;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFA 9
|||||
DB 108 RHNYGVFA 115

RESULT 4
OL9495 PRELIMINARY; PRT; 89 AA.
AC OL9495;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MHC class II beta 1 domain (Fragment).
GN B-LBI.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=15.151-5; TISSUE=BURSA;
RX MEDLINE=98179131; PubMed=9510552;
RA Pharr G.T., Dodgson J.B., Hunt H.D., Bacon L.D.;
RL "Class II MHC cDNAs in 1515 B-congenic chickens.";
DR EMBL; U91532; AAC15813.1; -.
DR InterPro; IPR000353; MHC_II_beta.
DR Pfam; PF00969; MHC_II_beta; 1.
DR ProDom; PD000328; MHC_II_beta; 1.
KW Glycoprotein; MHC II; Transmembrane.
FT NON_TER 1
FT NON_TER 89
FT NON_TER 89
SQ SEQUENCE 89 AA; 10724 MW; BC7D558B6AEB1379 CRC64;

Query Match 70.4%; Score 38; DB 7; Length 89;
Best Local Similarity 85.7%; Pred. No. 4.4;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
|||||
DB 75 RHNYGDF 81

RESULT 5
Q8UV27 PRELIMINARY; PRT; 469 AA.
AC Q8UV27;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Fushi tarazu factor 1-A.
GN FTZ-F1.
OS Clarias gariepinus (Sharptooth catfish) (African catfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
OC Clariidae; Clarias.
OX NCBI_TaxID=13013;
RN [1]
RP SEQUENCE FROM N.A.
RA Teves A.C.C., Zandbergen M.A., Bogerd J.;
RT "Molecular cloning and pubertal expression of two isoforms of FTZ-F1
RT messenger RNAs in the African catfish.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY014862; AAG49004.1; -.
DR InterPro; IPR000536; Hormone_rec_lig.
DR InterPro; IPR001723; Stdhrmn_receptor.
KW
```



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RP SEQUENCE FROM N.A.
RA Swarbrick P.A., Crawford A.M.;
RT "The MHC class II DRB intron 2 microsatellite of red deer.";
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U63080; AAB37780.1; -.
DR InterPro; IPR000353; MHC_II_beta.
DR Pfam; PF00969; MHC_II_beta.1.
DR ProDom; PD000328; MHC_II_beta.1.
KW Glycoprotein; MHC II; Transmembrane.
FT NON_TER 1
FT NON_TER 39
SQ SEQUENCE 39 AA; 4806 MW; C2188A16752A3C1D CRC64;

Query Match 66.7%; Score 36; DB 7; Length 39;
Best Local Similarity 85.7%; Pred. No. 4.4;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 25 RHNYGVF 31

RESULT 10
P79478 ID P79478 PRELIMINARY; PRT; 39 AA.
AC P79478;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II DRB (Fragment).
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
OC Cervidae; Cervinae; Cervus.
OX NCBI_TaxID=9860;
RN [1]
RP SEQUENCE FROM N.A.
RA Swarbrick P.A., Crawford A.M.;
RT "The MHC class II DRB intron 2 microsatellite of red deer.";
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U63081; AAB37781.1; -.
DR InterPro; IPR000353; MHC_II_beta.
DR Pfam; PF00969; MHC_II_beta.1.
DR ProDom; PD000328; MHC_II_beta.1.
KW Glycoprotein; MHC II; Transmembrane.
FT NON_TER 1
FT NON_TER 39
SQ SEQUENCE 39 AA; 4806 MW; C2188A16752A3C1D CRC64;

Query Match 66.7%; Score 36; DB 7; Length 39;
Best Local Similarity 85.7%; Pred. No. 4.4;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 25 RHNYGVF 31

RESULT 11
P79479 ID P79479 PRELIMINARY; PRT; 39 AA.
AC P79479;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II DRB (Fragment).
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
OC Cervidae; Cervinae; Cervus.
OX NCBI_TaxID=9860;
RN [1]
RP SEQUENCE FROM N.A.

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RA Swarbrick P.A., Crawford A.M.;
RT "The MHC class II DRB intron 2 microsatellite of red deer.";
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U63082; AAB37782.1; -.
DR InterPro; IPR000353; MHC_II_beta.
DR Pfam; PF00969; MHC_II_beta.1.
DR ProDom; PD000328; MHC_II_beta.1.
KW Glycoprotein; MHC II; Transmembrane.
FT NON_TER 1
FT NON_TER 39
SQ SEQUENCE 39 AA; 4806 MW; C2188A16752A3C1D CRC64;

Query Match 66.7%; Score 36; DB 7; Length 39;
Best Local Similarity 85.7%; Pred. No. 4.4;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 25 RHNYGVF 31

RESULT 12
Q8SP02 ID Q8SP02 PRELIMINARY; PRT; 67 AA.
AC Q8SP02;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE MHC class II antigen (Fragment).
GN HAGG-DRB.
OS Hapalemur griseus griseus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Strepsirhini; Lemuridae; Hapalemur.
OX NCBI_TaxID=122219;
RN [1]
RP SEQUENCE FROM N.A.
RA Go Y., Satta Y., Kawamoto Y., Rakotoarisoa G., Randrianjafy A.,
RA Koyama N., Hirai H.;
RT "Mhc-DRB genes evolution in lemurs.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB078220; BAB88434.1; -.
FT NON_TER 1
FT NON_TER 67
SQ SEQUENCE 67 AA; 8083 MW; 559300839F0EFA52 CRC64;

Query Match 66.7%; Score 36; DB 7; Length 67;
Best Local Similarity 85.7%; Pred. No. 8.1;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 59 RHNYGVF 65

RESULT 13
Q9TTM4 ID Q9TTM4 PRELIMINARY; PRT; 74 AA.
AC Q9TTM4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC(BOLA) class II DR-beta chain (Fragment).
GN BOLA-DRB3.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=JAPANESE BLACK;
RA Takeshima S., Ikegami M., Morita M., Nakai Y., Aida Y.;
RT "Identification of BOLA-DRB3 exon 2 of Japanese black cattle.";

```

RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB033388; BAA85470.1; -.
 DR InterPro: IPR000353; MHC_II_beta.
 DR Pfam; PF00969; MHC_II_beta; 1.
 DR ProDom; PD000328; MHC_II_beta; 1.
 KW Glycoprotein; MHC II; Transmembrane.
 FT NON_TER 1
 FT NON_TER 74
 SQ SEQUENCE 74 AA; 9132 MW; C5834842FOE38BA6 CRC64;

Query Match 66.7%; Score 36; DB 6; Length 74;
 Best Local Similarity 85.7%; Pred. No. 9;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
 Db 68 RHNYGVF 74

RESULT 14

Q9GIJ5 PRELIMINARY; PRT; 75 AA.
 AC Q9GIJ5;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE MHC(BOLA) class II DR-beta chain (Fragment).
 GN BOLA-DRB3.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]

SEQUENCE FROM N.A.

RC STRAIN-JAPANESE BLACK; TISSUE-PERIPHERAL BLOOD LYMPHOCYTE;
 RA Takeshima S., Ikegami M., Saitou N., Morita M., Inoko T., Aida Y.;
 RT "Nature and origin of polymorphism in BOLA-DRB3 gene."
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB053167; BAB20423.1; -.
 DR InterPro: IPR000353; MHC_II_beta.
 DR Pfam; PF00969; MHC_II_beta; 1.
 DR ProDom; PD000328; MHC_II_beta; 1.
 KW Glycoprotein; MHC II; Transmembrane.
 FT NON_TER 1
 FT NON_TER 75
 SQ SEQUENCE 75 AA; 9260 MW; C58310BD57BB7401 CRC64;

Query Match 66.7%; Score 36; DB 7; Length 75;
 Best Local Similarity 85.7%; Pred. No. 9.2;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
 Db 69 RHNYGVF 75

RESULT 15

Q9TPC2 PRELIMINARY; PRT; 76 AA.
 AC Q9TPC2;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE MHC class II antigen (Fragment).
 GN MAMU-DRB1.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]

SEQUENCE FROM N.A.

RP

RA Saueremann U., Khazand M., Nagy M., Peiberg C.;
 RT "Mhc-DO-DRB haplotype analysis in the rhesus macaque: evidence for a
 number of different haplotypes displaying a low allelic
 polymorphism."
 RL Tissue Antigens 0:0-0(1999).
 DR EMBL; AF175315; AAF07040.1; -.
 DR HSSP; P13758; 1DLH.
 DR InterPro: IPR000353; MHC_II_beta.
 DR Pfam; PF00969; MHC_II_beta; 1.
 DR ProDom; PD000328; MHC_II_beta; 1.
 KW Glycoprotein; MHC II; Transmembrane.
 FT NON_TER 1
 FT NON_TER 76
 SQ SEQUENCE 76 AA; 9315 MW; 1DC073E1B87A94D0 CRC64;

Query Match 66.7%; Score 36; DB 7; Length 76;
 Best Local Similarity 85.7%; Pred. No. 9.3;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
 Db 67 RHNYGVF 73

Search completed: November 18, 2002, 17:40:49
 Job time : 10.4912 secs

GenCore version 5.1.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:21:57 ; Search time 13.8235 Seconds
(without alignments)
96.394 Million cell updates/sec

Title: US-09-016-061-80
Perfect score: 54
Sequence: 1 ARHNGSFAA 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_101002.*
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23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	54	100.0	10	AAW76030	LM609 grafted anti
2	54	100.0	10	AAW76030	Mutant VH CDR3 pep
3	51	94.4	10	AAW76024	LM609 grafted anti
4	51	94.4	10	AAW76024	Mutant VH CDR3 pep
5	50	92.6	10	AAW76025	LM609 grafted anti
6	50	92.6	10	AAW76026	LM609 grafted anti
7	50	92.6	10	AAW76027	LM609 grafted anti
8	50	92.6	10	AAW76028	LM609 grafted anti
9	50	92.6	10	AAW76029	LM609 grafted anti
10	50	92.6	10	AAW76010	LM609 grafted anti

11	50	92.6	10	22	AAW76038	LM609 VH CDR3 pep
12	50	92.6	10	22	AAW76038	Mutant VH CDR3 pep
13	50	92.6	10	22	AAW76038	Mutant VH CDR3 pep
14	50	92.6	10	22	AAW76038	Mutant VH CDR3 pep
15	50	92.6	10	22	AAW76038	Mutant VH CDR3 pep
16	50	92.6	10	22	AAW76038	Mutant VH CDR3 pep
17	50	92.6	117	19	AAW76001	Vitaxin antibody h
18	50	92.6	117	19	AAW76003	LM609 antibody hea
19	50	92.6	117	20	AAW76038	Humanised LM609 an
20	50	92.6	117	20	AAW76038	Humanised LM609 an
21	50	92.6	117	22	AAW76038	A heavy chain vari
22	50	92.6	117	22	AAW76038	A heavy chain vari
23	50	92.6	117	22	AAW76038	Vitaxin heavy chai
24	50	92.6	117	22	AAW76038	Antibody LM609 hea
25	50	92.6	118	20	AAW76038	Humanised LM609 an
26	50	92.6	118	20	AAW76038	Humanised LM609 an
27	50	92.6	118	20	AAW76038	Humanised LM609 an
28	50	92.6	118	20	AAW76038	Humanised LM609 an
29	50	92.6	130	20	AAW76038	Humanised LM609 an
30	47	87.0	10	19	AAW76021	Murine monoclonal
31	47	87.0	10	22	AAW76038	LM609 grafted anti
32	46	85.2	10	19	AAW76037	Mutant VH CDR3 pep
33	46	85.2	10	19	AAW76039	LM609 grafted anti
34	46	85.2	10	19	AAW76040	LM609 grafted anti
35	46	85.2	10	19	AAW76022	LM609 grafted anti
36	46	85.2	10	19	AAW76023	LM609 grafted anti
37	46	85.2	10	22	AAW76038	Mutant VH CDR3 pep
38	46	85.2	10	22	AAW76038	Mutant VH CDR3 pep
39	46	85.2	10	22	AAW76038	Multiple mutant VH
40	46	85.2	10	22	AAW76038	Multiple mutant VH
41	46	85.2	10	22	AAW76038	Multiple mutant VH
42	46	85.2	10	19	AAW76020	LM609 grafted anti
43	45	83.3	10	22	AAW76038	Mutant VH CDR3 pep
44	42	77.8	110	20	AAW84099	Vitronectin alpha-
45	42	77.8	117	20	AAW84093	Murine vitronectin

ALIGNMENTS

RESULT 1
AAW76030
ID AAW76030 standard; Protein; 10 AA.
AC AAW76030;
XX
XX
DT 02-NOV-1998 (first entry)
XX
DE LM609 grafted antibody V-H region CDR3 protein fragment #12.

XX Vitaxin; antibody; variable region; heavy chain; Integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
XX
XX Mus sp.
XX
XX WO9833919-A2.
XX
XX
PD 06-AUG-1998.
XX
XX 30-JAN-1998; 98WO-US01826.
XX
XX 30-JAN-1997; 97US-0791391.
XX (IXSY-) IXSYS INC.
XX
XX Glaser SM, Huse WD;
XX
XX WPI; 1998-437472/37.
XX
XX N-PSDB; AAW49867.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
XX
XX Claim 62; Page 41; 129pp; English.
PS
CC AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
CC antibodies contain non-murine framework regions so are suitable for use
CC in humans. Enhanced types of LM609 have affinity more than 90 times
CC greater than that of parent the parent antibody.
XX
XX Sequence 10 AA;
SQ
Query Match 100.0%; Score 54; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.005;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ARHNYGSFAA 10
Db 1 ARHNYGSFAA 10
|||||
RESULT 2
AAB61388
ID AAB61388 standard; peptide; 10 AA.
XX
XX AAB61388;
XX
XX 03-APR-2001 (first entry)
XX
XX Mutant VH CDR3 peptide #11.
DE
XX
XX LM609; grafted antibody; alphavbeta3 integrin; angiogenesis;
KW inflammatory; cancer; retina; restenosis; osteoporosis.
KW
XX Unidentified.
OS
XX WO200078815-A1.
PN
XX
XX 28-DEC-2000.
PD
XX
XX 23-JUN-2000; 2000WO-US17454.
PF
XX
XX 24-JUN-1999; 99US-0339922.
PR
XX
XX (MOLE-) APPLIED MOLECULAR EVOLUTION.
PA
XX
XX Huse WD, Wu H;
PI
XX
XX WPI; 2001-050110/06.
DR
XX
XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
PT osteoporosis -
PT
XX
XX Disclosure; Page 41; 132pp; English.
PS
XX The present invention relates to enhanced LM609 grafted antibodies
CC exhibiting selective binding affinity to alphavbeta3 integrin or
CC their functional fragments. The antibodies or their functional
CC fragments can be used in the diagnosis and treatment of
CC alphavbeta3-mediated diseases such as angiogenesis, inflammatory

CC diseases (such as psoriasis and chronic articular rheumatism), of
CC disorders associated with inappropriate or inopportune invasion of
CC vessels (such as diabetic retinopathy, neovascular glaucoma and
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
CC diseases (such as macular degeneration), restenosis and
CC osteoporosis.
XX
XX Sequence 10 AA;
SQ
Query Match 100.0%; Score 54; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.005;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ARHNYGSFAA 10
Db 1 ARHNYGSFAA 10
|||||
RESULT 3
AAW76024
ID AAW76024 standard; Protein; 10 AA.
XX
XX AAW76024;
XX
XX 02-NOV-1998 (first entry)
DT
XX
XX LM609 grafted antibody V-H region CDR3 protein fragment #6.
DE
XX
XX Vitaxin; antibody; variable region; heavy chain; light chain; Integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
XX
XX Mus sp.
OS
XX
XX WO9833919-A2.
PN
XX
XX 06-AUG-1998.
PD
XX
XX 30-JAN-1998; 98WO-US01826.
PF
XX
XX 30-JAN-1997; 97US-0791391.
PR
XX
XX (IXSY-) IXSYS INC.
PA
XX
XX Glaser SM, Huse WD;
PI
XX
XX WPI; 1998-437472/37.
DR
XX
XX N-PSDB; AAV49861.
DR
XX
XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
XX Claim 62; Page 41; 129pp; English.
PS
XX
XX AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
CC antibodies contain non-murine framework regions so are suitable for use
CC in humans. Enhanced types of LM609 have affinity more than 90 times
CC greater than that of parent the parent antibody.
XX
XX Sequence 10 AA;
SQ

Query Match 94.4%; Score 51; DB 19; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.017;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFAA 10
 |||||
 Db 1 ARHNYGSFAS 10

RESULT 4

AAB61382
 ID AAB61382 standard; peptide; 10 AA.
 XX
 AC AAB61382;
 XX
 DT 03-APR-2001 (first entry)
 XX
 DE Mutant VH CDR3 peptide #5.
 XX
 KW LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis.
 XX
 OS Unidentified.
 XX
 PN WO200078815-A1.
 XX
 PD 28-DEC-2000.
 XX
 PF 23-JUN-2000; 2000WO-US17454.
 XX
 PR 24-JUN-1999; 99US-0339922.
 XX
 PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
 XX
 PI Huse WD, Wu H;
 XX
 DR WPI; 2001-050110/06.
 XX
 PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -
 XX
 PS Disclosure; Page 41; 132pp; English.

CC The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphavbeta_3 integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.

QY Sequence 10 AA;

Query Match 94.4%; Score 51; DB 22; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.017;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFAA 10
 |||||
 Db 1 ARHNYGSFAS 10

RESULT 5

AAW76025
 ID AAW76025 standard; Protein; 10 AA.
 XX

AC AAW76025;
 XX
 DT 02-NOV-1998 (first entry)
 XX
 DE LM609 grafted antibody V-H region CDR3 protein fragment #7.
 XX
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 XX
 OS Mus sp.
 XX
 PN WO9833919-A2.
 XX
 PD 06-AUG-1998.
 XX
 PF 30-JAN-1998; 98WO-US01826.
 XX
 PR 30-JAN-1997; 97US-0791391.
 XX
 PA (IXSY-) IXSYS INC.
 XX
 PI Glaser SM, Huse WD;
 XX
 DR WPI; 1998-437472/37.
 DR N-PSDB; AAV49862.
 XX
 PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 PS Claim 62; Page 41; 129pp; English.
 XX
 CC AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC Vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
 CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
 CC antibodies contain non-murine framework regions so are suitable for use
 CC in humans. Enhanced types of LM609 have affinity more than 90 times
 CC greater than that of parent the parent antibody.
 XX
 SQ Sequence 10 AA;
 Query Match 92.6%; Score 50; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.025;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ARHNYGSFA 9
 |||||
 Db 1 ARHNYGSFA 9
 RESULT 6
 AAW76026
 ID AAW76026 standard; Protein; 10 AA.
 XX
 AC AAW76026;
 XX
 DT 02-NOV-1998 (first entry)
 XX
 DE LM609 grafted antibody V-H region CDR3 protein fragment #8.
 XX
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;

KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.

XX Mus sp.
 PN WO9833919-A2.
 PD 06-AUG-1998.
 XX 30-JAN-1998; 98WO-US01826.
 PF 30-JAN-1997; 97US-0791391.
 XX (IXSY-) IXSYS INC.
 PA Glaser SM, Huse WD;
 PI WPI; 1998-437472/37.
 XX N-PSDB; AAV49863.
 DR Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 XX integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX Claim 62; Page 41; 129pp; English.
 PS AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
 XX LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
 CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
 CC antibodies contain non-murine framework regions so are suitable for use
 CC in humans. Enhanced types of LM609 have affinity more than 90 times
 CC greater than that of parent the parent antibody.
 XX Sequence 10 AA;
 SQ Query Match 92.6%; Score 50; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.025;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ARHNYGSFA 9
 DB | | | | | | | | | |
 1 ARHNYGSFA 9
 RESULT 7
 AAW76027
 ID AAW76027 standard; Protein; 10 AA.
 XX AAW76027;
 AC
 XX 02-NOV-1998 (first entry)
 DT LM609 grafted antibody V-H region CDR3 protein fragment #9.
 DE
 XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 XX Mus sp.
 OS
 XX WO9833919-A2.
 PN

XX 06-AUG-1998.
 XX 30-JAN-1998; 98WO-US01826.
 PF 30-JAN-1997; 97US-0791391.
 XX (IXSY-) IXSYS INC.
 PA Glaser SM, Huse WD;
 PI WPI; 1998-437472/37.
 XX N-PSDB; AAV49864.
 DR Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 XX integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX Claim 62; Page 41; 129pp; English.
 PS AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
 XX LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
 CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
 CC antibodies contain non-murine framework regions so are suitable for use
 CC in humans. Enhanced types of LM609 have affinity more than 90 times
 CC greater than that of parent the parent antibody.
 XX Sequence 10 AA;
 SQ Query Match 92.6%; Score 50; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.025;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ARHNYGSFA 9
 DB | | | | | | | | | |
 1 ARHNYGSFA 9
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 AAW76028
 ID AAW76028 standard; Protein; 10 AA.
 XX AAW76028;
 AC
 XX 02-NOV-1998 (first entry)
 DT LM609 grafted antibody V-H region CDR3 protein fragment #10.
 DE
 XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 XX Mus sp.
 OS
 XX WO9833919-A2.
 PN 06-AUG-1998.
 PD 30-JAN-1998; 98WO-US01826.
 PF 30-JAN-1997; 97US-0791391.
 XX (IXSY-) IXSYS INC.
 PA

```

XX PI Glaser SM, Huse WD;
XX DR WPI: 1998-437472/37.
XX DR N-PSDB; AAV49865.
XX
XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
XX integrin - and related grafted antibodies based on murine monoclonal
XX LM609, also related nucleic acid, used to treat, prevent or diagnose
XX PT angiogenesis or restenosis
XX
XX Claim 62; Page 41; 129pp; English.
XX
XX AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
XX LM609 heavy and light chain variable region. LM609 and the antibody
XX vitaxin bind selectively to integrin alphavbeta3 and can be used to
XX inhibit binding of alphavbeta3 to a ligand and thus block
XX integrin-mediated signal transduction. This is useful in the treatment,
XX prevention and diagnosis of alphavbeta3-mediated disease, specifically
XX angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
XX diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
XX rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
XX antibodies contain non-murine framework regions so are suitable for use
XX in humans. Enhanced types of LM609 have affinity more than 90 times
XX greater than that of parent the parent antibody.
XX
XX Sequence 10 AA;
XX
XX Query Match 92.6%; Score 50; DB 19; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 0.025;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 ARHNYGSEFA 9
XX | | | | | | | |
XX Db 1 ARHNYGSEFA 9
XX
XX RESULT 9
XX AAW76029
XX ID AAW76029 standard; Protein; 10 AA.
XX
XX AC AAW76029;
XX
XX DT 02-NOV-1998 (first entry)
XX
XX DE LM609 grafted antibody V-H region CDR3 protein fragment #11.
XX
XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
XX LM609; inhibitor; integrin-mediated signal transduction; treatment;
XX diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
XX neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
XX macular degeneration; osteoporosis; primer; V-H region; CDR;
XX complementarity determining region.
XX
XX OS Mus sp.
XX
XX PN WO9833919-A2.
XX
XX PD 06-AUG-1998.
XX
XX PF 30-JAN-1998; 98WO-US01826.
XX
XX PR 30-JAN-1997; 97US-0791391.
XX
XX PA (IXSY-) IXSYS INC.
XX
XX PI Glaser SM, Huse WD;
XX
XX DR WPI: 1998-437472/37.
XX DR N-PSDB; AAV49865.
XX
XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
XX integrin - and related grafted antibodies based on murine monoclonal
XX LM609, also related nucleic acid, used to treat, prevent or diagnose
XX PT angiogenesis or restenosis
XX
XX Disclosure; Page 40; 129pp; English.
XX
XX AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
XX LM609 heavy and light chain variable region. LM609 and the antibody
XX vitaxin bind selectively to integrin alphavbeta3 and can be used to

```

CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
 CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
 CC antibodies contain non-murine framework regions so are suitable for use
 CC in humans. Enhanced types of LM609 have affinity more than 90 times
 CC greater than that of parent the parent antibody.

XX Sequence 10 AA;

Query Match 92.6%; Score 50; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.025;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9
 |||||

Db 1 ARHNYGSFA 9

RESULT 11

AAB61368
 ID AAB61368 standard; peptide; 10 AA.

AC AAB61368;

DT 03-APR-2001 (first entry)

XX LM609 VH CDR3 peptide.

DE LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis.

XX Unidentified.

XX WO200078815-A1.

XX 28-DEC-2000.

PF 23-JUN-2000; 2000WO-US17454.

XX 24-JUN-1999; 99US-0339922.

XX (MOLE-) APPLIED MOLECULAR EVOLUTION.

PI Huse WD, Wu H;

XX WPI; 2001-050110/06.

XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -

XX Disclosure; Page 39; 132pp; English.

XX The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphavbeta_3 integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.

XX Sequence 10 AA;

Query Match 92.6%; Score 50; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.025;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9

|||||

Db 1 ARHNYGSFA 9

RESULT 12

AAB61383
 ID AAB61383 standard; peptide; 10 AA.

XX AAB61383;

DT 03-APR-2001 (first entry)

XX Mutant VH CDR3 peptide #6.

DE LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis.

XX Unidentified.

XX WO200078815-A1.

XX 28-DEC-2000.

PF 23-JUN-2000; 2000WO-US17454.

XX 24-JUN-1999; 99US-0339922.

XX (MOLE-) APPLIED MOLECULAR EVOLUTION.

PI Huse WD, Wu H;

XX WPI; 2001-050110/06.

XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -

XX Disclosure; Page 41; 132pp; English.

XX The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphavbeta_3 integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.

XX Sequence 10 AA;

Query Match 92.6%; Score 50; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.025;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9

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Db 1 ARHNYGSFA 9

RESULT 13

AAB61384
 ID AAB61384 standard; peptide; 10 AA.

XX AAB61384;

XX 03-APR-2001 (first entry)

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XX DE Mutant VH CDR3 peptide #7.
XX KW LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
XX KW inflammatory; cancer; retina; restenosis; osteoporosis.
XX OS Unidentified.
XX PN WO200078815-A1.
XX XX 28-DEC-2000.
XX PF 23-JUN-2000; 2000WO-US17454.
XX PR 24-JUN-1999; 99US-0339922.
XX PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX PI Huse WD, Wu H;
XX XX WPI; 2001-050110/06.
XX XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
XX PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
XX PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
XX PT osteoporosis.
XX PS Disclosure; Page 41; 132pp; English.
XX CC The present invention relates to enhanced LM609 grafted antibodies
XX CC exhibiting selective binding affinity to alphavbeta_3 integrin or
XX CC their functional fragments. The antibodies or their functional
XX CC fragments can be used in the diagnosis and treatment of
XX CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
XX CC diseases (such as psoriasis and chronic articular rheumatism),
XX CC disorders associated with inappropriate or inopportune invasion of
XX CC vessels (such as diabetic retinopathy, neovascular glaucoma and
XX CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
XX CC diseases (such as macular degeneration), restenosis and
XX CC osteoporosis.
XX SQ Sequence 10 AA;
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XX CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 ARHNYGSFA 9
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XX ID AAB61385 standard; peptide; 10 AA.
XX AC AAB61385;
XX XX 03-APR-2001 (first entry)
XX DT 03-APR-2001 (first entry)
XX DE Mutant VH CDR3 peptide #8.
XX XX LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
XX KW inflammatory; cancer; retina; restenosis; osteoporosis.
XX OS Unidentified.
XX PN WO200078815-A1.
XX XX 28-DEC-2000.
XX PF 23-JUN-2000; 2000WO-US17454.
XX PR 24-JUN-1999; 99US-0339922.
XX PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX PI Huse WD, Wu H;
XX XX WPI; 2001-050110/06.
XX XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
XX PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
XX PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
XX PT osteoporosis.
XX PS Disclosure; Page 41; 132pp; English.
XX CC The present invention relates to enhanced LM609 grafted antibodies
XX CC exhibiting selective binding affinity to alphavbeta_3 integrin or
XX CC their functional fragments. The antibodies or their functional
XX CC fragments can be used in the diagnosis and treatment of
XX CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
XX CC diseases (such as psoriasis and chronic articular rheumatism),
XX CC disorders associated with inappropriate or inopportune invasion of
XX CC vessels (such as diabetic retinopathy, neovascular glaucoma and
XX CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
XX CC diseases (such as macular degeneration), restenosis and
XX CC osteoporosis.
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XX ID AAB61386 standard; peptide; 10 AA.
XX AC AAB61386;
XX XX 03-APR-2001 (first entry)
XX DT 03-APR-2001 (first entry)
XX DE Mutant VH CDR3 peptide #9.
XX XX LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
XX KW inflammatory; cancer; retina; restenosis; osteoporosis.
XX OS Unidentified.
XX PN WO200078815-A1.
XX XX 28-DEC-2000.
XX PF 23-JUN-2000; 2000WO-US17454.
XX PR 24-JUN-1999; 99US-0339922.
XX PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX PI Huse WD, Wu H;
XX XX WPI; 2001-050110/06.
XX XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
XX PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
XX PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
XX PT osteoporosis.
XX PS Disclosure; Page 41; 132pp; English.

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PR 24-JUN-1999; 99US-0339922.
XX (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX PI Huse WD, Wu H;
XX XX WPI; 2001-050110/06.
XX XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
XX PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
XX PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
XX PT osteoporosis.
XX PS Disclosure; Page 41; 132pp; English.
XX CC The present invention relates to enhanced LM609 grafted antibodies
XX CC exhibiting selective binding affinity to alphavbeta_3 integrin or
XX CC their functional fragments. The antibodies or their functional
XX CC fragments can be used in the diagnosis and treatment of
XX CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
XX CC diseases (such as psoriasis and chronic articular rheumatism),
XX CC disorders associated with inappropriate or inopportune invasion of
XX CC vessels (such as diabetic retinopathy, neovascular glaucoma and
XX CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
XX CC diseases (such as macular degeneration), restenosis and
XX CC osteoporosis.
XX SQ Sequence 10 AA;
XX CC Query Match 92.6%; Score 50; DB 22; Length 10;
XX CC Best Local Similarity 100.0%; Pred. No. 0.025;
XX CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 ARHNYGSFA 9
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XX AC AAB61386;
XX XX 03-APR-2001 (first entry)
XX DT 03-APR-2001 (first entry)
XX DE Mutant VH CDR3 peptide #9.
XX XX LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
XX KW inflammatory; cancer; retina; restenosis; osteoporosis.
XX OS Unidentified.
XX PN WO200078815-A1.
XX XX 28-DEC-2000.
XX PF 23-JUN-2000; 2000WO-US17454.
XX PR 24-JUN-1999; 99US-0339922.
XX PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX PI Huse WD, Wu H;
XX XX WPI; 2001-050110/06.
XX XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
XX PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
XX PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
XX PT osteoporosis.
XX PS Disclosure; Page 41; 132pp; English.

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XX The present invention relates to enhanced LM609 grafted antibodies
CC exhibiting selective binding affinity to alphaVbeta3 integrin or
CC their functional fragments. The antibodies or their functional
CC fragments can be used in the diagnosis and treatment of
CC alphaVbeta3-mediated diseases such as angiogenesis, inflammatory
CC diseases (such as psoriasis and chronic articular rheumatism),
CC disorders associated with inappropriate or inopportune invasion of
CC vessels (such as diabetic retinopathy, neovascular glaucoma and
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
CC diseases (such as macular degeneration), restenosis and
CC osteoporosis.

XX SQ Sequence 10 AA;
Query Match 92.6%; Score 50; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ARHNYGSFA 9

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Job time : 13.8235 secs

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Title: US-09-016-061-80

Perfect score: 54

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Total number of hits satisfying chosen parameters: 97044

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	50	92.6	117	8	US-08-791-391A-6
5	36	66.7	14	1	US-08-677-599B-22
6	36	66.7	101	10	US-09-764-853-432
7	34	63.0	30	10	US-09-839-884-40
8	34	63.0	287	10	US-09-415-540-5
9	33	61.1	14	1	US-08-677-599B-21
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14	32	59.3	14	1	US-08-677-599B-15
15	32	59.3	14	1	US-08-677-599B-16
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Sequence 58, Appl
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ALIGNMENTS

RESULT 1
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; Sequence 2, Application US/08790540A
; Patent No. US2001001125A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,540A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-790-540A-2

Query Match 92.6%; Score 50; DB 8; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.005;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
|||||
Db 97 ARHNYGSFA 105

RESULT 2
US-08-790-540A-6
; Sequence 6, Application US/08790540A
; Patent No. US20010011125A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,540A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122

Query Match 92.6%; Score 50; DB 8; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.005;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
|||||
Db 97 ARHNYGSFA 105

RESULT 3
US-08-791-391A-2
; Sequence 2, Application US/08791391A
; Patent No. US200100116645A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122

Query Match 92.6%; Score 50; DB 8; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.005;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
|||||
Db 97 ARHNYGSFA 105

RESULT 4
US-08-791-391A-6
; Sequence 6, Application US/08791391A
; Patent No. US200100116645A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,391A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122

Query Match 92.6%; Score 50; DB 8; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.005;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
|||||
Db 97 ARHNYGSFA 105

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,391A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,391A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,391A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,391A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122

Query Match 92.6%; Score 50; DB 8; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.005;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
|||||
Db 97 ARHNYGSFA 105

RESULT 4
US-08-791-391A-6
; Sequence 6, Application US/08791391A
; Patent No. US200100116645A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,391A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122

Query Match 92.6%; Score 50; DB 8; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.005;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
|||||
Db 97 ARHNYGSFA 105

Query Match 92.6%; Score 50; DB 8; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.005;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSA 9
DB 97 ARHNYGSA 105

RESULT 5
US-08-677-599B-22
; Sequence 22, Application US/08677599B
; Patent No. US20020155117A1
; GENERAL INFORMATION:
; APPLICANT: Sucia-Foca, Nicole
; TITLE OF INVENTION: METHODS FOR DETECTING ORGAN ALLOGRAFT
; TITLE OF INVENTION: REJECTION AND USES THEREOF
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/677,599B
; FILING DATE: 08-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq., John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 50161-A
; TELEPHONE: 212/278/0400
; TELEFAX: 212/391/0525
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-677-599B-22

Query Match 66.7%; Score 36; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYG 6
DB 9 ARHNYG 14

RESULT 6
US-09-764-853-432
; Sequence 432, Application US/09764853
; Patent No. US20020090672A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJ206
; CURRENT APPLICATION NUMBER: US/09/764,853
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 939
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 432
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-853-432

Query Match 66.7%; Score 36; DB 10; Length 101;
Best Local Similarity 85.7%; Pred. No. 2.2;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYSF 8
DB 64 RHNYSF 70

RESULT 7
US-09-839-884-40
; Sequence 40, Application US/09839884
; Patent No. US20020076739A1
; GENERAL INFORMATION:
; APPLICANT: Abersold, Rudolf H.
; APPLICANT: Gelb, Michael H.
; APPLICANT: Gygi, Steven
; APPLICANT: Scott, C R
; APPLICANT: Turecek, Frantisek
; APPLICANT: Gerber, Scott A
; APPLICANT: Rist, Beate
; TITLE OF INVENTION: Rapid Quantitative Analysis of Proteins or Protein
; FILE REFERENCE: 64-98A
; CURRENT APPLICATION NUMBER: US/09/839,884
; CURRENT FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: 09/383,062
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 60/097,788
; PRIOR FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40
; LENGTH: 30
; TYPE: PRT
; ORGANISM: yeast
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (2)
; OTHER INFORMATION: C at position 2 is ICAT-labeled cysteinyl residue.
US-09-839-884-40

Query Match 63.0%; Score 34; DB 10; Length 30;
Best Local Similarity 83.3%; Pred. No. 1.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
DB 10 HNYGAF 15

RESULT 8
US-09-415-540-5
; Sequence 5, Application US/09415540
; Patent No. US20010010911A1
; GENERAL INFORMATION:
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: A NOVEL HUMAN PYROPHOSPHATASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/415,540
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/741,437
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0148 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 855-0555
TELEFAX: (415) 845-4166
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 287 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 4199
US-09-415-540-5

Query Match 63.0%; Score 34; DB 10; Length 287;
Best Local Similarity 83.3%; Pred. No. 16;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSP 8
DB 92 HNYGAF 97

RESULT 9
US-08-677-599B-21
Sequence 21, Application US/08677599B
Patent No. US20020155117A1
GENERAL INFORMATION:
APPLICANT: Sucia-Foca, Nicole
TITLE OF INVENTION: METHODS FOR DETECTING ORGAN ALLOGRAFT
TITLE OF INVENTION: REJECTION AND USES THEREOF
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/677,599B
FILING DATE: 08-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White Esq., John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 50161-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212/278/0400
TELEFAX: 212/391/0525
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:

LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-677-599B-21

Query Match 61.1%; Score 33; DB 1; Length 14;
Best Local Similarity 83.3%; Pred. No. 0.97;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYG 6
DB 9 SRHNYG 14

RESULT 10
US-08-677-599B-11
Sequence 11, Application US/08677599B
Patent No. US20020155117A1
GENERAL INFORMATION:
APPLICANT: Sucia-Foca, Nicole
TITLE OF INVENTION: METHODS FOR DETECTING ORGAN ALLOGRAFT
TITLE OF INVENTION: REJECTION AND USES THEREOF
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/677,599B
FILING DATE: 08-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White Esq., John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 50161-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212/278/0400
TELEFAX: 212/391/0525
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-677-599B-11

Query Match 59.3%; Score 32; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHNYG 6
DB 10 RHNYG 14

RESULT 11
US-08-677-599B-12
Sequence 12, Application US/08677599B
Patent No. US20020155117A1
GENERAL INFORMATION:
APPLICANT: Sucia-Foca, Nicole
TITLE OF INVENTION: METHODS FOR DETECTING ORGAN ALLOGRAFT

;; TITLE OF INVENTION: REJECTION AND USES THEREOF
;; NUMBER OF SEQUENCES: 23
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Cooper & Dunham LLP
;; STREET: 1185 Avenue of the Americas
;; CITY: New York
;; STATE: New York
;; COUNTRY: USA
;; ZIP: 10036
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/677,599B
;; FILING DATE: 08-JUL-1996
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: White Esq., John P.
;; REGISTRATION NUMBER: 28,678
;; REFERENCE/DOCKET NUMBER: 50161-A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 212/278/0400
;; TELEFAX: 212/391/0525
;; INFORMATION FOR SEQ ID NO: 12:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 14 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-08-677-599B-12

Query Match 59.3%; Score 32; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHNYG 6
Db 10 RHNYG 14

RESULT 12
US-08-677-599B-13
; Sequence 13, Application US/08677599B
; Patent No. US20020155117A1
; GENERAL INFORMATION:
; APPLICANT: Sucia-Foca, Nicole
; TITLE OF INVENTION: METHODS FOR DETECTING ORGAN ALLOGRAFT
; REJECTION AND USES THEREOF
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/677,599B
; FILING DATE: 08-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq., John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 50161-A
; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: 212/278/0400
;; TELEFAX: 212/391/0525
;; INFORMATION FOR SEQ ID NO: 13:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 14 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-08-677-599B-13

Query Match 59.3%; Score 32; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHNYG 6
Db 10 RHNYG 14

RESULT 13
US-08-677-599B-14
; Sequence 14, Application US/08677599B
; Patent No. US20020155117A1
; GENERAL INFORMATION:
; APPLICANT: Sucia-Foca, Nicole
; TITLE OF INVENTION: METHODS FOR DETECTING ORGAN ALLOGRAFT
; REJECTION AND USES THEREOF
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/677,599B
; FILING DATE: 08-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq., John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 50161-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212/278/0400
; TELEFAX: 212/391/0525
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-677-599B-14

Query Match 59.3%; Score 32; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHNYG 6
Db 10 RHNYG 14

RESULT 14
US-08-677-599B-15
; Sequence 15, Application US/08677599B

Patent No. US20020155117A1
GENERAL INFORMATION:
APPLICANT: Sucia-Foca, Nicole
TITLE OF INVENTION: METHODS FOR DETECTING ORGAN ALLOGRAFT
REJECTION AND USES THEREOF
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/677,599B
FILING DATE: 08-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White Esq., John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 50161-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212/278/0400
TELEFAX: 212/391/0525
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-677-599B-15

Query Match 59.3%; Score 32; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHNYG 6
|||||
Db 10 RHNYG 14

RESULT 15
US-08-677-599B-16
Sequence 16, Application US/08677599B
Patent No. US20020155117A1
GENERAL INFORMATION:
APPLICANT: Sucia-Foca, Nicole
TITLE OF INVENTION: METHODS FOR DETECTING ORGAN ALLOGRAFT
REJECTION AND USES THEREOF
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/677,599B
FILING DATE: 08-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: White Esq., John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 50161-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212/278/0400
TELEFAX: 212/391/0525
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-677-599B-16

Query Match 59.3%; Score 32; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHNYG 6
|||||
Db 10 RHNYG 14

Search completed: November 18, 2002, 18:45:17
Job time : 1.96078 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:01 ; Search time 4.2402 Seconds
(without alignments)
69.390 Million cell updates/sec

Title: US-09-016-061-80
Perfect score: 54
Sequence: 1 ARHNYGSFAA 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	36	66.7	94	3	US-09-147-550-45
3	36	66.7	94	3	US-09-147-550-48
4	36	66.7	94	3	US-09-147-550-77
5	36	66.7	94	3	US-09-147-550-84
6	36	66.7	94	3	US-09-147-550-90
7	36	66.7	94	3	US-09-147-550-101
8	36	66.7	94	4	US-09-557-917-14
9	36	66.7	94	4	US-09-557-917-45
10	36	66.7	94	4	US-09-557-917-48
11	36	66.7	94	4	US-09-557-917-77
12	36	66.7	94	4	US-09-557-917-84
13	36	66.7	94	4	US-09-557-917-90
14	36	66.7	94	4	US-09-557-917-101
15	36	66.7	119	3	US-08-767-128-6
16	34	63.0	191	4	US-09-443-041A-24
17	34	63.0	236	4	US-09-443-041A-30
18	34	63.0	260	4	US-09-443-041A-10
19	34	63.0	261	4	US-09-443-041A-26
20	34	63.0	269	4	US-09-443-041A-28
21	34	63.0	271	4	US-09-443-041A-32
22	34	63.0	271	4	US-09-443-041A-33
23	34	63.0	286	2	US-08-809-267-3
24	34	63.0	286	5	PCT-US95-13662A-3
25	34	63.0	287	2	US-08-741-437-5
26	34	63.0	287	2	US-09-134-593-5
27	32	59.3	15	1	US-08-618-464-7

28 32 59.3 15 4 US-09-107-615-7 Sequence 7, Appl1
29 32 59.3 16 4 US-09-181-896-2 Sequence 2, Appl1
30 32 59.3 25 2 US-08-480-130-44 Sequence 44, Appl
31 32 59.3 25 2 US-08-488-379-44 Sequence 44, Appl
32 32 59.3 25 5 PCT-US93-07545-44 Sequence 44, Appl
33 32 59.3 36 1 US-08-053-131-84 Sequence 84, Appl
34 32 59.3 36 1 US-08-645-641-84 Sequence 84, Appl
35 32 59.3 36 1 US-07-853-408B-84 Sequence 84, Appl
36 32 59.3 36 2 US-08-096-762-84 Sequence 84, Appl
37 32 59.3 36 2 US-08-308-865-84 Sequence 84, Appl
38 32 59.3 36 4 US-09-042-353-281 Sequence 129, App
39 32 59.3 36 4 US-08-758-417A-129 Sequence 129, App
40 32 59.3 36 5 PCT-US92-10983-84 Sequence 84, Appl
41 32 59.3 80 1 US-08-264-250A-1 Sequence 1, Appl1
42 32 59.3 89 1 US-08-025-038-30 Sequence 30, Appl
43 32 59.3 89 1 US-08-039-137-17 Sequence 17, Appl
44 32 59.3 90 2 US-08-485-133-23 Sequence 23, Appl
45 32 59.3 94 3 US-09-147-550-12 Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-09-147-550-14
; Sequence 14, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-14

Query Match 66.7% Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
Db 80 RHNYGVF 86
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RESULT 2
US-09-147-550-45
; Sequence 45, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979

; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-45

Query Match 66.7%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 2 RHNYGSF 8
| | | | |
Db 80 RHNYGVF 86

RESULT 3

US-09-147-550-48
; Sequence 48, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-48

Query Match 66.7%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 2 RHNYGSF 8
| | | | |
Db 80 RHNYGVF 86

RESULT 4

US-09-147-550-77
; Sequence 77, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 77
; LENGTH: 94

; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-77

Query Match 66.7%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 2 RHNYGSF 8
| | | | |
Db 80 RHNYGVF 86

RESULT 5

US-09-147-550-84
; Sequence 84, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-84

Query Match 66.7%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 2 RHNYGSF 8
| | | | |
Db 80 RHNYGVF 86

RESULT 6

US-09-147-550-90
; Sequence 90, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 90
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-90

Query Match 66.7%; Score 36; DB 3; Length 94;

Best Local Similarity 85.7%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
Db 80 RHNYGVF 86

RESULT 7
US-09-147-550-101
; Sequence 101, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-101

Query Match 66.7%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
Db 80 RHNYGVF 86

RESULT 8
US-09-557-917-14
; Sequence 14, Application US/09557917
; Patent No. 6284457
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; PRIOR APPLICATION NUMBER: 2000-04-21
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-14

Query Match 66.7%; Score 36; DB 4; Length 94;
Best Local Similarity 85.7%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
Db 80 RHNYGVF 86

RESULT 9
US-09-557-917-45
; Sequence 45, Application US/09557917
; Patent No. 6284457
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-45

Query Match 66.7%; Score 36; DB 4; Length 94;
Best Local Similarity 85.7%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
Db 80 RHNYGVF 86

RESULT 10
US-09-557-917-48
; Sequence 48, Application US/09557917
; Patent No. 6284457
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-48

Query Match 66.7%; Score 36; DB 4; Length 94;
Best Local Similarity 85.7%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8

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Db      80 RHNYGVF 86

RESULT 11
US-09-557-917-77
; Sequence 77, Application US/09557917
; Patent No. 6284457
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 77
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-77

Query Match      66.7%; Score 36; DB 4; Length 94;
Best Local Similarity 85.7%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

QY      2 RHNYGSF 8
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Db      80 RHNYGVF 86

RESULT 12
US-09-557-917-84
; Sequence 84, Application US/09557917
; Patent No. 6284457
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-84

Query Match      66.7%; Score 36; DB 4; Length 94;
Best Local Similarity 85.7%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

QY      2 RHNYGSF 8
      ||||| |
Db      80 RHNYGVF 86

RESULT 13
US-09-557-917-90
; Sequence 90, Application US/09557917
; Patent No. 6284457
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 90
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-90

Query Match      66.7%; Score 36; DB 4; Length 94;
Best Local Similarity 85.7%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 RHNYGSF 8
      ||||| |
Db      80 RHNYGVF 86

RESULT 14
US-09-557-917-101
; Sequence 101, Application US/09557917
; Patent No. 6284457
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-101

Query Match      66.7%; Score 36; DB 4; Length 94;
Best Local Similarity 85.7%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 RHNYGSF 8
      ||||| |
Db      80 RHNYGVF 86
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Search completed: November 18, 2002, 17:43:39
Job time : 5.2402 secs

RESULT 15
US-08-767-128-6
; Sequence 6, Application US/08767128
; Patent No. 6111079
; GENERAL INFORMATION:
; APPLICANT: WYLIE, DWANE E.
; APPLICANT: LOPEZ, OSVALDO
; APPLICANT: MURRAY, PETER JOSEPH
; APPLICANT: GOEBEL, PETER
; TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
; TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
; STREET: 3100 No. 6111079west Center, 90 South Seventh St
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/767,128
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE: 04-DEC-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/09258
; FILING DATE: 05-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/541,373
; FILING DATE: 10-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/462,798
; FILING DATE: 05-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G.
; REGISTRATION NUMBER: 35,093
; REFERENCE/DOCKET NUMBER: 8648.49USF1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/371-5278
; TELEFAX: 612/332-9081
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; US-08-767-128-6

Query Match 66.7%; Score 36; DB 3; Length 119;
Best Local Similarity 66.7%; Pred. No. 20;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9

|||:|:|

Db 97 ARHHYGYA 105

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:01 ; Search time 6.37255 Seconds
(without alignments)
196.114 Million cell updates/sec

Title: US-09-016-061-82

Perfect score: 72

Sequence: 1 QASQSISNLFHWY 13

Scoring table: BLOSUM62

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Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	65	90.3	106	2	PL0267
2	65	90.3	123	2	S35479
3	62	86.1	122	2	S40370
4	61	84.7	107	2	S32188
5	60	83.3	96	2	G33730
6	60	83.3	103	2	S19975
7	59	81.9	95	2	PH0867
8	59	81.9	102	2	S26346
9	59	81.9	104	2	B43413
10	59	81.9	107	2	B45722
11	59	81.9	107	2	A45722
12	59	81.9	138	2	A26471
13	58	80.6	62	2	S42265
14	58	80.6	87	2	I52592
15	58	80.6	88	2	S34088
16	58	80.6	88	2	S34087
17	58	80.6	95	2	PH0862
18	58	80.6	107	2	C45722
19	58	80.6	108	2	S19674
20	58	80.6	110	2	S44118
21	58	80.6	117	2	S43528
22	58	80.6	117	2	S42263
23	58	80.6	127	2	S40367
24	58	80.6	129	1	K1HUWK
25	58	80.6	129	2	S52789
26	55	76.4	122	2	S40314
27	54	75.0	92	1	KVR838
28	54	75.0	93	2	S38564
29	54	75.0	106	2	PC4282

30 54 75.0 107 2 B28044 Ig kappa chain V r
31 54 75.0 107 2 A28044 Ig kappa chain V r
32 54 75.0 107 2 D48677 Ig kappa chain V-J
33 54 75.0 107 2 B49026 Ig kappa chain V r
34 54 75.0 107 2 S69901 Ig kappa chain (cl
35 54 75.0 107 2 S69906 Ig kappa chain (cl
36 54 75.0 108 1 KVM5AR Ig kappa chain V r
37 54 75.0 108 2 C28405 Ig kappa chain V r
38 54 75.0 108 2 B30551 Ig kappa chain V r
39 54 75.0 108 2 PL0282 Ig kappa chain V r
40 54 75.0 108 2 S38862 Ig kappa chain V r
41 54 75.0 108 2 S69903 Ig kappa chain (cl
42 54 75.0 108 2 S69900 Ig kappa chain (cl
43 54 75.0 108 2 S69902 Ig kappa chain (cl
44 54 75.0 115 2 JL0080 Ig kappa chain pre
45 54 75.0 115 2 A53276 Ig kappa chain V r

ALIGNMENTS

RESULT 1

PL0267

Ig kappa chain V region (anti-DNA, DPL2VK) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000

C:Accession: PL0267

R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein J. Exp. Med. 171, 265-297, 1990

A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat

A:Reference number: PL0231; MUID:90111618; PMID:2104919

A:Accession: PL0267

A:Molecule type: mRNA

A:Residues: 1-106 <SHL>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-23/Region: framework 1

F:16-90/Domain: immunoglobulin homology <IMM>

F:24-34/Region: complementarity-determining 1

F:35-49/Region: framework 2

F:50-56/Region: complementarity-determining 2

F:57-88/Region: framework 3

F:89-97/Region: complementarity-determining 3

F:98-106/Region: framework 4

Query Match 90.3%; Score 65; DB 2; Length 106;
Best Local Similarity 84.6%; Pred.No. 0.00031;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQSISNLFHWY 13

Db 24 RASQSISNLFHWY 36

RESULT 2

S35479

Ig kappa chain precursor V region - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 19-Mar-1997 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000

C:Accession: S35479

R:Takeda, Y.; Wise, K.S.; Hoffman, R.W.

Nucleic Acids Res. 20, 4099, 1992

A:Title: Nucleotide sequences of immunoglobulin heavy and light chain V-regions from anti-glycoprotein

A:Reference number: S35479

A:Accession: S35479

A:Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-123 <TAK>

C:Cross-references: EMBL:M93959; NID:g197572; PIDN:AAA39079.1; PID:g554148

C:Genetics:

A:Map position: 6

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-12/Domain: signal sequence (fragment) #status predicted <SIG>
F:13-123/Product: Ig kappa chain V region (fragment) #status predicted <MAT>
F:28-102/Domain: immunoglobulin homology <IMM>

Query Match 90.3%; Score 65; DB 2; Length 123;
Best Local Similarity 84.6%; Pred. No. 0.00036;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQTSISNLFHWY 13
:|||||:|||||
Db 36 RASQTSISNLFHWY 48

RESULT 3
S40370
Ig kappa chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40370
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40370
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-122 <KLE>
A:Cross-references: EMBL:X72480; NID:g441428; PIDN:CAA51148.1; PID:g441429
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:30-104/Domain: immunoglobulin homology <IMM>

Query Match 86.1%; Score 62; DB 2; Length 122;
Best Local Similarity 84.6%; Pred. No. 0.0012;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQTSISNLFHWY 13
:|||||:|||||
Db 38 RASQTSISNLFHWY 50

RESULT 4
S32188
Ig kappa chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C:Accession: S32188
R:Izui, S.
submitted to the EMBL Data Library, February 1993
A:Reference number: S32185
A:Accession: S32188
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-107 <IZU>
A:Cross-references: EMBL:X70090; NID:g288253; PIDN:CAA49695.1; PID:g288254
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 84.7%; Score 61; DB 2; Length 107;
Best Local Similarity 76.9%; Pred. No. 0.0016;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQTSISNLFHWY 13
:|||||:|||||
Db 24 RASQTSISNLFHWY 36

RESULT 5
G33730
Ig kappa chain V region (23.32) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 21-Jan-2000

C:Accession: G33730
R:Lawler, A.M.; Kearney, J.F.; Kuehl, M.; Gearhart, P.J.
Proc. Natl. Acad. Sci. U.S.A. 86, 6744-6747, 1989
A:Title: Early rearrangements of genes encoding murine immunoglobulin kappa-chains, u
A:Reference number: A33730; MUID:89367325; PMID:2505260
A:Accession: G33730
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-96 <LAW>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 83.3%; Score 60; DB 2; Length 96;
Best Local Similarity 76.9%; Pred. No. 0.0021;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQTSISNLFHWY 13
:|||||:|||||
Db 24 RASQTSISNLFHWY 36

RESULT 6
SI9975
Ig kappa chain V region (M-T408) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C:Accession: SI9975
R:Weissenhorn, W.; Riethmuller, G.; Weiss, E.M.; Rieber, E.P.
submitted to the EMBL Data Library, March 1992
A:Description: Structural characterization of CD4 mAb.
A:Reference number: SI9963
A:Accession: SI9975
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-103 <WEI>
A:Cross-references: EMBL:X65097; NID:g52296; PIDN:CAA46225.1; PID:g52297
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:11-85/Domain: immunoglobulin homology <IMM>

Query Match 83.3%; Score 60; DB 2; Length 103;
Best Local Similarity 76.9%; Pred. No. 0.0022;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQTSISNLFHWY 13
:|||||:|||||
Db 19 RASQTSISNLFHWY 31

RESULT 7
PH0867
Ig kappa chain V region (anti-DNA, R3.5H5G) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 21-Jan-2000
C:Accession: PH0867
R:Mauchelme-Lory, A.; Katz, J.B.; Pillinger, M.; Gosselin, C.; Smith, A.; Diamond, B.
J. Exp. Med. 174, 1639-1652, 1991
A:Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idiot
A:Reference number: PH0862; MUID:92078875; PMID:1660528
A:Accession: PH0867
A:Molecule type: DNA
A:Residues: 1-95 <MAN>
C:Comment: This antibody is produced by Epstein-Barr virus-transformed B cell that be
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-23/Region: framework 1
F:16-90/Domain: immunoglobulin homology <IMM>
F:24-34/Region: complementarity-determining 1
F:35-49/Region: framework 2
F:50-56/Region: complementarity-determining 2
F:57-88/Region: framework 3
F:89-95/Region: complementarity-determining 3

Query Match 81.9%; Score 59; DB 2; Length 95;
 Best Local Similarity 76.9%; Pred. No. 0.003;
 Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISNLFHWY 13
 :|||||:|||||
 Db 24 RASQISNLFHWY 36

RESULT 8
 S26346
 Ig kappa chain V region - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
 C:Accession: S26346
 R:Stark, S.E.; Caton, A.J.
 J. Exp. Med. 174, 613-624, 1991
 A:Title: Antibodies that are specific for a single amino acid interchange in a protein e
 A:Reference number: S26309; MUID:91341421; PMID:1908510
 A:Accession: S26346
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-102 <STA>
 A:Cross-references: EMBL:X59211; NID:g52338; PIDN:CAA41921.1; PID:g1334075
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:14-88/Domain: immunoglobulin homology <IMM>

Query Match 81.9%; Score 59; DB 2; Length 102;
 Best Local Similarity 84.6%; Pred. No. 0.0033;
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISNLFHWY 13
 :|||||:|||||
 Db 22 RASQISNLFHWY 34

RESULT 9
 B43413
 Ig kappa chain V region - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
 C:Accession: B43413
 R:Tomiya, Y.; Brojer, E.; Ruggeri, Z.M.; Shattil, S.J.; Smiltneck, J.; Gorski, J.; Kun
 J. Biol. Chem. 267, 18085-18092, 1992
 A:Title: A molecular model of RGD ligands. Antibody D gene segments that direct specific
 A:Reference number: A43413; MUID:92388177; PMID:1517241
 A:Accession: B43413
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: nucleic acid
 A:Residues: 1-104 <TOM>
 A:Note: sequence extracted from NCBI backbone (NCBIP:112818)
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:13-87/Domain: immunoglobulin homology <IMM>

Query Match 81.9%; Score 59; DB 2; Length 104;
 Best Local Similarity 84.6%; Pred. No. 0.0034;
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISNLFHWY 13
 :|||||:|||||
 Db 21 RASQISNLFHWY 33

RESULT 10
 B45722
 anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 33) - mouse (fr
 C:Species: Mus musculus (house mouse)
 C:Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
 C:Accession: B45722
 R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Vasqu

J. Virol. 67, 489-496, 1993
 A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on
 A:Reference number: A45722; MUID:93100833; PMID:7677958
 A:Accession: B45722
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: nucleic acid
 A:Residues: 1-107 <SIM>
 A:Note: sequence extracted from NCBI backbone (NCBIP:120590)
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: glycoprotein
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 81.9%; Score 59; DB 2; Length 107;
 Best Local Similarity 84.6%; Pred. No. 0.0035;
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISNLFHWY 13
 :|||||:|||||
 Db 24 RASQISNLFHWY 36

RESULT 11
 A45722
 anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 5) - mouse (C
 C:Species: Mus musculus (house mouse)
 C:Date: 03-Mar-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
 C:Accession: A45722
 R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Va
 J. Virol. 67, 489-496, 1993
 A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on
 A:Reference number: A45722; MUID:93100833; PMID:7677958
 A:Accession: A45722
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-107 <SIM>
 A:Note: sequence extracted from NCBI backbone (NCBIP:120589)
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: glycoprotein
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 81.9%; Score 59; DB 2; Length 107;
 Best Local Similarity 84.6%; Pred. No. 0.0035;
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISNLFHWY 13
 :|||||:|||||
 Db 24 RASQISNLFHWY 36

RESULT 12
 A26471
 Ig kappa chain precursor V region (MAK33) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 23-Jul-1999
 C:Accession: A26471
 R:Buckel, P.; Hubner-Parajsz, C.; Mattes, R.; Lenz, H.; Haug, H.; Beaucamp, K.
 Gene 51, 13-19, 1987
 A:Title: Cloning and nucleotide sequence of heavy- and light-chain cDNAs from a creat
 A:Reference number: A91572; MUID:87248058; PMID:3110009
 A:Accession: A26471
 A:Molecule type: mRNA
 A:Residues: 1-138 <BUG>
 A:Cross-references: GB:M16162; NID:g196893; PIDN:AAA38823.1; PID:g196894
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-20/Domain: signal sequence #status predicted <SIG>
 F:21-138/Product: Ig kappa chain V region #status predicted <MAT>

Query Match 81.9%; Score 59; DB 2; Length 138;
 Best Local Similarity 84.6%; Pred. No. 0.0045;
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISNLFHWY 13

Db 44 RASQISNNLHWY 56
:|||||

RESULT 13

S42265
Ig kappa chain V region (018) - human
C:Species: Homo sapiens (man)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 17-Mar-1999
C:Accession: S42265
R:Scott, M.G.; Crimmins, D.L.; McCourt, D.W.; Chung, G.; Schaeble, K.F.; Thiebe, R.; Que
J. Immunol. 147, 4007-4013, 1991
A:Title: Clonal characterization of the human IgG antibody repertoire to Haemophilus inf
A:Reference number: S42263; MUID:92043792; PMID:1940382
A:Accession: S42265
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-62 <SCD>
A:Cross-references: EMBL:M64856
C:Genetics:
A:Introns: 19/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 80.6%; Score 58; DB 2; Length 62;
Best Local Similarity 76.9%; Pred. No. 0.0029;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISNFLHWY 13
|||||
Db 24 QASQDISNLYNWY 36

RESULT 14

I52592
Ig kappa chain V region - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
C:Accession: I52592
R:Wagner, S.D.; Martinelli, V.; Luzzatto, L.
Blood 83, 3647-3653, 1994
A:Title: Similar patterns of V kappa gene usage but different degrees of somatic mutatio
A:Reference number: I52592; MUID:94264318; PMID:8204889
A:Accession: I52592
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-87 <RES>
A:Cross-references: GB:S71057; NID:g547053; PIDN:AAB30971.1; PID:g547054
C:Genetics:
A:Gene: IGV
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F;9-83/Domain: immunoglobulin homology <IMM>

Query Match 80.6%; Score 58; DB 2; Length 87;
Best Local Similarity 76.9%; Pred. No. 0.0041;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISNFLHWY 13
|||||
Db 17 QASQDISNLYNWY 29

RESULT 15

S34088
Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C:Accession: S34088
R:Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A:Title: V kappa gene segments rearranged in chronic lymphocytic leukemia are distribute
A:Reference number: S34076; MUID:93170387; PMID:8436174
A:Accession: S34088

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-88 <WAG>
A:Cross-references: EMBL:X67172
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;9-83/Domain: immunoglobulin homology <IMM>

Query Match 80.6%; Score 58; DB 2; Length 88;
Best Local Similarity 76.9%; Pred. No. 0.0042;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISNFLHWY 13
|||||
Db 17 QASQDISNLYNWY 29

Search completed: November 18, 2002, 17:47:08
Job time : 6.37255 secs

GenCore version 5.1.3

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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:00 ; Search time 3.18627 Seconds
(without alignments)
169.223 Million cell updates/sec

Title: US-09-016-061-82

Perfect score: 72

Sequence: 1 QASQSTSNFLHWY 13

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	58	80.6	129	1 KVIW_HUMAN	P04431 homo sapien
2	54	75.0	92	1 KV09_RABIT	P01690 oryctolagus
3	54	75.0	108	1 KV5K_MOUSE	P01644 mus musculus
4	54	75.0	108	1 KV5L_MOUSE	P01645 mus musculus
5	54	75.0	108	1 KV5M_MOUSE	P01646 mus musculus
6	54	75.0	117	1 KV10_RABIT	P01691 oryctolagus
7	53	73.6	108	1 KV1B_HUMAN	P01594 homo sapien
8	53	73.6	108	1 KV5U_MOUSE	P04946 mus musculus
9	52	72.2	108	1 KV1P_HUMAN	P01608 homo sapien
10	52	72.2	108	1 KV5J_MOUSE	P01643 mus musculus
11	51	70.8	108	1 KV1H_HUMAN	P01600 homo sapien
12	51	70.8	108	1 KV5N_MOUSE	P01647 mus musculus
13	51	70.8	108	1 KV5Q_MOUSE	P01648 mus musculus
14	50	69.4	108	1 KV1A_HUMAN	P01593 homo sapien
15	49	68.1	115	1 KV3I_HUMAN	P04433 homo sapien
16	48	66.7	115	1 KV5I_MOUSE	P01642 mus musculus
17	48	66.7	117	1 KV1J_HUMAN	P01602 homo sapien
18	48	66.7	129	1 KV3H_HUMAN	P04207 homo sapien
19	47	65.3	107	1 KV04_RABIT	P01685 oryctolagus
20	47	65.3	108	1 KV1M_HUMAN	P01605 homo sapien
21	47	65.3	108	1 KV1N_HUMAN	P01606 homo sapien
22	46.5	64.6	109	1 KV3D_HUMAN	P01622 homo sapien
23	46	63.9	108	1 KV08_RABIT	P01689 oryctolagus
24	46	63.9	108	1 KV1O_HUMAN	P01607 homo sapien
25	46	63.9	111	1 KV12_RABIT	P01693 oryctolagus
26	45	62.5	107	1 KV1D_HUMAN	P01596 homo sapien
27	45	62.5	108	1 KV07_RABIT	P01688 oryctolagus
28	45	62.5	108	1 KV3V_MOUSE	P01674 mus musculus
29	44.5	62.5	109	1 KV03_RABIT	P01684 oryctolagus
30	44.5	61.8	109	1 KV3F_HUMAN	P01624 homo sapien
31	44	61.1	104	1 KV17_RABIT	P01698 oryctolagus
32	44	61.1	108	1 KV1C_HUMAN	P01595 homo sapien
33	44	61.1	108	1 KV1E_HUMAN	P01597 homo sapien

ALIGNMENTS

RESULT 1

```

KVIW_HUMAN
ID KVIW_HUMAN STANDARD; PRT; 129 AA.
AC P04431;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Walker precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85014148; PubMed=6091049;
RA Klobbeck H.G., Combrato G., Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
RT lymphoid cell lines are closely related.";
RL Nucleic Acids Res. 12:6995-7006(1984).
CC -----
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CC -----
CC EMBL; X00965; CAA25477.1; ALT_TERM.
DR PIR; A01883; K1HUWK.
DR HSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 22
FT CHAIN 23 129 IG KAPPA CHAIN V-I REGION WALKER.
FT DOMAIN 23 45 FRAMEWORK-1.
FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 57 71 FRAMEWORK-2.
FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 79 110 FRAMEWORK-3.
FT DOMAIN 111 119 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 120 129 FRAMEWORK-4.
FT DISULFID 45 110 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14069 MW; F941FA07D4AFC2F9 CRC64;

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Query Match 80.6%; Score 58; DB 1; Length 129;

Best Local Similarity 76.9%; Pred. No. 0.002;

Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQSTSNFLHWY 13

:|||||:|

Db 46 RASQSTSNFLHWY 58


```
RESULT 2
KV09_RABIT STANDARD; PRT; 92 AA.
ID KV09_RABIT STANDARD; PRT; 92 AA.
AC P01630;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V region 3381 (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RN SEQUENCE.
RP MEDLINE=75176905; PubMed=1094456;
RX Margolies M.N., Cannon L.E. III, Strosberg A.D., Haber E.;
RA "Diversity of light chain variable region sequences among rabbit
RT antibodies elicited by the same antigens.";
RL Proc. Natl. Acad. Sci. U.S.A. 72:2180-2184(1975).
CC -I- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM ANTIBODY TO TYPE III
CC PNEUMOCOCCI AND WAS ISOLATED FROM THE SERUM OF A SINGLE RABBIT.
DR PIR; A01953; KYRB38.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34 FRAMEWORK-1.
FT DOMAIN 35 49 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 50 56 FRAMEWORK-2.
FT DOMAIN 57 88 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 89 92 FRAMEWORK-3.
FT DOMAIN 93 92 COMPLEMENTARITY-DETERMINING-3.
FT NON_TER 92 92
FT SEQUENCE 92 AA; 9730 MW; 9A36B15913CB3BEE CRC64;
Query Match 75.0%; Score 54; DB 1; Length 92;
Best Local Similarity 76.9%; Pred. No. 0.007; Indels 0; Gaps 0;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 QASQISNFWHY 13
Db 24 QASEISNFWLAWY 36
!!!:!!!:!!

RESULT 3
KV5K_MOUSE STANDARD; PRT; 108 AA.
ID KV5K_MOUSE STANDARD; PRT; 108 AA.
AC P01644;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-V region HP R16.7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE.
RP STRAIN=A/J;
RX MEDLINE=82150934; PubMed=6801658;
RA Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived
RT from five monoclonal anti-p-azophenylarsenate antibodies differing
RT with respect to a crossreactive idiotype.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -I- MISCELLANEOUS: ANTI-ARSONATE HYBRIDOMA PROTEIN.
DR PIR; A01927; KVM5AR.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Antiarsonate antibody.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 108 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
FT SEQUENCE 108 AA; 11954 MW; 22F4642C63EFF58E CRC64;
Query Match 75.0%; Score 54; DB 1; Length 108;
Best Local Similarity 69.2%; Pred. No. 0.0084;
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 1 QASQISNFWHY 13
Db 24 RASQDISNFWLWY 36
!!!:!!!:!!

RESULT 4
KV5L_MOUSE STANDARD; PRT; 108 AA.
ID KV5L_MOUSE STANDARD; PRT; 108 AA.
AC P01645;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-V region HP 93G7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE.
RP STRAIN=A/J;
RX MEDLINE=82150934; PubMed=6801658;
RA Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived
RT from five monoclonal anti-p-azophenylarsenate antibodies differing
RT with respect to a crossreactive idiotype.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -I- MISCELLANEOUS: ANTI-ARSONATE HYBRIDOMA PROTEIN.
DR PIR; A01927; KVM5AR.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Antiarsonate antibody.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 108 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
FT SEQUENCE 108 AA; 11954 MW; 22F4642C63EFF58E CRC64;
Query Match 75.0%; Score 54; DB 1; Length 108;
Best Local Similarity 69.2%; Pred. No. 0.0084;
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 1 QASQISNFWHY 13
Db 24 RASQDISNFWLWY 36
!!!:!!!:!!
```

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RESULT 5
KV5M_MOUSE
ID KV5M_MOUSE STANDARD; PRT; 108 AA.
AC P01646;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-V region HP 133E6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=82150934; PubMed=6801658;
RA Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived
RT from five monoclonal anti-p-azophenylarsenate antibodies differing
RT with respect to a crossreactive idioType";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -1- MISCELLANEOUS: ANTI-ARSONATE HYBRIDOMA PROTEIN.
DR PIR; A01927; KMSAR.
DR HSP; P01607; IREI.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Antiarsonate antibody.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 108 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11989 MW; 4C98599C08EBA09A CRC64;

Query Match 75.0%; Score 54; DB 1; Length 108;
Best Local Similarity 69.2%; Pred. No. 0.0084;
Matches 9; Conservative 3; Mismatches 1; Indels 0; Caps 0;

QY 1 QASQSIISNLFHWY 13
: ||| ||| : |||
Db 24 RASQDISNYLWY 36

RESULT 6
KV10_RABBIT
ID KV10_RABBIT STANDARD; PRT; 117 AA.
AC P01691;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V region 12F2 precursor (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83273646; PubMed=6410392;
RA Dreher K.L., Emorine L., Kindt T.J., Max E.E.;
RT "cDNA clone encoding a complete rabbit immunoglobulin kappa light
RT chain of b4 allotype.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:4489-4493(1983).
CC -1- MISCELLANEOUS: THIS CLONE WAS DERIVED FROM THE RABBIT-MOUSE
CC HYBRIDOMA 12F2; THE CHAIN PRODUCED IS A MONOCLONAL ANTIBODY
CC AGAINST STREPTOCOCCAL GROUP C VACCINE.
CC
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CC -----
DR EMBL; K01358; AAB59259.1; ALT_TERM.
DR PIR; A01954; K4RBF2.
DR HSP; P01607; IREI.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Monoclonal antibody; Hybridoma; Signal.
FT NON_TER 1 1
FT SIGNAL <1 6
FT CHAIN 7 117 IG KAPPA CHAIN V REGION 12F2.
FT DOMAIN 7 29 FRAMEWORK-1.
FT DOMAIN 30 40 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 41 55 FRAMEWORK-2.
FT DOMAIN 56 62 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 63 94 FRAMEWORK-3.
FT DOMAIN 95 106 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 107 116 FRAMEWORK-4.
FT DISULFID 29 86 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12288 MW; E24A7582389E4439 CRC64;

Query Match 75.0%; Score 54; DB 1; Length 117;
Best Local Similarity 76.9%; Pred. No. 0.0092;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Caps 0;

QY 1 QASQSIISNLFHWY 13
: ||| ||| : |||
Db 30 QASQSIISYLSWY 42

RESULT 7
KV1B_HUMAN
ID KV1B_HUMAN STANDARD; PRT; 108 AA.
AC P01594;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region AU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72189444; PubMed=5028201;
RA Schiechl H., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
RT protein Au).";
RL Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).
RN [2]
RP X-RAY CRYSTALLOGRAPHY.
RX MEDLINE=77022433; PubMed=1234024;
RA Fehlgammer H., Schiffer M., Epp O., Colman P.M., Latzman E.E.,
RA Schwager P., Steigemann W., Schramm H.J.;
RT "The structure determination of the variable portion of the
RT Bence-Jones protein Au.";
RL Biophys. Struct. Mech. 1:139-146(1975).
CC -1- MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY
CC MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V
CC REGION OF THE KAPPA CHAIN REI.
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENGE-JONES PROTEIN.
DR PIR; A01862; K1HUAU.
DR HSP; P01607; IREI.

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DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11939 MW; E8011187EE6F6FB9 CRC64;

Query Match 73.6%; Score 53; DB 1; Length 108;
Best Local Similarity 69.2%; Pred. No. 0.013;
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISNLFHWY 13
   ||| |||:|
Db 24 QASQDISYLNWY 36

RESULT 8
KV5U_MOUSE STANDARD; PRT; 108 AA.
AC P04946;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-V region N05-89.4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83271467; PubMed=6877353;
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT "mRNA sequences define an unusually restricted IgG response to 2-phenylloxazalone and its early diversification.";
RL Nature 304:320-324(1983).
CC -!- MISCELLANEOUS: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.
CC -----
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CC -----
CC EMBL: K00745; AAA38690.1; -.
CC HSSP; P01607; IREI.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region; Hybridoma.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11866 MW; DB2C885920DC6DD CRC64;

Query Match 73.6%; Score 53; DB 1; Length 108;
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Best Local Similarity 75.0%; Pred. No. 0.013;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ASQSISNLFHWY 13
   ||| |||:|
Db 25 ASQDISYLNWY 36

RESULT 9
KV1P_HUMAN STANDARD; PRT; 108 AA.
AC P01608;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Roy.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=68362076; PubMed=5595110;
RA Hilschmann N.;
RT "Chemical structure of 2 kappa-type Bence Jones proteins (Roy and Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080(1967)).";
RL Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080(1967).
RN [2]
RP REVISIONS TO 39 AND 41.
RA Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H., Steinmetz-Kayne M., Suter L., Watanabe S.;
RL (In) Franek F., Shugar D. (eds.);
RL Gamma globulins: structure and function, pp.57-74, Academic Press, New York (1969).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2) MARKER.
CC -----
CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR; A01874; KIHURY.
DR HSSP; P80362; 1WTL.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11782 MW; F5ACEDE5A313DF3A CRC64;

Query Match 72.2%; Score 52; DB 1; Length 108;
Best Local Similarity 76.9%; Pred. No. 0.019;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QASQISNLFHWY 13
   ||| |||:|
Db 24 QASQDISYLNWY 36

RESULT 10
KV5J_MOUSE STANDARD; PRT; 108 AA.
AC P01643;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-V region MOPC 173.
OS Mus musculus (Mouse).
```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=76091934; PubMed=812696;
 RA Schiff C., Fougereau M.;
 RT "Determination of the primary structure of a mouse IgG2a
 immunoglobulin. Amino-acid sequence of the light chain.";
 RL Eur. J. Biochem. 59:525-537(1975).
 CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
 DR PIR; A01926; KVM573.
 DR HSSP; P01607; IREI.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 34
 FT DOMAIN 35 49
 FT DOMAIN 50 56
 FT DOMAIN 57 88
 FT DOMAIN 89 97
 FT DOMAIN 98 108
 FT DISULFID 23 88
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11819 MW; 2AD29D92A72AA0A3 CRC64;
 Query Match 72.2%; Score 52; DB 1; Length 108;
 Best Local Similarity 75.0%; Pred. No. 0.019; 2; Indels 0; Gaps 0;
 Matches 9; Conservative 1; Mismatches 2;
 QY 2 ASQSISNFWY 13
 DB 25 ASQSIGNLWY 36
 RESULT 11
 ID KVLH_HUMAN STANDARD; PRT; 108 AA.
 AC P01600;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-I region Hau.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=71032830; PubMed=4097974;
 RA Watanabe S., Hilschmann N.;
 RT "The primary structure of a monoclonal kappa-type immunoglobulin L-
 chain of subgroup I (Bence-Jones Protein Hau): subdivision within
 subgroups.";
 RL Hoppe-Sevler's Z. Physiol. Chem. 351:1291-1295(1970).
 CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
 DR PIR; A01868; KIHUHU.
 DR HSSP; P80362; LWTL.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 KW Immunoglobulin V region; Bence-Jones protein.
 FT DOMAIN 1 23
 FT DOMAIN 24 34
 FT DOMAIN 35 49
 FT DOMAIN 50 56
 FT DOMAIN 57 88
 FT DOMAIN 89 97
 COMPLEMENTARITY-DETERMINING-1.
 COMPLEMENTARITY-DETERMINING-2.
 COMPLEMENTARITY-DETERMINING-3.

FT DOMAIN 98 107
 FT DISULFID 23 88
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11671 MW; 08D3A616D08D0618 CRC64;
 Query Match 70.8%; Score 51; DB 1; Length 108;
 Best Local Similarity 69.2%; Pred. No. 0.028;
 Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QASQISNFWY 13
 DB 24 RASQSISSYLSWY 36
 RESULT 12
 ID KVS_N_MOUSE STANDARD; PRT; 108 AA.
 AC P01647;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-V region HP 124E1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=A/J;
 RX MEDLINE=82150934; PubMed=6801658;
 RA Siegelman M., Capra J.D.;
 RT "Complete amino acid sequence of light chain variable regions derived
 from five monoclonal anti-p-azophenylarsenate antibodies differing
 with respect to a crossreactive idiotype.";
 RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
 CC -!- MISCELLANEOUS: ANTI-ARSONATE HYBRIDOMA PROTEIN.
 DR PIR; A01927; KVM5AR.
 DR HSSP; P01607; IREI.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 KW Immunoglobulin V region; Antiarsonate antibody.
 FT DOMAIN 1 23
 FT DOMAIN 24 34
 FT DOMAIN 35 49
 FT DOMAIN 50 56
 FT DOMAIN 57 88
 FT DOMAIN 89 97
 FT DOMAIN 98 108
 FT DISULFID 23 88
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11965 MW; 39971BC653EFEFA2 CRC64;
 Query Match 70.8%; Score 51; DB 1; Length 108;
 Best Local Similarity 61.5%; Pred. No. 0.028;
 Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QASQISNFWY 13
 DB 24 RASQDINNLYNWY 36
 RESULT 13
 ID KVSQ_MOUSE STANDARD; PRT; 108 AA.
 AC P01648;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-V region HP 91A3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RC SEQUENCE.
RC STRAIN=A/J;
RA MEDLINE=82150934; PubMed=6801658;
RX Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived
from five monoclonal anti-p-azophenylarsenate antibodies differing
with respect to a crossreactive idiotype.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CL -!- MISCELLANEOUS: ANTI-ARSONATE HYBRIDOMA PROTEIN.
DR PIR: A01927; KVSAR.
DR HSSP: P01607; IREI.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Antiarsenate antibody.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 FRAMEWORK-4.
FT DOMAIN 98 108 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11961 MW; D52EDA5E9A45291C CRC64;

Query Match 70.8%; Score 51; DB 1; Length 108;
Best Local Similarity 61.5%; Pred. No. 0.028;
Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISNLFHWY 13
DB 24 RASQDINLYNWY 36

RESULT 14
KVIA_HUMAN
ID KVIA_HUMAN STANDARD; PRT; 108 AA.
AC P01593;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region AG.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RC SEQUENCE.
RX MEDLINE=69234734; PubMed=4893682;
RA Titani K., Shinoda T., Putnam F.W.;
RT "The amino acid sequence of a kappa type Bence-Jones protein. 3. The
complete sequence and the location of the disulfide bridges.";
RL J. Biol. Chem. 244:3550-3560(1969).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR: A01861; KIHUAG.
DR HSSP: P01607; IREI.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.

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FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11992 MW; E3B3B246C18F0C4F CRC64;

Query Match 69.4%; Score 50; DB 1; Length 108;
Best Local Similarity 61.5%; Pred. No. 0.043;
Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISNLFHWY 13
DB 24 QASQDINLYNWY 36

RESULT 15
KV3I_HUMAN
ID KV3I_HUMAN STANDARD; PRT; 115 AA.
AC P04433;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region VG precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RC SEQUENCE FROM N.A.
RP MEDLINE=85087932; PubMed=6440122;
RX Pech M., Zachau H.G.;
RT "Immunoglobulin genes of different subgroups are interdigitated
within the VK locus.";
RL Nucleic Acids Res. 12:9229-9236(1984).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
CC EMBL; X01668; -; NOT_ANNOTATED_CDS.
DR PIR: A01900; K3HUVG.
DR HSSP: P80362; 1WTL.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 >115 IG KAPPA CHAIN V-III REGION VG.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 69 FRAMEWORK-2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 77 108 FRAMEWORK-3.
FT DOMAIN 109 115 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12575 MW; 2DE47CDA3A17D555 CRC64;

Query Match 68.1%; Score 49; DB 1; Length 115;
Best Local Similarity 61.5%; Pred. No. 0.069;
Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISNLFHWY 13
DB 44 RASQSVSYLWY 56

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Search completed: November 18, 2002, 17:33:30
Job time : 4.18627 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:01 ; Search time 13.5735 Seconds
(without alignments)
197.341 Million cell updates/sec

Title: US-09-016-061-82
Perfect score: 72
Sequence: 1 QASQSISNFWY 13

Scoring table: BLOSUM62
Gapop 10.0 , Capext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					
Result No.	Score	Query Match	Length	ID	Description
1	58	80.6	107	4 Q9UL81	Q9UL81 homo sapien
2	54	75.0	234	11 Q91WF8	Q91WF8 mus musculus
3	53	73.6	107	4 Q96SA9	Q96SA9 homo sapien
4	53	73.6	108	4 Q9UL77	Q9UL77 homo sapien
5	53	73.6	234	11 Q9R062	Q9R062 mus musculus
6	51	70.8	108	4 Q9UL70	Q9UL70 homo sapien
7	51	70.8	116	4 Q96PF6	Q96PF6 homo sapien
8	48.5	67.4	101	11 Q9UL78	Q9UL78 mus musculus
9	47	65.3	278	17 Q978G1	Q978G1 thermoplasm
10	47	65.3	307	3 Q9680	Q9680 schizosacch
11	46	63.9	233	11 Q91WS9	Q91WS9 mus musculus
12	45	62.5	99	11 Q9JL74	Q9JL74 mus musculus
13	43	59.7	108	4 Q9UL83	Q9UL83 homo sapien
14	43	59.7	109	4 Q9UL85	Q9UL85 homo sapien
15	43	59.7	130	8 Q80033	Q80033 exoneurella
16	43	59.7	130	8 Q80034	Q80034 exoneurella

17	43	59.7	131	8 Q79124	Q79124 braunsapis
18	43	59.7	131	8 Q79125	Q79125 brevineura
19	43	59.7	131	8 Q79126	Q79126 exoneurella
20	43	59.7	156	8 Q9G462	Q9G462 diadasia co
21	43	59.7	192	8 Q9G7A3	Q9G7A3 brevineura
22	43	59.7	192	8 Q9G798	Q9G798 xylocopa bo
23	43	59.7	198	8 Q9G7A2	Q9G7A2 xylocopa m1
24	43	59.7	198	8 Q9G7A1	Q9G7A1 xylocopa tr
25	43	59.7	198	8 Q9G799	Q9G799 xylocopa v1
26	43	59.7	198	8 Q9G797	Q9G797 xylocopa ta
27	43	59.7	198	8 Q9G796	Q9G796 xylocopa si
28	43	59.7	198	8 Q9G795	Q9G795 xylocopa v1
29	43	59.7	198	8 Q9G794	Q9G794 xylocopa su
30	43	59.7	198	8 Q9G793	Q9G793 xylocopa ar
31	43	59.7	198	8 Q9G792	Q9G792 xylocopa li
32	43	59.7	198	8 Q9G791	Q9G791 xylocopa pu
33	43	59.7	198	8 Q9G790	Q9G790 xylocopa sc
34	43	59.7	198	8 Q9G789	Q9G789 xylocopa n1
35	43	59.7	198	8 Q9G788	Q9G788 xylocopa f1
36	43	59.7	198	8 Q9G787	Q9G787 xylocopa ol
37	43	59.7	198	8 Q9G786	Q9G786 xylocopa la
38	43	59.7	198	8 Q9G785	Q9G785 xylocopa ac
39	43	59.7	198	8 Q9G784	Q9G784 xylocopa ap
40	43	59.7	198	8 Q9G783	Q9G783 xylocopa m1
41	43	59.7	198	8 Q9G781	Q9G781 xylocopa gu
42	43	59.7	198	8 Q9G780	Q9G780 xylocopa fr
43	43	59.7	283	5 Q9NJVO	Q9NJVO haemochus
44	43	59.7	347	8 Q9G511	Q9G511 apis mellif
45	43	59.7	347	8 Q959V5	Q959V5 apis cerana

ALIGNMENTS

RESULT 1
Q9UL81
ID Q9UL81 PRELIMINARY; PRT; 107 AA.
AC Q9UL81;
DC 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 13, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region (Fragment).
DE OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035033; AAD56269.1; -;
DR HSSP; P01607; 1REI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match 80.6%; Score 58; DB 4; Length 107;
Best Local Similarity 76.9%; Pred. No. 0.0058;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QASQSISNFWY 13
Db 24 RASQSISNFWY 36

RESULT 2

Q91WF8 PRELIMINARY; PRT; 234 AA.
AC Q91WF8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical 25.9 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COLON;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC015292; AAH15292.1; -;
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001865; Ribosomal_S2.
DR Pfam; PF00047; ig; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE; PS00962; RIBOSOMAL_S2_1; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25929 MW; B0D0B0E6E7812D2 CRC64;

Query Match 75.0%; Score 54; DB 11; Length 234;
Best Local Similarity 69.2%; Pred. No. 0.071;
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISNLFHWY 13

Db 44 RASQDISNYLWY 56

RESULT 3

Q96SA9 PRELIMINARY; PRT; 107 AA.
AC Q96SA9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Anti-streptococcal/anti-myoisin immunoglobulin kappa light chain
DE variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98375893; PubMed=9712075;
RA Aderson E.E., Shikhan A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyreactive monoclonal antibodies from
RT rheumatic carditis; human anti-N-acetylglucosamine/anti-myoisin
RT antibody V region genes";
RL J. Immunol. 161:2020-2031(1998).
DR EMBL; U96396; AAB68785.1; -;
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig; 1.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;

Query Match 73.6%; Score 53; DB 4; Length 107;
Best Local Similarity 69.2%; Pred. No. 0.047;
Matches 9; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQISNLFHWY 13

Db 24 RASQDISNYLWY 36

RESULT 4

Q9UL77 PRELIMINARY; PRT; 108 AA.
AC Q9UL77;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035037; AAD56273.1; -;
DR HSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IgV; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match 73.6%; Score 53; DB 4; Length 108;
Best Local Similarity 69.2%; Pred. No. 0.047;
Matches 9; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQISNLFHWY 13

Db 24 RASQDISNYLWY 36

RESULT 5

Q8R062 PRELIMINARY; PRT; 234 AA.
AC Q8R062;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 25.9 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COLON;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC027418; AAH27418.1; -;
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25857 MW; 4EB08C81426AEAB1 CRC64;

Query Match 73.6%; Score 53; DB 11; Length 234;
Best Local Similarity 75.0%; Pred. No. 0.11;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ASQISNLFHWY 13

Db 45 ASQISNLFHWY 56

RESULT 6

Q9UL70 PRELIMINARY; PRT; 108 AA.
ID Q9UL70

AC Q9UL70;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Myosin-reactive immunoglobulin light chain variable region
 DE (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 RT fetus";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035044; AAD56280.1; -;
 DR HSP; P01607; IREI.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 FT NON_TER 1
 FT NON_TER 108
 SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match 70.8%; Score 51; DB 4; Length 108;
 Best Local Similarity 69.2%; Pred. No. 0.11;
 Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 QASQISNFWLHWY 13

DB 24 RASQISNFWLHWY 36

RESULT 7
 Q96PF6
 ID Q96PF6 PRELIMINARY; PRT; 116 AA.
 AC Q96PF6;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE kappa 1 light chain variable region (Fragment).
 GN SDNK1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21361171; PubMed=11468171;
 RA Comezo R.L., Zhang Y., Martinez C., Osman K., Herrera G.A.;
 RT "The tropism of organ involvement in primary systemic amyloidosis:
 RT contributions of Ig V(L) germ line gene use and clonal plasma cell
 RT burden";
 RL Blood 98:714-720(2001).
 DR EMBL; AE361758; AAK51465.1; -;
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig; 1.
 FT NON_TER 1
 FT NON_TER 116
 SQ SEQUENCE 116 AA; 12735 MW; E796FC2217BFCF57 CRC64;

Query Match 70.8%; Score 51; DB 4; Length 116;
 Best Local Similarity 69.2%; Pred. No. 0.12;
 Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 QASQISNFWLHWY 13

DB 24 QASQISNFWLHWY 36

RESULT 8
 Q9JL78
 ID Q9JL78 PRELIMINARY; PRT; 101 AA.
 AC Q9JL78;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Anti-myosin immunoglobulin light chain variable region
 DE (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=A.CA;
 RX MEDLINE=20448942; PubMed=10992488;
 RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
 RT "T-Cell-dependent antibody response to the dominant epitope of
 RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
 RT with cardiac myosin";
 RL Infect. Immun. 68:5803-5808(2000).
 DR EMBL; AF206028; AAF69326.1; -;
 DR HSP; P01679; 2FBJ.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 FT NON_TER 1
 FT NON_TER 101
 SQ SEQUENCE 101 AA; 10778 MW; 0A7F65E6A7E6F14D CRC64;

Query Match 67.4%; Score 48.5; DB 11; Length 101;
 Best Local Similarity 76.9%; Pred. No. 0.29;
 Matches 10; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 2 ASQSI-SNFWLHWY 13
 DB 17 ASSISNFWLHWY 29

RESULT 9
 Q978G1
 ID Q978G1 PRELIMINARY; PRT; 278 AA.
 AC Q978G1;
 DT 01-OCT-2001 (TREMBLrel. 18, Created)
 DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Hypothetical protein TV1454.
 GN TV1454 OR TVGI506196.
 OS Thermoplasma volcanium.
 OC Archaea; Euryarchaeota; Thermoplasma; Thermoplasmales;
 OC Thermoplasmataceae; Thermoplasma.
 OX NCBI_TaxID=50339;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=GSSI / DSM 4299 / JCM 9571;
 RX MEDLINE=20570466; PubMed=11121031;
 RA Kawashima T., Amano N., Koike H., Makino S.-I., Higuchi S.,
 RA Kawashima-Ohta Y., Watanabe K., Yamazaki M., Kanehori K., Kawamoto T.,
 RA Nunoshima T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.;
 RT "Archaeal adaptation to higher temperatures revealed by genomic
 RT sequence of Thermoplasma volcanium";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000).
 DR EMBL; AP000996; BAB60596.1; -;
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 278 AA; 33022 MW; BADDCCD7163042CD3 CRC64;

Query Match 65.3%; Score 47; DB 17; Length 278;
 Best Local Similarity 70.0%; Pred. No. 1.6;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 OSISNLFHWY 13
|||:|:|:|
Db 236. QSIDDFVHWY 245

RESULT 10

OS9680 PRELIMINARY; PRT; 307 AA.
AC OS9680;
DT 01-JAN-1999 (TREMBLrel. 09, Created)
DT 01-JUN-1999 (TREMBLrel. 09, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE Probable cytochrome C1, heme protein precursor.
GN SPC29A3.18.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
[1]
RN
RP
RC
RC STRAIN=972;
RA Lyne M., Rajandream M.A., Barrell B.G., Volkert G.G.
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: THIS IS THE HEME-CONTAINING COMPONENT OF THE CYTOCHROME
CC B-C1 COMPLEX, WHICH ACCEPTS ELECTRONS FROM RIESKE PROTEIN AND
CC TRANSFERS ELECTRONS TO CYTOCHROME C IN THE MITOCHONDRIAL
CC RESPIRATORY CHAIN.
CC -!- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CC CYTOCHROME C1 AND THE RIESKE PROTEIN.
CC -!- SUBCELLULAR LOCATION: ANCHORED IN THE INNER MITOCHONDRIAL MEMBRANE
CC WITH ITS N-TERMINUS PROTRUDING INTO THE MITOCHONDRIAL
CC INTERMEMBRANE SPACE (BY SIMILARITY).
EMBL: AL022299; CAAL8395.1; -
DR InterPro: IPR000345; CytC_heme_bind.
DR InterPro: IPR002326; Cyt_C1.
DR Pfam: PF02167; Cytochrome_C1; 1.
DR PRINTS: PR00603; CYTOCHROME.C1.
DR PROSITE: PS00190; CYTOCHROME.C; UNKNOWN.1.
KW Electron transport; Respiratory chain; Oxidative phosphorylation;
KW Heme; Mitochondrion; Transmembrane; Transit peptide.
FT TRANSIT 1 62 MITOCHONDRION (BY SIMILARITY).
FT CHAIN 63 307 PROBABLE CYTOCHROME C1, HEME PROTEIN.
FT BINDING 102 102 HEME (COVALENT) (BY SIMILARITY).
FT BINDING 105 105 HEME (COVALENT) (BY SIMILARITY).
FT METAL 106 106 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT METAL 225 225 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT TRANSMEM 273 287 ANCHORS TO THE MEMBRANE (BY SIMILARITY).
SQ SEQUENCE 307 AA; 34340 MW; FAD8B9D3A9A3C1B3 CRC64;

Query Match 65.3%; Score 47; DB 3; Length 307;
Best Local Similarity 58.3%; Pred. No. 1.8; Mismatches 2; Indels 0; Gaps 0;
Matches 7; Conservative 3;
QY 1 QASQISNLFHW 12
|||:|:|:|
Db 246 QAKDVVNLHW 257

RESULT 11

Q91WS9 PRELIMINARY; PRT; 233 AA.
AC Q91WS9;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Hypothetical 25.8 kDa protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN
RP SEQUENCE FROM N.A.

RC TISSUE=COLON;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC013496; AAH13496.1; -
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig; 2.
DR PROSITE: PS00290; IG_MHC; UNKNOWN.1.
KW Hypothetical protein.
FT NON_TER 1 1
SQ SEQUENCE 233 AA; 25781 MW; B1C184DA149A16EB CRC64;

Query Match 63.9%; Score 46; DB 11; Length 233;
Best Local Similarity 63.6%; Pred. No. 2; Mismatches 3; Indels 0; Gaps 0;
Matches 7; Conservative 3;

QY 3 SOSISNLFHWY 13
|||:|:|:|
Db 45 SGIANYLHWY 55

RESULT 12

Q9JL74 PRELIMINARY; PRT; 99 AA.
AC Q9JL74;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Anti-myosin immunoglobulin light chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=20448942; PubMed=10992488;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin";
RL Infect. Immun. 68:5803-5808(2000).
DR EMBL: AF206032; AAF69330.1; -
DR HSSP: P80362; 1WTL.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_LV.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
FT NON_TER 1 1
FT NON_TER 99 99
SQ SEQUENCE 99 AA; 10939 MW; 3B25D0E784533324 CRC64;

Query Match 62.5%; Score 45; DB 11; Length 99;
Best Local Similarity 61.5%; Pred. No. 1.2; Mismatches 8; Conservative 3; Indels 0; Gaps 0;

QY 1 QASQISNLFHWY 13
|||:|:|:|
Db 16 KASQSVNDVAVY 28

RESULT 13

Q9UL83 PRELIMINARY; PRT; 108 AA.
ID Q9UL83
AC Q9UL83;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
[1]
RN
RP SEQUENCE FROM N.A.

OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 RT fetus."
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL: AF035031; AAD56267.1; -;
 DR HSSP: P80362; IWTL.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IGV; 1.
 DR NON_TER 1
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11834 MW; 9F9C5A92EBA96EEA CRC64;

 Query Match 59.7%; Score 43; DB 4; Length 108;
 Best Local Similarity 61.5%; Pred. No. 3.1;
 Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

 Qy 1 QASQISNFWY 13
 Db 24 RASQSVSSNLAWY 36
 :|||:|:| |

 RESULT 14
 Q9UL85 PRELIMINARY; PRT; 109 AA.
 AC Q9UL85;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DE 01-DEC-2001 (TrEMBLrel. 13, Last annotation update)
 DE Myosin-reactive immunoglobulin kappa chain variable region
 DE (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 RT fetus."
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL: AF035029; AAD56265.1; -;
 DR HSSP: P80362; IWTL.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IGV; 1.
 DR NON_TER 1
 FT NON_TER 109 109
 SQ SEQUENCE 109 AA; 11761 MW; FB1E43E7C7AFACCC CRC64;

Query Match 59.7%; Score 43; DB 4; Length 109;
 Best Local Similarity 75.0%; Pred. No. 3.1;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

 Qy 2 ASQISNFWY 13
 Db 25 ASQISNFWY 36
 |||||:| |

RESULT 15
 O80033 PRELIMINARY; PRT; 130 AA.
 ID O80033
 AC O80033;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)

DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Cytochrome c oxidase polypeptide I (EC 1.9.3.1) (Fragment).
 OS Exoneurella lawsoni.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 OC Apoidea; Apidae; Exoneurella.
 OX NCBI_TaxID=78187;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Reyes S.G., Cooper S.J.B., Schwarz M.P.;
 RT "Species phylogeny of the bee genus Exoneurella Michener (Hymenoptera:
 RT Apidae: Allodapini): evidence from molecular and morphological data
 RT sets."
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
 CC CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNIT 1-
 CC 3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. CO I IS THE
 CC CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
 CC CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
 CC AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
 CC AND COPPER B (BY SIMILARITY).
 CC -!- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) -> 4 FERROCYTOCHROME
 CC C + 2 H(2)O.
 CC -!- COFACTOR: HEMES A, A3, AND COPPER B (BY SIMILARITY).
 CC -!- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC INNER MEMBRANE (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
 DR EMBL: AF072661; AAC24880.1; -;
 DR InterPro: IPR000883; COX1.
 DR Pfam: PF00115; COX1; 1.
 KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
 KW Respiratory chain; Transmembrane.
 FT NON_TER 1
 FT NON_TER 130 130
 SQ SEQUENCE 130 AA; 15339 MW; 11CF4F1F1EAE22F2 CRC64;

 Query Match 59.7%; Score 43; DB 8; Length 130;
 Best Local Similarity 75.0%; Pred. No. 3.8;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ISNFWY 13
 Db 19 ISSFIHWY 26
 ||:|:|

Search completed: November 18, 2002, 17:40:50
 Job time : 14.6235 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:21:57 : Search time 17.9706 Seconds
(without alignments)
96.394 Million cell updates/sec

Title: US-09-016-061-82

Perfect score: 72

Sequence: 1 QASQSISNPLHWY 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_101002.*

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15:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
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17:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
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19:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
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21:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	72	100.0	13	19	AAW76031
2	72	100.0	13	22	AAW76031
3	68	94.4	259	21	AAW76011
4	65	90.3	13	19	AAW76011
5	65	90.3	13	22	AAW76011
6	65	90.3	107	19	AAW76006
7	65	90.3	107	19	AAW76002
8	65	90.3	107	19	AAW76004
9	65	90.3	107	22	AAW76004
10	65	90.3	107	22	AAW76004

11	65	90.3	107	22	AAW76031	Vitaxin light chain
12	65	90.3	107	22	AAW76031	Antibody LM609 lig
13	65	90.3	107	22	AAW76031	Light chain variab
14	61	84.7	105	20	AAW87456	Jk gene product.
15	61	84.7	105	20	AAW87456	Humanised anti- α
16	61	84.7	107	20	AAW84098	Humanised anti- α
17	61	84.7	108	20	AAW84094	Murine vitronectin
18	61	84.7	109	20	AAW06380	Murine monoclonal
19	61	84.7	111	22	AAW63629	Amino acid sequenc
20	61	84.7	112	20	AAW84100	Vitronectin alpha-
21	61	84.7	299	22	AAW63633	Amino acid sequenc
22	61	84.7	299	22	AAW63638	Amino acid sequenc
23	60	83.3	88	21	AAW56654	Partial peptide fr
24	60	83.3	107	20	AAW30203	The variable light
25	60	83.3	107	20	AAW30205	The variable light
26	60	83.3	107	21	AAW71240	Humanised antibody
27	60	83.3	107	22	AAW80987	Murine antiCD40 re
28	60	83.3	107	23	AAW47721	Light chain of ant
29	60	83.3	107	23	AAW47723	Light chain of ant
30	60	83.3	108	17	AAW00241	Esf receptor chime
31	60	83.3	124	21	AAW56719	Amino acid sequenc
32	60	83.3	128	20	AAW30199	Light chain variab
33	60	83.3	128	23	AAW47724	Light chain variab
34	60	83.3	214	20	AAW30202	Light chain sequen
35	60	83.3	214	23	AAW47727	Light chain of Chi
36	59	81.9	107	13	AAW25729	Humanised VL regio
37	59	81.9	107	13	AAW69677	Murine CMV5 antibo
38	59	81.9	107	22	AAW69678	Humanised CMV5 ant
39	59	81.9	107	22	AAW69690	Human WOL antibody
40	59	81.9	108	12	AAW15438	Light chain variab
41	59	81.9	109	20	AAW89176	Anti-p53 monoclonal
42	59	81.9	127	15	AAW34093	Sequence of mouse
43	59	81.9	127	22	AAW69687	Murine CMV5 antibo
44	59	81.9	240	12	AAW15443	Single chain Fv fr
45	58	80.6	75	19	AAW62818	Amino acid sequenc

ALIGNMENTS

RESULT 1

AAW76031
ID AAW76031 standard; Protein; 13 AA.

XX AAW76031;

AC AAW76031;

DT 02-NOV-1998 (first entry)

XX LM609 grafted antibody V-L region CDR1 protein fragment #2.

DE Vitaxin; antibody; variable region; heavy chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-L region; CDR;
KW complementarity determining region.

XX Mus sp.

PN WO9833919-A2.

XX 06-AUG-1998.

PF 30-JAN-1998; 98WO-US01826.

PR 30-JAN-1997; 97US-0791391.

XX (IXSY-) IxSYS INC.

PI Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

DR N-PSDB; AAW49868.

XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
PT Integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
XX Claim 62; Page 41; 129pp; English.
PS
XX AAM76007-w76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphaVbeta3 and can be used to
CC inhibit binding of alphaVbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphaVbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
CC antibodies contain non-murine framework regions so are suitable for use
CC in humans. Enhanced types of LM609 have affinity more than 90 times
CC greater than that of parent the parent antibody.
XX
XX Sequence 13 AA;
SQ
Query Match 100.0%; Score 72; DB 19; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.6e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QASQSISNLFHWY 13
DB 1 QASQSISNLFHWY 13
|||||
RESULT 2
AAB61389
ID AAB61389 standard; peptide; 13 AA.
XX
AC AAB61389;
XX
DT 03-APR-2001 (first entry)
XX
DE Mutant VL CDR1 peptide.
XX
XX LM609; grafted antibody; alphaVbeta3 integrin; angiogenesis;
KW inflammatory; cancer; retina; restenosis; osteoporosis.
XX
XX Unidentified.
XX WO200078815-A1.
PN
XX 28-DEC-2000.
XX
XX 23-JUN-2000; 2000WO-US17454.
PF
XX 24-JUN-1999; 99US-0339922.
PR
XX (MOLE-) APPLIED MOLECULAR EVOLUTION.
PA
XX Huse WD, Wu H;
PI WPI; 2001-050110/06.
XX
XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
PT osteoporosis -
XX
XX Disclosure; Page 41; 132pp; English.
PS
XX The present invention relates to enhanced LM609 grafted antibodies
CC exhibiting selective binding affinity to alphaVbeta3 integrin or
CC their functional fragments. The antibodies or their functional
CC fragments can be used in the diagnosis and treatment of
CC alphaVbeta3-mediated diseases such as angiogenesis, inflammatory

CC diseases (such as psoriasis and chronic articular rheumatism),
CC disorders associated with inappropriate or inopportune invasion of
CC vessels (such as diabetic retinopathy, neovascular glaucoma and
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
CC diseases (such as macular degeneration), restenosis and
CC osteoporosis.
XX
XX Sequence 13 AA;
SQ
Query Match 100.0%; Score 72; DB 22; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.6e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QASQSISNLFHWY 13
DB 1 QASQSISNLFHWY 13
|||||
RESULT 3
AAB09775
ID AAB09775 standard; Protein; 259 AA.
XX
XX AAB09775;
AC
XX 06-SEP-2000 (first entry)
DT
XX TMV 30K movement protein and scFv fusion protein scFv 30-1 SEQ ID NO:29.
DE
XX Molecular pathogenicide; plant disease; resistance; antibody; scFv;
KW gene construct; pathogen; toxin; fusion protein; antimicrobial;
KW deoxyribonuclease; RNase; ribosome inactivator; immunomodulator.
XX
XX Tobacco mosaic virus.
OS
XX WO200023593-A2.
PN
XX 27-APR-2000.
PD
XX 15-OCT-1999; 99WO-EP07844.
PF
XX 16-OCT-1998; 98EP-0119630.
PR
XX 16-OCT-1998; 98IN-0000666.
PR
XX (FRAU) FRAUNHOFER GES FOERDERUNG ANGEWANDTEN.
PA
XX Fischer R, Schillberg S, Naehring J, Sack M, Monecke M, Liao Y;
PI Spiegel H, Zimmerman S, Emans N, Holzem A;
PI
XX WPI; 2000-339692/29.
DR
XX New fusion proteins and gene constructs for expressing agents
XX (antibodies, enzymes, vectors or molecular pathogenicides), useful for
XX protecting plants against pathogens and increasing resistance to
XX disease -
XX
XX Example 5; Page 149-150; 193pp; English.
PS
XX The present invention describes a fusion protein (I) comprising at least
CC one binding domain specifically recognising an epitope of a plant
CC pathogen and at least one further domain comprising a protein or peptide
CC sequence which is toxic to the pathogen or detrimental to its
CC replication, transmission or life cycle. Also described is a
CC pathogenicide (II) comprising (I) and a cellular targeting sequence
CC and/or membrane localisation sequence and/or motif that leads to
CC membrane anchoring; or at least one binding domain that specifically
CC recognises a viral movement and/or replicase protein. The fusion
CC protein, pathogenicide, polynucleotide, vectors, and compositions from
CC the present invention are useful for the protection of a plant against
CC the action of a pathogen. The kit from the present invention is useful
CC for carrying out the methods and may be employed in different
CC applications, for example in the diagnostic field or as research tools.
CC The kit or its components, such as the fusion protein, pathogenicide,
CC polynucleotides, vectors or compositions are useful in plant cell and

CC plant tissue culture, in agriculture. They are extremely useful for
 CC breeding new varieties of plants that display improved properties such as
 CC resistance to pathogens. AAS56587 to AAS56702 and AAB09774 to B097820
 CC represent sequences used in the exemplification of the present
 CC invention.

XX
 XX Sequence 259 AA;

Query Match 94.4%; Score 68; DB 21; Length 259;
 Best Local Similarity 92.3%; Pred. No. 0.0057;
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QASQISISNHLHWY 13
 Db 155 RASQISNHLHWY 167

RESULT 4

AAW76011
 ID AAW76011 standard; Protein; 13 AA.

XX AC AAW76011;

XX 02-NOV-1998 (first entry)

XX DE LM609 grafted antibody V-L region CDR1 protein fragment #1.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-L region; CDR;
 KW complementarity determining region.

XX Mus sp.

XX PN WO9833919-A2.

XX PD 06-AUG-1998.

XX PF 30-JAN-1998; 98WO-US01826.

XX PR 30-JAN-1997; 97US-0791391.

XX PA (IXSY-) IXSYS INC.

XX PI Glaser SM, Huse WD;

XX DR WPI; 1998-437472/37.

XX DR N-PSDB; AAV49848.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

XX PS Disclosure; Page 40; 129pp; English.

XX AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
 CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
 CC antibodies contain non-murine framework regions so are suitable for use
 CC in humans. Enhanced types of LM609 have affinity more than 90 times
 CC greater than that of parent the parent antibody.

XX Sequence 13 AA;

Query Match 90.3%; Score 65; DB 19; Length 13;
 Best Local Similarity 92.3%; Pred. No. 0.00072;
 Matches 12; Conservative 0; Mismatches 1; Indels 7 0; Gaps 0;

Qy 1 QASQISISNHLHWY 13
 Db 1 QASQISISNHLHWY 13

RESULT 5

AAW76011

ID AAB61369 standard; peptide; 13 AA.

XX AC AAB61369;

XX 03-APR-2001 (first entry)

XX DE LM609 VL CDR1 peptide.

XX KW LM609; grafted antibody; alphavbeta3 integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis.

XX OS Unidentified.

XX PN WO200078815-A1.

XX PD 28-DEC-2000.

XX PF 23-JUN-2000; 2000WO-US17454.

XX PR 24-JUN-1999; 99US-0339922.

XX PA (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX PI Huse WD, Wu H;

XX DR WPI; 2001-050110/06.

XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis

XX PS Disclosure; Page 39; 132pp; English.

XX The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphavbeta3 integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphavbeta3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.

XX SQ Sequence 13 AA;

Query Match 90.3%; Score 65; DB 22; Length 13;
 Best Local Similarity 92.3%; Pred. No. 0.00072;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QASQISISNHLHWY 13
 Db 1 QASQISISNHLHWY 13

RESULT 6

AAW76006

ID AAW76006 standard; Protein; 107 AA.

XX AC AAW76006;

```

XX 02-NOV-1998 (first entry)
XX LM609 grafted antibody light chain variable region protein fragment.
XX
XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
XX LM609; inhibitor; integrin-mediated signal transduction; treatment;
XX diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
XX neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
XX macular degeneration; osteoporosis.
XX
XX Mus sp.
XX
XX Key Location/Qualifiers
XX Misc-difference 49
XX /label= Arg, Met
XX
XX WO9833919-A2.
XX
XX 06-AUG-1998.
XX
XX 30-JAN-1998; 98WO-US01826.
XX
XX 30-JAN-1997; 97US-0791391.
XX
XX (IXSY-) IXSYS INC.
XX
XX Glaser SM, Huse WD;
XX
XX WPI; 1998-437472/37.
XX
XX N-PSDB; AAV49843.
XX
XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
XX integrin - and related grafted antibodies based on murine monoclonal
XX LM609, also related nucleic acid, used to treat, prevent or diagnose
XX angiogenesis or restenosis
XX
XX Claim 19; Fig 7; 129pp; English.
XX
XX This sequence represents a LM609 grafted antibody variable light chain
XX region. LM609 and the antibody vitaxin bind selectively to integrin
XX alphavbeta3 and can be used to inhibit binding of alphavbeta3 to a
XX ligand and thus block integrin-mediated signal transduction. This is
XX useful in the treatment, prevention and diagnosis of alphavbeta3-mediated
XX disease, specifically angiogenesis and restenosis (but also e.g. (non-)immune
XX inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
XX psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
XX etc.). The antibodies contain non-murine framework regions so are
XX suitable for use in humans. Enhanced types of LM609 have affinity
XX more than 90 times greater than that of parent the antibody.
XX
XX .SQ Sequence 107 AA;
XX
XX Query Match 90.3%; Score 65; DB 19; Length 107;
XX Best Local Similarity 92.3%; Pred. No. 0.0066;
XX Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 QASQISINFLHWY 13
XX | | | | | | | | | |
XX DB 24 QASQISINHLHWY 36
XX
XX RESULT 7
XX AAW76002
XX ID AAW76002 standard; Protein; 107 AA.
XX
XX AC AAW76002;
XX
XX 02-NOV-1998 (first entry)
XX
XX Vitaxin antibody light chain variable region protein fragment.
XX
XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;

```

```

KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis.
XX
XX Mus sp.
XX
XX WO9833919-A2.
XX
XX 06-AUG-1998.
XX
XX 30-JAN-1998; 98WO-US01826.
XX
XX 30-JAN-1997; 97US-0791391.
XX
XX (IXSY-) IXSYS INC.
XX
XX Glaser SM, Huse WD;
XX
XX WPI; 1998-437472/37.
XX
XX N-PSDB; AAV49821.
XX
XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
XX integrin - and related grafted antibodies based on murine monoclonal
XX LM609, also related nucleic acid, used to treat, prevent or diagnose
XX angiogenesis or restenosis
XX
XX Claim 1; Fig 1b; 129pp; English.
XX
XX This sequence represents the vitaxin antibody variable light chain
XX region. Vitaxin and the antibody LM609 bind selectively to integrin
XX alphavbeta3 and can be used to inhibit binding of alphavbeta3 to a
XX ligand and thus block integrin-mediated signal transduction. This is
XX useful in the treatment, prevention and diagnosis of alphavbeta3-mediated
XX disease, specifically angiogenesis and restenosis (but also e.g.
XX (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,
XX cancer, psoriasis, rheumatoid arthritis, macular degeneration,
XX osteoporosis etc.). The antibodies contain non-murine framework regions
XX so are suitable for use in humans. Enhanced types of LM609 have affinity
XX more than 90 times greater than that of parent the antibody.
XX
XX .SQ Sequence 107 AA;
XX
XX Query Match 90.3%; Score 65; DB 19; Length 107;
XX Best Local Similarity 92.3%; Pred. No. 0.0066;
XX Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 QASQISINFLHWY 13
XX | | | | | | | | | |
XX DB 24 QASQISINHLHWY 36
XX
XX RESULT 8
XX AAW76004
XX ID AAW76004 standard; Protein; 107 AA.
XX
XX AC AAW76004;
XX
XX 02-NOV-1998 (first entry)
XX
XX LM609 antibody light chain variable region protein fragment.
XX
XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
XX LM609; inhibitor; integrin-mediated signal transduction; treatment;
XX diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
XX neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
XX macular degeneration; osteoporosis.
XX
XX Mus sp.
XX
XX WO9833919-A2.
XX
XX 06-AUG-1998.

```


XX New LM609 grafted antibody exhibiting selective binding affinity to
PT alphavbeta3, comprising at least one LM609 grafted heavy and light
PT chain polypeptide, useful for diagnosing and treating e.g. inflammatory
PT disorders or cancer
XX
PS Disclosure; Fig 2B; 25pp; English.
XX
CC The present sequence represents the light chain variable region of the
CC monoclonal antibody LM609. LM609 is a murine antibody which specifically
CC recognises the integrin alphavbeta3, and inhibits its functional activity.
CC The specification describes a LM609 grafted antibody which has the
CC complementarity determining regions (CDRs) substituted into a non-murine
CC framework. Nucleic acids encoding LM609 grafted heavy and light chain
CC polypeptides and fragments are useful in diagnostic and therapeutic
CC purposes, such as in the production of LM609 grafted antibodies and
CC fragments having binding specificity and inhibitory activity against
CC the integrin alphavbeta3. The antibody can be used for the diagnosis
CC or treatment of alphavbeta3-mediated diseases (e.g. inflammatory
CC disorders, chronic articular rheumatism, psoriasis, disorders
CC associated with inappropriate or inopportune invasion of vessels such
CC as diabetic retinopathy, neovascular glaucoma and capillary
CC proliferation in atherosclerotic plaques, or cancers), and to inhibit
CC binding activity of alphavbeta3 that are necessary for progression of
CC an alphavbeta3-mediated disease.
XX
SQ Sequence 107 AA;

Query Match 90.3%; Score 65; DB 22; Length 107;
Best Local Similarity 92.3%; Pred. No. 0.0066;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISNHLHWY 13
| | | | | | | | | |
Db 24 QASQISNHLHWY 36

RESULT 11
AAB61360
ID AAB61360 standard; protein; 107 AA.
XX
AC AAB61360;
XX
XX 03-APR-2001 (first entry)
XX
DE Vitaxin light chain variable region protein.
XX
XX LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
KW inflammatory; cancer; retina; restenosis; osteoporosis.
XX
OS Unidentified.
XX
XX WO200078815-A1.
XX
XX 28-DEC-2000.
XX
XX 23-JUN-2000; 2000WO-US17454.
XX
XX 24-JUN-1999; 99US-0339922.
XX
XX (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX
XX Huse WD, Wu H;
XX
XX WPI; 2001-050110/06.
XX
XX WO200078815-A1.
XX
XX 28-DEC-2000.
XX
XX 23-JUN-2000; 2000WO-US17454.
XX
XX 24-JUN-1999; 99US-0339922.
XX
XX (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX
XX Huse WD, Wu H;
XX
XX WPI; 2001-050110/06.
XX
XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
PT osteoporosis -
XX
PS Disclosure; Fig 1; 132pp; English.

CC The present invention relates to enhanced LM609 grafted antibodies
CC exhibiting selective binding affinity to alphavbeta_3 integrin or
CC their functional fragments. The antibodies or their functional
CC fragments can be used in the diagnosis and treatment of
CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
CC diseases (such as psoriasis and chronic articular rheumatism),
CC disorders associated with inappropriate or inopportune invasion of
CC vessels (such as diabetic retinopathy, neovascular glaucoma and
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
CC diseases (such as macular degeneration), restenosis and
XX osteoporosis.
SQ Sequence 107 AA;

Query Match 90.3%; Score 65; DB 22; Length 107;
Best Local Similarity 92.3%; Pred. No. 0.0066;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISNHLHWY 13
| | | | | | | | | |
Db 24 QASQISNHLHWY 36

RESULT 12
AAB61362
ID AAB61362 standard; protein; 107 AA.
XX
AC AAB61362;
XX
XX 03-APR-2001 (first entry)
XX
DE Antibody LM609 light chain variable region protein.
XX
XX LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
KW inflammatory; cancer; retina; restenosis; osteoporosis.
XX
OS Unidentified.
XX
XX WO200078815-A1.
XX
XX 28-DEC-2000.
XX
XX 23-JUN-2000; 2000WO-US17454.
XX
XX 24-JUN-1999; 99US-0339922.
XX
XX (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX
XX Huse WD, Wu H;
XX
XX WPI; 2001-050110/06.
XX
XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
PT osteoporosis -
XX
XX Disclosure; Fig 2; 132pp; English.
XX
CC The present invention relates to enhanced LM609 grafted antibodies
CC exhibiting selective binding affinity to alphavbeta_3 integrin or
CC their functional fragments. The antibodies or their functional
CC fragments can be used in the diagnosis and treatment of
CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
CC diseases (such as psoriasis and chronic articular rheumatism),
CC disorders associated with inappropriate or inopportune invasion of
CC vessels (such as diabetic retinopathy, neovascular glaucoma and
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
CC diseases (such as macular degeneration), restenosis and
XX osteoporosis.
SQ Sequence 107 AA;

Query Match 90.3%; Score 65; DB 22; Length 107;
 Best Local Similarity 92.3%; Pred. No. 0.0066;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISNHLHWY 13
 DB 24 QASQISNHLHWY 36

RESULT 13
 AAB61364
 ID AAB61364 standard; protein; 107 AA.
 AC AAB61364;
 XX
 DT 03-APR-2001 (first entry)
 DE
 XX
 DE Light chain variable region of LM609.
 XX
 KW LM609; grafted antibody; alphaVbeta_3 integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis.
 XX
 OS Unidentified.
 XX
 PN WO200078815-A1.
 XX
 PD 28-DEC-2000.
 XX
 PF 23-JUN-2000; 2000WO-US17454.
 XX
 PR 24-JUN-1999; 99US-0339922.
 XX
 PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
 XX
 PI Huse WD, Wu H;
 XX
 DR WPI; 2001-050110/06.
 XX
 PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis.
 XX
 PS Disclosure; Fig 7; 132pp; English.
 XX
 CC The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphaVbeta_3 integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphaVbeta_3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.
 XX
 SQ Sequence 107 AA;

Query Match 90.3%; Score 65; DB 22; Length 107;
 Best Local Similarity 92.3%; Pred. No. 0.0066;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISNHLHWY 13
 DB 24 QASQISNHLHWY 36

RESULT 14
 AAW87456
 ID AAW87456 standard; Protein; 105 AA.
 XX
 AC AAW87456;

XX
 DT 15-MAR-1999 (first entry)
 XX
 DE Jk gene product.
 XX
 KW Humanised antibody; monoclonal antibody; MAb; antibody engineering;
 KW mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;
 KW cancer; metastasis; rheumatoid arthritis; atherosclerosis;
 KW angiogenesis; diabetic retinopathy; inflammation;
 KW macular degeneration; osteoporosis; Paget's disease;
 KW hyperparathyroidism; hypercalcaemia; therapy; immunotherapy;
 KW D12HZREI; Jk protein.
 XX
 OS Mus sp.
 XX
 PN WO9840488-A1.
 XX
 PD 17-SEP-1998.
 XX
 PF 12-MAR-1998; 98WO-US04987.
 XX
 PR 12-MAR-1997; 97US-0039609.
 XX
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 XX
 PI Johanson KO, Jonak ZL, Taylor AH;
 XX
 DR WPI; 1999-034590/03.
 DR N-PSDB; AAV71803.
 XX
 PT New anti alpha_v beta_3 vitronectin receptor antibodies - used for
 PT immunotherapeutic treatment of e.g. diabetic retinopathy,
 PT inflammatory disorders, atherosclerosis, restenosis, cancers or
 PT osteoporosis
 XX
 PS Example 14; Page 66; 97pp; English.
 XX
 CC This polypeptide is encoded by a Jk synthetic gene segment (see
 CC AAV71803). It was utilising in novel D12HZREI humanised light chain
 CC variable region (see AAW87458), which comprises a human REI framework
 CC and complementarity determining regions from the anti-human alpha-v
 CC beta-3 vitronectin receptor monoclonal antibody D12. Humanised D12
 CC antibodies can be used for passive immunotherapy of disorders
 CC mediated by the alpha-v beta-3 vitronectin receptor, e.g. restenosis
 CC and angiogenic associated diseases.
 XX
 SQ Sequence 105 AA;

Query Match 84.7%; Score 61; DB 20; Length 105;
 Best Local Similarity 84.6%; Pred. No. 0.028;
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISNHLHWY 13
 DB 24 RASQISNHLHWY 36

RESULT 15
 AAW87458
 ID AAW87458 standard; Protein; 105 AA.
 XX
 AC AAW87458;
 XX
 DT 15-MAR-1999 (first entry)
 XX
 DE Humanised anti-alpha-v beta-3 MAb D12HZLCREI VL.
 XX
 KW Humanised antibody; monoclonal antibody; MAb; antibody engineering;
 KW mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;
 KW cancer; metastasis; rheumatoid arthritis; atherosclerosis;
 KW angiogenesis; diabetic retinopathy; inflammation;
 KW macular degeneration; osteoporosis; Paget's disease;
 KW hyperparathyroidism; hypercalcaemia; therapy; immunotherapy;

KW D12HZLCREI.
XX Homo sapiens.
OS Synthetic.
XX WO9804088-A1.
XX 17-SEP-1998.
XX 12-MAR-1998; 98WO-US04987.
XX 12-MAR-1997; 97US-0039609.
XX (SMIK) SMITHKLINE BEECHAM CORP.
XX Johanson KO, Jonak ZL, Taylor AH;
XX WPI; 1999-034590/03.
XX N-PSDB; AAV71805.
XX New anti alpha_v beta_3 vitronectin receptor antibodies - used for
PT immunotherapeutic treatment of e.g. diabetic retinopathy,
PT inflammatory disorders, atherosclerosis, restenosis, cancers or
PT osteoporosis
XX
XX Example 14; Page 68-69; 97pp; English.
XX This is the amino acid sequence of the light chain variable region
CC (VL) of humanised anti-alpha_v beta_3 vitronectin receptor
CC monoclonal antibody D12HZLCREI. It is based on a synthetic
CC humanised kappa chain based on a modified human REI kappa
CC framework and complementarity determining regions from the murine
CC anti-human alpha_v beta_3 vitronectin receptor monoclonal antibody
CC D12 (see AAW84094). Humanised antibodies of the invention can be used
CC for passive immunotherapy of a disorder mediated by the alpha_v
CC beta_3 receptor, e.g. cardiovascular disorders or angio-genic-
CC related disorders, such as angiogenesis associated with diabetic
CC retinopathy, atherosclerosis and restenosis, chronic inflammatory
CC disorders, macular degeneration, rheumatoid arthritis and cancer,
CC e.g. solid tumour metastasis, and diseases where bone resorption is
CC associated with pathology such as osteoporosis, hyperparathyroidism,
CC Paget's disease, hypercalcaemia of malignancy, osteolytic lesions
CC produced by bone metastasis, bone loss due to immobilisation or sex
CC hormone deficiency. They can also be used for targeted drug
CC therapy, and for detection and diagnosis.
XX
SQ Sequence 105 AA;
Query Match 84.7%; Score 61; DB 20; Length 105;
Best Local Similarity 84.6%; Pred. No. 0.028;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 QASQISINFLHWY 13
Db :|||||
24 RASQISINHLHWY 36

Search completed: November 18, 2002, 17:31:39
Job time : 17.9706 secs

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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:54:45 ; search time 2.54902 Seconds
(without alignments)
76.811 Million cell updates/sec

Title: US-09-016-061-82
Perfect score: 72
Sequence: 1 QASQSISNLFHWY 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 97044 seqs, 15060890 residues

Total number of hits satisfying chosen parameters: 97044

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
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- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
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- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES											
Result No.	Score	Query Match	Length	DB ID	Description						
1	65	90.3	107	8	US-08-790-540A-4	Sequence 4, Appli					
2	65	90.3	107	8	US-08-790-540A-8	Sequence 8, Appli					
3	65	90.3	107	8	US-08-791-391A-4	Sequence 4, Appli					
4	65	90.3	107	8	US-08-791-391A-8	Sequence 8, Appli					
5	65	90.3	107	8	US-08-791-391A-32	Sequence 32, Appli					
6	60	83.3	88	10	US-09-905-243-31	Sequence 31, Appli					
7	58	80.6	90	10	US-09-864-761-34739	Sequence 34739, A					
8	58	80.6	108	10	US-09-905-243-68	Sequence 68, Appli					
9	57	79.2	124	12	US-10-066-895-10	Sequence 10, Appli					
10	56	77.8	88	10	US-09-905-243-36	Sequence 36, Appli					
11	55	76.4	31	9	US-09-956-206A-3	Sequence 3, Appli					
12	55	76.4	107	10	US-09-850-165-93	Sequence 93, Appli					
13	55	76.4	108	10	US-09-056-160B-12	Sequence 12, Appli					
14	55	76.4	109	10	US-09-811-123-6	Sequence 6, Appli					
15	55	76.4	234	10	US-09-800-729-150	Sequence 150, App					
16	54	75.0	30	9	US-09-956-206A-7	Sequence 7, Appli					
17	54	75.0	31	9	US-09-956-206A-5	Sequence 5, Appli					
18	54	75.0	108	10	US-09-905-243-73	Sequence 73, Appli					
19	54	75.0	108	12	US-10-140-555-4	Sequence 4, Appli					

Query Match 90.3%; Score 65; DB 8; Length 107;
Best Local Similarity 92.3%; Pred. No. 0.0016;

20	54	75.0	131	1	US-08-779-784-21	Sequence 21, Appli
21	53	73.6	88	10	US-09-905-243-63	Sequence 63, Appli
22	53	73.6	88	12	US-10-066-895-9	Sequence 9, Appli
23	53	73.6	95	12	US-10-025-687-22	Sequence 22, Appli
24	53	73.6	107	10	US-09-056-160B-13	Sequence 13, Appli
25	53	73.6	107	10	US-09-056-160B-15	Sequence 15, Appli
26	53	73.6	108	10	US-09-056-160B-8	Sequence 8, Appli
27	53	73.6	108	10	US-09-056-160B-10	Sequence 10, Appli
28	53	73.6	108	10	US-09-056-160B-126	Sequence 126, App
29	53	73.6	110	10	US-09-056-160B-103	Sequence 103, App
30	53	73.6	110	10	US-09-056-160B-105	Sequence 105, App
31	53	73.6	110	10	US-09-056-160B-107	Sequence 107, App
32	53	73.6	110	10	US-09-056-160B-117	Sequence 117, App
33	53	73.6	128	10	US-09-764-304-10	Sequence 10, Appli
34	53	73.6	128	10	US-09-764-304-19	Sequence 19, Appli
35	53	73.6	128	12	US-10-006-773-6	Sequence 6, Appli
36	53	73.6	237	10	US-09-056-160B-100	Sequence 100, App
37	53	73.6	240	9	US-09-968-561A-2	Sequence 2, Appli
38	53	73.6	240	10	US-09-192-85A-2	Sequence 2, Appli
39	53	73.6	491	12	US-10-011-125-2	Sequence 2, Appli
40	52	72.2	102	10	US-09-864-761-48570	Sequence 48570, A
41	51	70.8	88	10	US-09-905-243-29	Sequence 29, Appli
42	51	70.8	88	10	US-09-905-243-30	Sequence 30, Appli
43	51	70.8	88	10	US-09-905-243-62	Sequence 62, Appli
44	51	70.8	125	10	US-09-809-739-1	Sequence 1, Appli
45	51	70.8	127	10	US-09-809-739-10	Sequence 10, Appli

ALIGNMENTS

RESULT 1
US-08-790-540A-4
; Sequence 4, Application US/08790540A
; Patent No. US20010011125A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,540A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-790-540A-4


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Query Match      90.3%; Score 65; DB 8; Length 107;
Best Local Similarity 92.3%; Pred. No. 0.0016;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QASQSIISNHLHWY 13
Db 24 QASQSIISNHLHWY 36

RESULT 5
US-08-791-391A-32
; Sequence 32, Application US/08791391A
; Patent No. US20010016645A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,391A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-391A-32

Query Match      90.3%; Score 65; DB 8; Length 107;
Best Local Similarity 92.3%; Pred. No. 0.0016;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QASQSIISNHLHWY 13
Db 24 QASQSIISNHLHWY 36

RESULT 6
US-09-905-243-31
; Sequence 31, Application US/09905243
; Patent No. US20020062009A1
; GENERAL INFORMATION:
; APPLICANT: Taylor, Alexander H
; TITLE OF INVENTION: Monoclonal Antibodies with Reduced
; TITLE OF INVENTION: Immunogenicity
; FILE REFERENCE: P50770
; CURRENT APPLICATION NUMBER: US/09/905,243
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/300,970
; PRIOR FILING DATE: 1999-04-28
```

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; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 31
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Pan troglodytes
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (24)...(34)
; OTHER INFORMATION: CDRI
; NAME/KEY: DOMAIN
; LOCATION: (50)...(66)
; OTHER INFORMATION: CDRII
US-09-905-243-31

Query Match      83.3%; Score 60; DB 10; Length 88;
Best Local Similarity 84.6%; Pred. No. 0.0075;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QASQSIISNHLHWY 13
Db 24 QASQSIISNHLHWY 36

RESULT 7
US-09-864-761-34739
; Sequence 34739, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; FILE REFERENCE: Acomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
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;; PRIOR FILING DATE: 2001-01-29
;; NUMBER OF SEQ ID NOS: 49117
;; SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
;; SEQ ID NO 34739
;; LENGTH: 90
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: MAP TO AC009958.1
;; OTHER INFORMATION: EXPRESSED IN HEL100, SIGNAL = 2.6
;; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.8
;; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 84
;; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 15
;; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.91
;; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 5.9
;; OTHER INFORMATION: EST_HUMAN HIT: AW404507.1, EVALUAE 4.00e-46
;; OTHER INFORMATION: SWISSPROT HIT: P01608, EVALUAE 3.00e-43
US-09-864-761-34739

Query Match 80.6%; Score 58; DB 10; Length 90;
Best Local Similarity 76.9%; Pred. No. 0.015;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISNFLHWY 13
||| |||:|:|
Db 16 QASQDISNLYNWY 28

RESULT 8
US-09-905-243-68
; Sequence 68, Application US/09905243
; Patent No. US20020062009A1
; GENERAL INFORMATION:
; APPLICANT: Taylor, Alexander H
; TITLE OF INVENTION: Monoclonal Antibodies with Reduced
; FILE REFERENCE: P50770
; CURRENT APPLICATION NUMBER: US/09/905,243
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/300,970
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 68
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: rat/chimpanzee sequence
US-09-905-243-68

Query Match 80.6%; Score 58; DB 10; Length 108;
Best Local Similarity 69.2%; Pred. No. 0.018;
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISNFLHWY 13
||:|:| |||
Db 24 RASESVSTFLHWY 36

RESULT 9
US-10-066-895-10
; Sequence 10, Application US/10066895
; Patent No. US20020141990A1
; GENERAL INFORMATION:
; APPLICANT: Deen, Keith C.
; Dillon, Susan B.
; Porter, Terence C.
; Sweet, Raymond A.
; TITLE OF INVENTION: Human Monoclonal Antibodies
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation

;; STREET: 709 Swedeland Road
;; CITY: King of Prussia
;; STATE: PA
;; COUNTRY: U.S.A.
;; ZIP: 19046
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSEQ for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/10/066,895
;; FILING DATE: 04-Feb-2002
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 09/297,344
;; FILING DATE: 1999-JUN-09
;; APPLICATION NUMBER: 60/030,149
;; FILING DATE: 01-NOV-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Geiger, Kathleen
;; REGISTRATION NUMBER: 35,880
;; REFERENCE/DOCKET NUMBER: P50504
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 610-270-5968
;; TELEFAX: 610-270-5090
;; TELEX: <Unknown>
;; INFORMATION FOR SEQ ID NO: 10:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 124 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-066-895-10

Query Match 79.2%; Score 57; DB 12; Length 124;
Best Local Similarity 69.2%; Pred. No. 0.029;
Matches 9; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQISNFLHWY 13
:|:|:| |||:|
Db 41 RATQSVSNFLNWY 53

RESULT 10
US-09-905-243-36
; Sequence 36, Application US/09905243
; Patent No. US20020062009A1
; GENERAL INFORMATION:
; APPLICANT: Taylor, Alexander H
; TITLE OF INVENTION: Monoclonal Antibodies with Reduced
; FILE REFERENCE: P50770
; CURRENT APPLICATION NUMBER: US/09/905,243
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/300,970
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Pan troglodytes
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (24)...(34)
; OTHER INFORMATION: CDRI
; NAME/KEY: DOMAIN
; LOCATION: (50)...(66)
; OTHER INFORMATION: CDRII
US-09-905-243-36

Query Match 77.8%; Score 56; DB 10; Length 88;
Best Local Similarity 76.9%; Pred. No. 0.03;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISNLFHWY 13
DB 24 RASQISNLSWY 36

RESULT 11
US-09-956-206A-3
; Sequence 3, Application US/09956206A
; Patent No. US20020164339A1
; GENERAL INFORMATION:
; APPLICANT: DO COUTO, FERNANDO J.R.
; CERIANT, ROBERTO L.
; PETERSON, JERRY A.
; TITLE OF INVENTION: MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND
; METHODS OF HUMANIZING ANTIBODY PEPTIDES
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/956.206A
; FILING DATE: 19-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/525,539
; FILING DATE: 14-SEP-1995
; APPLICATION NUMBER: PCT/US95/11683
; FILING DATE: 14-SEP-1995
; APPLICATION NUMBER: 08/487,598
; FILING DATE: 7-JUNE-1995
; APPLICATION NUMBER: 08/307,868
; FILING DATE: 16-SEPT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: WITT, ERIC
; REGISTRATION NUMBER: 44,408
; REFERENCE/DOCKET NUMBER: 276332000101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-956-206A-3

Query Match 76.4%; Score 55; DB 9; Length 31;
Best Local Similarity 76.9%; Pred. No. 0.017;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QASQISNLFHWY 13
DB 11 RASQISNLSWY 23

RESULT 12
US-09-850-165-93
; Sequence 93, Application US/09850165
; Patent No. US20020150580A1
; GENERAL INFORMATION:
; APPLICANT: NEWMAN, ROLAND A.
; APPLICANT: HANNA, NABIL
; APPLICANT: RAAB, RONALD W.
; TITLE OF INVENTION: RECOMBINANT ANTIBODIES FOR HUMAN THERAPY
; FILE REFERENCE: 037003-0280614
; CURRENT APPLICATION NUMBER: US/09/850,165
; CURRENT FILING DATE: 2001-05-08
; PRIOR APPLICATION NUMBER: 09/082,472
; PRIOR FILING DATE: 1998-05-21
; PRIOR APPLICATION NUMBER: 08/476,237
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/397,072
; PRIOR FILING DATE: 1995-04-17
; PRIOR APPLICATION NUMBER: 07/912,292
; PRIOR FILING DATE: 1992-07-10
; PRIOR APPLICATION NUMBER: 07/856,281
; PRIOR FILING DATE: 1992-03-23
; PRIOR APPLICATION NUMBER: 07/735,064
; PRIOR FILING DATE: 1991-07-25
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 93
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: monkey clone
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (13)
; OTHER INFORMATION: Val or Ala
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (77)
; OTHER INFORMATION: Arg, Gly or Ser
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (83)
; OTHER INFORMATION: Ile or Phe
US-09-850-165-93

Query Match 76.4%; Score 55; DB 10; Length 107;
Best Local Similarity 76.9%; Pred. No. 0.05;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QASQISNLFHWY 13
DB 24 QASQSVSNLLAWY 36

RESULT 13
US-09-056-160B-12
; Sequence 12, Application US/09056160B
; Patent No. US20020032315A1
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; APPLICANT: Wells, James A.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Lowman, Henry B.
; APPLICANT: Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California

; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/056,160B
; FILING DATE: 06-Apr-1998
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/054,856
; FILING DATE: 06-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: P1093R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1896
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-056-160B-12

Query Match 76.4%; Score 55; DB 10; Length 108;
Best Local Similarity 76.9%; Pred. No. 0.051;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QASQSIISFLHWY 13
Db 24 RASQSIISFLHWY 36

RESULT 14
US-09-811-123-6
; Sequence 6, Application US/09811123
; Patent No. US20020001587A1
; GENERAL INFORMATION:
; APPLICANT: Sharon Erickson
; APPLICANT: Ralph Schwall
; APPLICANT: Mark Sliwkowski
; TITLE OF INVENTION: METHODS OF TREATMENT USING ANTI-ErbB
; FILE REFERENCE: GENENT.073A2
; CURRENT APPLICATION NUMBER: US/09/811,123
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/238,327
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 09/602,530
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized Antibody Sequence
US-09-811-123-6

Query Match 76.4%; Score 55; DB 10; Length 109;
Best Local Similarity 76.9%; Pred. No. 0.051;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QASQSIISFLHWY 13
Db 24 RASQSIISFLHWY 36

RESULT 15
US-09-800-729-150
; Sequence 150, Application US/09800729
; Patent No. US20020068319A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 32 Human secreted proteins
; FILE REFERENCE: P2044P1
; CURRENT APPLICATION NUMBER: US/09/800,729
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: PCT/US00/26013
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/155,709
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 150
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (120)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-800-729-150

Query Match 76.4%; Score 55; DB 10; Length 234;
Best Local Similarity 69.2%; Pred. No. 0.099;
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QASQSIISFLHWY 13
Db 44 QASQDIANYLNWY 56

Search completed: November 18, 2002, 18:45:18
Job time : 3.54902 secs

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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:01 ; Search time 5.51225 Seconds
(without alignments)
69.390 Million cell updates/sec

Title: US-09-016-061-82

Perfect score: 72

Sequence: 1 QASQSISNFIHWY 13

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Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	60	83.3	107	4	US-09-438-954-3
5	60	83.3	108	2	US-08-378-939-20
6	60	83.3	108	4	US-09-247-352-1
7	60	83.3	108	4	US-09-466-635-1
8	60	83.3	214	4	US-09-247-352-4
9	60	83.3	214	4	US-09-466-635-4
10	59	81.9	100	1	US-08-436-463-19
11	59	81.9	103	1	US-08-436-463-21
12	59	81.9	107	1	US-07-634-278-62
13	59	81.9	107	1	US-07-634-278-63
14	59	81.9	107	1	US-07-634-278-87
15	59	81.9	107	1	US-08-477-728-62
16	59	81.9	107	1	US-08-477-728-63
17	59	81.9	107	1	US-08-477-728-87
18	59	81.9	107	1	US-08-474-040-62
19	59	81.9	107	1	US-08-474-040-63
20	59	81.9	107	1	US-08-474-040-87
21	59	81.9	107	1	US-08-487-200-62
22	59	81.9	107	1	US-08-487-200-63
23	59	81.9	107	1	US-08-487-200-87
24	59	81.9	107	1	US-08-484-537-62
25	59	81.9	107	4	US-08-484-537-63
26	59	81.9	107	4	US-08-484-537-87
27	59	81.9	108	4	US-09-157-370-4

28 59 81.9 127 1 US-07-634-278-83 Sequence 83, Appl
29 59 81.9 127 1 US-08-477-728-83 Sequence 83, Appl
30 59 81.9 127 1 US-08-474-040-83 Sequence 83, Appl
31 59 81.9 127 1 US-08-487-200-83 Sequence 83, Appl
32 59 81.9 127 1 US-08-436-463-4 Sequence 4, Appl
33 59 81.9 127 1 US-08-436-463-18 Sequence 18, Appl
34 59 81.9 127 4 US-08-484-537-83 Sequence 83, Appl
35 59 80.6 76 4 US-08-851-362D-20 Sequence 20, Appl
36 58 80.6 105 4 US-08-851-362D-28 Sequence 28, Appl
37 58 80.6 105 4 US-08-851-362D-34 Sequence 34, Appl
38 58 80.6 105 4 US-08-851-362D-38 Sequence 38, Appl
39 58 80.6 107 2 US-08-652-558-36 Sequence 36, Appl
40 58 80.6 107 2 US-08-378-939-14 Sequence 14, Appl
41 58 80.6 107 4 US-09-240-274-173 Sequence 173, App
42 58 80.6 108 1 US-08-276-852-102 Sequence 102, App
43 58 80.6 108 1 US-08-899-575-102 Sequence 102, App
44 58 80.6 108 1 US-08-899-575-102 Sequence 102, App
45 58 80.6 108 2 US-08-378-939-30 Sequence 30, Appl

ALIGNMENTS

RESULT 1

US-08-737-560A-9
; Sequence 9, Application US/08737560A
; Patent No. 5928893
; GENERAL INFORMATION:
; APPLICANT: KANG, Chang-Yuill
; APPLICANT: KIM, Joong-Gon
; TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC FOR HUMAN
; TITLE OF INVENTION: 4-1BB AND CELL LINE PRODUCING SAME
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KANG, Chang-Yuill
; STREET: Professor Apt. Ka-302, #244-2, Bongchun 7-dong,
; STREET: Kwanak-gu
; CITY: Seoul
; STATE: Seoul
; COUNTRY: Republic of Korea
; ZIP: 151-057
; ADDRESSEE: KIM, Joong-Gon
; STREET: Hanyang Apt. 72-1213, Appujung-dong, Kangnam-gu
; CITY: Seoul
; STATE: Seoul
; COUNTRY: Republic of Korea
; ZIP: 135-110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5inch, 1.44MB storage
; COMPUTER: IBM PC/AT
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/737,560A
; FILING DATE: 13-NOV-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: KR 95-8176
; FILING DATE: 08-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 96 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:

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; OTHER INFORMATION: VK23.32'CL
US-08-737-560A-9

Query Match      83.3%; Score 60; DB 2; Length 96;
Best Local Similarity 76.9%; Pred. No. 0.0048;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQISISNLFHWY 13
Db 24 RASQISISDYLHWY 36

RESULT 2
US-09-247-352-8
; Sequence 8, Application US/09247352
; Patent No. 6312693
; GENERAL INFORMATION:
; APPLICANT: Aruffo, Alejandro A.
; APPLICANT: Siadak, Anthony W.
; APPLICANT: Berry, Karen K.
; APPLICANT: Harris, Linda
; APPLICANT: Thorne, Barbara A.
; APPLICANT: Bajorath, Jurgen
; APPLICANT: Huse, William D.
; APPLICANT: Wu, Herren
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: ANTIBODIES AGAINST HUMAN CD40
; FILE REFERENCE: DB2a SEQUENCE
; CURRENT APPLICATION NUMBER: US/09/247,352
; CURRENT FILING DATE: 1999-02-10
; EARLIER APPLICATION NUMBER: 09/026,291
; EARLIER FILING DATE: 1998-02-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Human and Mouse
US-09-247-352-8

Query Match      83.3%; Score 60; DB 4; Length 107;
Best Local Similarity 76.9%; Pred. No. 0.0054;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQISISNLFHWY 13
Db 24 RASQISISDYLHWY 36

RESULT 3
US-09-247-352-12
; Sequence 12, Application US/09247352
; Patent No. 6312693
; GENERAL INFORMATION:
; APPLICANT: Aruffo, Alejandro A.
; APPLICANT: Siadak, Anthony W.
; APPLICANT: Berry, Karen K.
; APPLICANT: Harris, Linda
; APPLICANT: Thorne, Barbara A.
; APPLICANT: Bajorath, Jurgen
; APPLICANT: Huse, William D.
; APPLICANT: Wu, Herren
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: ANTIBODIES AGAINST HUMAN CD40
; FILE REFERENCE: DB2a SEQUENCE
; CURRENT APPLICATION NUMBER: US/09/247,352
; CURRENT FILING DATE: 1999-02-10
; EARLIER APPLICATION NUMBER: 09/026,291
; EARLIER FILING DATE: 1998-02-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 107

; TYPE: PRT
; ORGANISM: Human and Mouse
US-09-247-352-12

Query Match      83.3%; Score 60; DB 4; Length 107;
Best Local Similarity 76.9%; Pred. No. 0.0054;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQISISNLFHWY 13
Db 24 RASQISISDYLHWY 36

RESULT 4
US-09-438-954-3
; Sequence 3, Application US/09438954
; Patent No. 6458934
; GENERAL INFORMATION:
; APPLICANT: HONG, Hyo Jeong
; APPLICANT: PARK, Sung Sup
; APPLICANT: KANG, Young Jun
; APPLICANT: KANG, Chang-Yuil
; APPLICANT: YOON, Sung Kwan
; TITLE OF INVENTION: HUMANIZED ANTIBODY SPECIFIC FOR HUMAN 4-1BB AND
; FILE REFERENCE: 1303-124P
; CURRENT APPLICATION NUMBER: US/09/438,954
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Variable
; OTHER INFORMATION: region of light chain of humanized antibody
; OTHER INFORMATION: H24B4-2
US-09-438-954-3

Query Match      83.3%; Score 60; DB 4; Length 107;
Best Local Similarity 76.9%; Pred. No. 0.0054;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQISISNLFHWY 13
Db 24 RASQISISDYLHWY 36

RESULT 5
US-08-378-939-20
; Sequence 20, Application US/08378939
; Patent No. 5876961
; GENERAL INFORMATION:
; APPLICANT: CROWE, JAMES SCOTT
; APPLICANT: LEWIS, ALAN PETER
; TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
; STREET: 555 THIRTEENTH ST. N.W.
; CITY: WASHINGTON
; STATE: D. C.
; COUNTRY: U.S.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/378,939
; FILING DATE:
```

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/952640
FILING DATE: 01-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: ERNST, BARBARA G
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1808-118
TELEPHONE: (202) 783-6040
TELEFAX: (202) 783-6031
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-378-939-20

Query Match 83.3%; Score 60; DB 2; Length 108;
Best Local Similarity 76.9%; Pred. No. 0.0054;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQISNLFHWY 13
Db 24 QASQSLNLYNWY 36

RESULT 6

US-09-247-352-1
Sequence 1, Application US/09247352
Patent No. 6312693
GENERAL INFORMATION:
APPLICANT: Aruffo, Alejandro A.
APPLICANT: Sladak, Anthony W.
APPLICANT: Berry, Karen K.
APPLICANT: Harris, Linda
APPLICANT: Thorne, Barbara A.
APPLICANT: Bajorath, Jurgan
APPLICANT: Huse, William D.
APPLICANT: Wu, Herren
APPLICANT: Watkins, Jeffrey D.
TITLE OF INVENTION: ANTIBODIES AGAINST HUMAN CD40
FILE REFERENCE: DB2a SEQUENCE
CURRENT APPLICATION NUMBER: US/09/247,352
CURRENT FILING DATE: 1999-02-10
EARLIER APPLICATION NUMBER: 09/026,291
EARLIER FILING DATE: 1998-02-19
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 108
TYPE: PRT
ORGANISM: Human and Mouse
US-09-247-352-1

Query Match 83.3%; Score 60; DB 4; Length 108;
Best Local Similarity 76.9%; Pred. No. 0.0054;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQISNLFHWY 13
Db 24 RASQISDYLHWY 36

RESULT 7

US-09-466-635-1
Sequence 1, Application US/09466635
Patent No. 6413514
GENERAL INFORMATION:
APPLICANT: Aruffo, Alejandro A.
APPLICANT: Sladak, Anthony W.
APPLICANT: Berry, Karen K.

APPLICANT: Harris, Linda
APPLICANT: Thorne, Barbara A.
APPLICANT: Bajorath, Jurgan
TITLE OF INVENTION: ANTIBODIES AGAINST HUMAN CD40
FILE REFERENCE: DB2 SEQUENCE
CURRENT APPLICATION NUMBER: US/09/466,635
CURRENT FILING DATE: 1999-12-17
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 108
TYPE: PRT
ORGANISM: Human and Mouse
US-09-466-635-1

Query Match 83.3%; Score 60; DB 4; Length 108;
Best Local Similarity 76.9%; Pred. No. 0.0054;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQISNLFHWY 13
Db 24 RASQISDYLHWY 36

RESULT 8

US-09-247-352-4
Sequence 4, Application US/09247352
Patent No. 6312693
GENERAL INFORMATION:
APPLICANT: Aruffo, Alejandro A.
APPLICANT: Sladak, Anthony W.
APPLICANT: Berry, Karen K.
APPLICANT: Harris, Linda
APPLICANT: Thorne, Barbara A.
APPLICANT: Bajorath, Jurgan
APPLICANT: Huse, William D.
APPLICANT: Wu, Herren
APPLICANT: Watkins, Jeffrey D.
TITLE OF INVENTION: ANTIBODIES AGAINST HUMAN CD40
FILE REFERENCE: DB2a SEQUENCE
CURRENT APPLICATION NUMBER: US/09/247,352
CURRENT FILING DATE: 1999-02-10
EARLIER APPLICATION NUMBER: 09/026,291
EARLIER FILING DATE: 1998-02-19
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 214
TYPE: PRT
ORGANISM: Human and Mouse
US-09-247-352-4

Query Match 83.3%; Score 60; DB 4; Length 214;
Best Local Similarity 76.9%; Pred. No. 0.011;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQISNLFHWY 13
Db 24 RASQISDYLHWY 36

RESULT 9

US-09-466-635-4
Sequence 4, Application US/09466635
Patent No. 6413514
GENERAL INFORMATION:
APPLICANT: Aruffo, Alejandro A.
APPLICANT: Sladak, Anthony W.
APPLICANT: Berry, Karen K.
APPLICANT: Harris, Linda
APPLICANT: Thorne, Barbara A.
APPLICANT: Bajorath, Jurgan
TITLE OF INVENTION: ANTIBODIES AGAINST HUMAN CD40

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; FILE REFERENCE: DB2 SEQUENCE
; CURRENT APPLICATION NUMBER: US/09/466,635
; CURRENT FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Human and Mouse
US-09-466-635-4

Query Match      83.3%; Score 60; DB 4; Length 214;
Best Local Similarity 76.9%; Pred. No. 0.011;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQISNLFHWY 13
:|||||:||||
Db 24 RASQISDYLHWY 36

RESULT 10
US-08-436-463-19
; Sequence 19, Application US/08436463
; Patent No. 5760185
; GENERAL INFORMATION:
; APPLICANT: KIMACHI, Kazuhiko
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: NISHIYAMA, Kiyoto
; APPLICANT: TOKIYOSHI, Sachio
; TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT
; TITLE OF INVENTION: ANTIBODY AND GENE FRAGMENT CODING FOR SAID ANTIBODY
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,463
; FILING DATE: 26-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION NUMBER: JP 341255/1992
; FILING DATE: 28-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: KIMACHI=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 100 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-436-463-19

Query Match      81.9%; Score 59; DB 1; Length 100;
Best Local Similarity 84.6%; Pred. No. 0.0073;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISNLFHWY 13
:|||||:||||
Db 24 RASQISDYLHWY 36

RESULT 11
US-08-436-463-21
; Sequence 21, Application US/08436463
; Patent No. 5760185
; GENERAL INFORMATION:
; APPLICANT: KIMACHI, Kazuhiko
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: NISHIYAMA, Kiyoto
; APPLICANT: TOKIYOSHI, Sachio
; TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT
; TITLE OF INVENTION: ANTIBODY AND GENE FRAGMENT CODING FOR SAID ANTIBODY
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,463
; FILING DATE: 26-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION NUMBER: JP 341255/1992
; FILING DATE: 28-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: KIMACHI=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 103 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-436-463-21

Query Match      81.9%; Score 59; DB 1; Length 103;
Best Local Similarity 84.6%; Pred. No. 0.0075;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISNLFHWY 13
:|||||:||||
Db 22 RASQISNLFHWY 34

RESULT 12
US-07-634-278-62
; Sequence 62, Application US/07634278
; Patent No. 5530101
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: GOELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
```

ADDRESSEE: Townsend and Townsend Kourile and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-634-278-62

Query Match 81.9%; Score 59; DB 1; Length 107;
Best Local Similarity 84.6%; Pred. No. 0.0078;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QASQTSISNFLHWY 13
:|||||
Db 24 RASQTSISNFLHWY 36

RESULT 13
US-07-634-278-63
Sequence 63, Application US/07634278
Patent No. 5530101
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourile and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-634-278-63
Query Match 81.9%; Score 59; DB 1; Length 107;
Best Local Similarity 84.6%; Pred. No. 0.0078;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 QASQTSISNFLHWY 13
:|||||
Db 24 RASQTSISNFLHWY 36
RESULT 14
US-07-634-278-87
Sequence 87, Application US/07634278
Patent No. 5530101
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourile and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252

;; FILING DATE: 13-FEB-1989
;; PRIOR APPLICATION DATA: US 07/290,975
;; FILING DATE: 28-DEC-1988
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Smith, William M.
;; REGISTRATION NUMBER: 30,223
;; REFERENCE/DOCKET NUMBER: 11823-002600
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 326-2400
;; TELEFAX: (415) 326-2422
;; INFORMATION FOR SEQ ID NO: 87:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 107 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-07-634-278-87

Query Match 81.9%; Score 59; DB 1; Length 107;
Best Local Similarity 84.6%; Pred. No. 0.0078;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQSISNHLHWY 13
Db 24 RASQSISNHLHWY 36

RESULT 15

US-08-477-728-62
; Sequence 62, Application US/08477728
; Patent No. 5585089
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,728
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400

;; TELEFAX: (415) 326-2422
;; INFORMATION FOR SEQ ID NO: 62:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 107 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-08-477-728-62

Query Match 81.9%; Score 59; DB 1; Length 107;
Best Local Similarity 84.6%; Pred. No. 0.0078;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQSISNHLHWY 13
Db 24 RASQSISNHLHWY 36

Search completed: November 18, 2002, 17:43:39
Job time : 5.51225 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:01 ; Search time 5.39216 Seconds
(without alignments)
196.114 Million cell updates/sec

Title: US-09-016-061-84
Perfect score: 49
Sequence: 1 LLIRYSSQSIS 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR.73.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	43	87.8	69	2 PH1080	Ig light chain V r
2	43	87.8	96	2 G33730	Ig kappa chain V r
3	43	87.8	104	2 B43413	Ig kappa chain V r
4	43	87.8	106	2 PL0367	Ig kappa chain V r
5	43	87.8	107	2 B45722	anti-glycoprotein
6	43	87.8	107	2 C45722	anti-glycoprotein
7	43	87.8	107	2 A45722	anti-glycoprotein
8	43	87.8	115	2 S10146	Ig kappa chain pre
9	43	87.8	138	2 A26471	Ig kappa chain pre
10	40	81.6	87	2 PH1082	Ig light chain V r
11	40	81.6	102	2 C26346	Ig kappa chain V r
12	40	81.6	108	2 S30502	Ig kappa chain V r
13	40	81.6	115	1 KVM5U7	Ig kappa chain pre
14	40	81.6	123	2 S35479	Ig kappa chain pre
15	40	81.6	128	2 PN0445	Ig kappa chain pre
16	39	79.6	67	2 PH1081	Ig light chain V r
17	39	79.6	103	2 S19975	Ig kappa chain V r
18	39	79.6	114	2 S00996	Ig kappa chain pre
19	37	75.5	500	2 S56276	probable membrane
20	36	73.5	3344	2 JQ1899	genome polypotein
21	35	71.4	284	2 G90470	hypothetical prote
22	35	71.4	613	1 Q0BE33	BBRfl protein - hu
23	35	71.4	675	2 D85065	receptor protein k
24	35	71.4	847	1 S36337	histidine decarbox
25	34	69.4	141	2 C83768	hypothetical prote
26	33	67.3	66	2 G98059	hypothetical prote
27	33	67.3	399	2 AE0549	probable efflux pu
28	33	67.3	406	2 B82147	conserved hypothet
29	33	67.3	407	2 D85643	hypothetical prote

30 33 67.3 422 2 A93783 probable tail tip
31 33 67.3 459 2 T11256 NADH2 dehydrogenas
32 33 67.3 598 2 T28238 ORF MSV077 hypothe
33 33 67.3 998 2 T04842 genome polyprotein
34 33 67.3 3125 1 GNVSPS genome polyprotein
35 33 67.3 3140 1 GNVSRA genome polyprotein
36 33 67.3 3140 2 S47508 genome polyprotein
37 33 67.3 3141 1 GNVSPD hypothetical prote
38 32 65.3 121 2 AB2315 hypothetical prote
39 32 65.3 225 2 C85475 NADH2 dehydrogenas
40 32 65.3 290 2 S26028 transcription regu
41 32 65.3 365 2 F82398 methylease Llapi -
42 32 65.3 380 2 B47029 probable poly(A) b
43 32 65.3 545 2 F84635 hypothetical prote
44 32 65.3 547 1 D64249 site-specific DNA -
45 32 65.3 622 2 S35122

ALIGNMENTS

RESULT 1

PH1080
Ig light chain V region (clone 165.60) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 15-Jun-1996
C:Accession: PH1080
R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective
A:Reference number: PH0971; MUID:92381444; PMID:1512540
A:Accession: PH1080
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-69 <TIL>
A:Experimental source: B cell, strain [N2B x NZW]F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin

Query Match 87.8%; Score 43; DB 2; Length 69;
Best Local Similarity 81.8%; Pred. No. 0.063;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIRYSSQSIS 11
Db 17 LLIKVASQSIS 27
||||:|||||

RESULT 2

G33730
Ig kappa chain V region (23.32) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 21-Jan-2000
C:Accession: G33730
R:Lawler, A.M.; Kearney, J.F.; Kuehl, M.; Gearhart, P.J.
Proc. Natl. Acad. Sci. U.S.A. 86, 6744-6747, 1989
A:Title: Early rearrangements of genes encoding murine immunoglobulin kappa-chains, u
A:Reference number: A33730; MUID:89367325; PMID:2505260
A:Accession: G33730
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-96 <LAW>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F16-90/Domain: immunoglobulin homology <IMM>

Query Match 87.8%; Score 43; DB 2; Length 96;
Best Local Similarity 81.8%; Pred. No. 0.089;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIRYSSQSIS 11
Db 46 LLIKVASQSIS 56
||||:|||||


```

RESULT 3
B43413
Ig kappa chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: B43413
R:Tomiya, Y.; Brojer, E.; Ruggeri, Z.M.; Shattil, S.J.; Smiltneck, J.; Gorski, J.; Kun
J. Biol. Chem. 267, 18085-18092, 1992
A:Title: A molecular model of RGD ligands. Antibody D gene segments that direct specific
A:Reference number: A43413; MUID:92388177; PMID:1517241
A:Accession: B43413
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-104 <TOM>
A:Note: sequence extracted from NCBI backbone (NCBIP:112818)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:13-87/Domain: immunoglobulin homology <IMM>

Query Match      87.8%; Score 43; DB 2; Length 104;
Best Local Similarity 81.8%; Pred. No. 0.097;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIRYSQSIS 11
    |||:|:|||||
Db 43 LLIKYASQSIS 53

RESULT 4
PL0267
Ig kappa chain V region (anti-DNA, DP12VK) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C:Accession: PL0267
R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A
J. Exp. Med. 171, 265-297, 1990
A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
A:Reference number: PL0231; MUID:90111618; PMID:2104919
A:Accession: PL0267
A:Molecule type: mRNA
A:Residues: 1-106 <SHL>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:1-23/Region: framework 1
F:16-90/Domain: immunoglobulin homology <IMM>
F:24-34/Region: complementarity-determining 1
F:35-49/Region: framework 2
F:50-56/Region: complementarity-determining 2
F:57-88/Region: framework 3
F:89-97/Region: complementarity-determining 3
F:98-106/Region: framework 4

Query Match      87.8%; Score 43; DB 2; Length 106;
Best Local Similarity 81.8%; Pred. No. 0.099;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIRYSQSIS 11
    |||:|:|||||
Db 46 LLIKYASQSIS 56

RESULT 5
B45722
anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 33) - mouse (fr
C:Species: Mus musculus (house mouse)
C:Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: B45722
R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Vasqu
J. Virol. 67, 489-496, 1993
A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on hu
A:Reference number: A45722; MUID:93100833; PMID:7677958

```

```

A:Accession: B45722
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-107 <SIM>
A:Note: sequence extracted from NCBI backbone (NCBIP:120590)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: glycoprotein
F:16-90/Domain: immunoglobulin homology <IMM>

```

```

Query Match      87.8%; Score 43; DB 2; Length 107;
Best Local Similarity 81.8%; Pred. No. 0.1;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 LLIRYSQSIS 11
    |||:|:|||||
Db 46 LLIKYASQSIS 56

```

```

RESULT 6
C45722
anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 115) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: C45722
R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Va
J. Virol. 67, 489-496, 1993
A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on
A:Reference number: A45722; MUID:93100833; PMID:7677958
A:Accession: C45722
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-107 <SIM>
A:Note: sequence extracted from NCBI backbone (NCBIP:120591)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: glycoprotein
F:16-90/Domain: immunoglobulin homology <IMM>

```

```

Query Match      87.8%; Score 43; DB 2; Length 107;
Best Local Similarity 81.8%; Pred. No. 0.1;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 LLIRYSQSIS 11
    |||:|:|||||
Db 46 LLIKYASQSIS 56

```

```

RESULT 7
A45722
anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 5) - mouse (
C:Species: Mus musculus (house mouse)
C:Date: 03-Mar-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: A45722
R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Va
J. Virol. 67, 489-496, 1993
A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on
A:Reference number: A45722; MUID:93100833; PMID:7677958
A:Accession: A45722
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-107 <SIM>
A:Note: sequence extracted from NCBI backbone (NCBIP:120589)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: glycoprotein
F:16-90/Domain: immunoglobulin homology <IMM>

```

```

Query Match      87.8%; Score 43; DB 2; Length 107;
Best Local Similarity 81.8%; Pred. No. 0.1;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 LLIRYSQSIS 11
    |||:|:|||||
Db 46 LLIKYASQSIS 56

```

```
RESULT 8
S10146
Ig kappa chain precursor V region (A14) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 21-Jan-2000
C:Accession: S10146
R:Straubinger, B.; Thiebe, R.; Huber, C.; Osterholzer, E.; Zachau, H.G.
Biol. Chem. Hoppe-Seyler 369, 601-607, 1988
A:Title: Two unusual human immunoglobulin V-kappa genes.
A:Reference number: S00996; MUID:89134397; PMID:2852016
A:Accession: S10146
A:Molecule type: DNA
A:Residues: 1-115 <STR>
A:Cross-references: EMBL:M27751; NID:q185916; PIDN:AAA58913.1; PID:q185917
A:Note: this sequence was determined from the germline gene
C:Genetics:
A:Introns: 17/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-115/Product: Ig kappa chain V region #status predicted <MAT>
F:36-110/Domain: immunoglobulin homology <IMM>
F:43-108/Disulfide bonds: #status predicted

Query Match      87.8%; Score 43; DB 2; Length 115;
Best Local Similarity 81.8%; Pred. No. 0.11;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLIRYSSQSIS 11
Db 66 LLIKYASQSIS 76

RESULT 9
A26471
Ig kappa chain precursor V region (MAK33) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 03-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 23-Jul-1999
C:Accession: A26471
R:Buckel, P.; Hubner-Parajsz, C.; Mattes, R.; Lenz, H.; Haug, H.; Beaucamp, K.
Gene 51, 13-19, 1987
A:Title: Cloning and nucleotide sequence of heavy- and light-chain cDNAs from a creatine
A:Reference number: A91572; MUID:87248036; PMID:3110009
A:Accession: A26471
A:Molecule type: mRNA
A:Residues: 1-138 <BUC>
A:Cross-references: GB:M16162; NID:q196893; PIDN:AAA38823.1; PID:q196894
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-138/Product: Ig kappa chain V region #status predicted <MAT>

Query Match      87.8%; Score 43; DB 2; Length 138;
Best Local Similarity 81.8%; Pred. No. 0.13;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLIRYSSQSIS 11
Db 66 LLIKYASQSIS 76

RESULT 10
PH1082
Ig light chain V region (clone 165.54) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C:Accession: PH1082
R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B c
A:Reference number: PH0971; MUID:92381444; PMID:1512540
A:Accession: PH1082
```

```
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-87 <TIL>
A:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Cross-references: GB:M21907; NID:q197071; PIDN:AAA38907.1; PID:q197072
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-80/Domain: immunoglobulin homology <IMM>

Query Match      81.6%; Score 40; DB 2; Length 87;
Best Local Similarity 72.7%; Pred. No. 0.35;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLIRYSSQSIS 11
Db 36 LLIKYASESIS 46

RESULT 11
S26346
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C:Accession: S26346
R:Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A:Title: Antibodies that are specific for a single amino acid interchange in a protei
A:Reference number: S26309; MUID:91341421; PMID:1908510
A:Accession: S26346
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-102 <STA>
A:Cross-references: EMBL:X59211; NID:g52338; PIDN:CAA41921.1; PID:gl334075
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:14-88/Domain: immunoglobulin homology <IMM>

Query Match      81.6%; Score 40; DB 2; Length 102;
Best Local Similarity 81.8%; Pred. No. 0.41;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LLIRYSSQSIS 11
Db 44 LLIKYVSQSIS 54

RESULT 12
C30502
Ig kappa chain V region (D444) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 03-Nov-1988 #sequence_revision 03-Nov-1988 #text_change 21-Jan-2000
C:Accession: C30502
R:Eilat, D.; Webster, D.M.; Rees, A.R.
J. Immunol. 141, 1745-1753, 1988
A:Title: V region sequences of anti-DNA and anti-RNA autoantibodies from NZB/NZW F-1
A:Reference number: A30502; MUID:88315787; PMID:2457627
A:Accession: C30502
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-108 <EIL>
A:Cross-references: GB:M21907; NID:q197071; PIDN:AAA38907.1; PID:q197072
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match      81.6%; Score 40; DB 2; Length 108;
Best Local Similarity 72.7%; Pred. No. 0.44;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLIRYSSQSIS 11
Db 46 LLIKYASESIS 56
```

RESULT 13

KVMSL7

Ig kappa chain precursor V region (L7) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 18-Dec-1981 #sequence_revision 18-Dec-1981 #text_change 22-Jun-1999

C:Accession: A01925

R:Pech, M.; Hochtl, J.; Schnell, H.; Zachau, H.G.

Nature 291, 668-670, 1981

A:Title: Differences between germ-line and rearranged immunoglobulin V-kappa coding sequences

A:Reference number: A93259; MUID:81220975; PMID:6264318

A:Accession: A01925

A:Molecule type: DNA

A:Residues: 1-115 <PEC>

A:Cross-references: GB:V01564; GB:J00574; NID:951718; PIDN:CAA24884.1; PID:g758153

A:Note: the sequence was determined from the germline gene

A:Note: there appear to be two possible splice junctions at the 3' end of the intron; the

C:Genetics:

A:Introns: 17/1

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-115/Product: Ig kappa chain V region (L7) #status predicted <MAT>

F:36-110/Domain: immunoglobulin homology <IMM>

F:43-108/Disulfide bonds: #status predicted

Query Match 81.6%; Score 40; DB 1; Length 115;

Best Local Similarity 72.7%; Pred. No. 0.47;

Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIRYSQSIS 11

|||:|:|:|

Db 66 LLIKYASESIS 76

RESULT 14

S35479

Ig kappa chain precursor V region - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 19-Mar-1997 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000

C:Accession: S35479

R:Takeda, Y.; Wise, K.S.; Hoffman, R.W.

Nucleic Acids Res. 20, 4099, 1992

A:Title: Nucleotide sequences of immunoglobulin heavy and light chain V-regions from a mouse

A:Reference number: S35479; MUID:92375706; PMID:1387203

A:Accession: S35479

A:Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-123 <TAK>

A:Cross-references: EMBL:M93959; NID:g197572; PIDN:AAA39079.1; PID:g554148

C:Genetics:

A:Map position: 6

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-12/Domain: signal sequence (fragment) #status predicted <SIG>

F:13-123/Product: Ig kappa chain V region (fragment) #status predicted <MAT>

F:28-102/Domain: immunoglobulin homology <IMM>

Query Match

81.6%; Score 40; DB 2; Length 123;

Best Local Similarity 81.8%; Pred. No. 0.5;

Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLIRYSQSIS 11

|||:|:|:|

Db 58 LLIKYVSQSIS 68

RESULT 15

PN0445

Ig kappa chain precursor V-I region - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:00 ; Search time 2.69608 Seconds
(without alignments)
169.223 Million cell updates/sec

Title: US-09-016-061-84
Perfect score: 49
Sequence: 1 LLIRYSSQSIS 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	81.6	115	1 KV51_MOUSE	P01642 mus musculus
2	37	75.5	500	1 YFJ1_YEAST	P43601 saccharomyc
3	36	73.5	3344	1 POLG_PPSVH	Q01901 p genome po
4	35	71.4	613	1 UL06_EBV	P03213 Epstein-bar
5	35	71.4	847	1 DCHS_DROME	Q05733 drosophila
6	33	67.3	459	1 NU4M_CERSI	Q03204 ceratotheri
7	33	67.3	459	1 NU4M_RH1UN	Q96068 rhinoceros
8	33	67.3	1786	1 YCF1_ARATH	P56785 arabidopsis
9	33	67.3	3125	1 POLG_PPVNA	P17766 p genome po
10	33	67.3	3140	1 POLG_PPVRA	P17767 p genome po
11	33	67.3	3140	1 POLG_PPVSK	Q84934 p genome po
12	33	67.3	3141	1 POLG_PPVD	P13529 p genome po
13	32	65.3	547	1 V447_MYCGE	P47685 mycoplasma
14	32	65.3	622	1 MTL1_LACLA	P35516 lactococcus
15	32	65.3	3066	1 POLG_SBMVG	Q90069 s genome po
16	32	65.3	3066	1 POLG_SBMVN	P21231 s genome po
17	31	63.3	112	1 RSR1_VIBCH	Q34419 vibrio chol
18	31	63.3	201	1 RACG_DICDI	O8qps0 dictyosteli
19	31	63.3	265	1 YBCM_ECOLI	P77634 escherichia
20	31	63.3	290	1 NUIM_ASCSU	P24875 ascaris suu
21	31	63.3	348	1 ABRB_ECOLI	P75747 escherichia
22	31	63.3	453	1 RADA_PSEAE	P69693 pseudomonas
23	31	63.3	474	1 YE91_MYCPN	P75295 mycoplasma
24	31	63.3	488	1 DP2S_THEAC	Q9H1K5 thermoplas
25	31	63.3	542	1 KCPY_CANAL	P30574 candida alb
26	31	63.3	686	1 KLC_STRPU	Q05090 strongyloce
27	31	63.3	717	1 PAL1_PRUAV	O64963 prunus aviu
28	31	63.3	812	1 SUN1_HUMAN	O94901 homo sapien
29	30	61.2	161	1 YD03_MYCTU	Q10619 mycobacteri
30	30	61.2	185	1 YCXB_BACSU	Q08793 bacillus su
31	30	61.2	297	1 HSLQ_PSEAE	Q9ntz6 pseudomonas
32	30	61.2	332	1 GALR_HAEIN	P31766 haemophilus
33	30	61.2	363	1 NUI1C_OENHO	Q9mth7 oenothera h

34 30 61.2 376 1 FHAE_BORPE Q00879 bordetella
35 30 61.2 582 1 HEX3_ADE12 P36712 human adeno
36 30 61.2 585 1 HEX3_ADE02 P03279 human adeno
37 30 61.2 585 1 HEX3_ADE05 P12537 human adeno
38 30 61.2 1014 1 CIN1_YEAST P40987 saccharomyc
39 30 61.2 1209 1 THR_DROME P42286 drosophila
40 30 61.2 1366 1 CA21_HUMAN P08123 homo sapien
41 29 59.2 145 1 VPRE_HUMAN P12018 homo sapien
42 29 59.2 155 1 CRT_CLODI P45361 clostridium
43 29 59.2 176 1 YQ33_BACAN Q9rmz9 bacillus an
44 29 59.2 258 1 TPIS_STRCO Q9z520 streptomyces
45 29 59.2 300 1 YB87_ARATH O81004 arabidopsis

ALIGNMENTS

RESULT 1
KV51_MOUSE
ID KV51_MOUSE STANDARD; PRT; 115 AA.
AC P01642;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-V region L7 precursor (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=812203975; Pubmed=6264318;
RA Pech M., Hochtl J., Schnell H., Zachau H.G.;
RT "Differences between germ-line and rearranged immunoglobulin V kappa
RT coding sequences suggest a localized mutation mechanism.";
RL Nature 291:668-670(1981).
CC -!- MISCELLANEOUS: THERE APPEAR TO BE TWO POSSIBLE SPLICE JUNCTIONS AT
CC THE 3' END OF THE INTRON. THE ALTERNATE WOULD CODE FOR A PROTEIN
CC LACKING RESIDUES 17-19.
DR PIR; A01925; KVM5L7.
DR HSSP; P80362; LWTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 >115 IG KAPPA CHAIN V-V REGION L7.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 69 FRAMEWORK-2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 77 108 FRAMEWORK-3.
FT DOMAIN 109 >115 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12615 MW; C17BEC758C577E00 CRC64;

Query Match 81.6%; Score 40; DB 1; Length 115;
Best Local Similarity 72.7%; Pred. No. 0.13;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIRYSSQSIS 11
DB 66 LLIKYASESIS 76
||||:|||||

RESULT 2
YFJ1_YEAST
ID YFJ1_YEAST STANDARD; PRT; 500 AA.
AC P43601;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 55.1 kDa Trp-Asp repeats containing protein in FABL-PES4
DE intergenic region.
GN YFR021W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c / AB972;
RX MEDLINE=95400292; PubMed=7670463;
RA Murakami Y., Naitou M., Hagiwara H., Shibata T., Ozawa M.,
RA Sasanuma S.-I., Sasanuma M., Tsuchiya Y., Soeda E., Yokoyama K.,
RA Yamazaki M., Tashiro H., Eki T.;
RT "Analysis of the nucleotide sequence of chromosome VI from
RT Saccharomyces cerevisiae";
RL Nat. Genet. 10:261-268(1995).
CC -1- SIMILARITY: CONTAINS 2 WD REPEATS (TRP-ASP DOMAINS).
CC -1- SIMILARITY: TO YEAST YGR223C.
CC -----
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CC -----
DR EMBL; D50617; BAA09260.1; -;
DR SGD; S0001917; YFR021W.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 2.
DR SMART; SM00320; WD40; 2.
DR PROSITE; PS00678; WD_REPEATS.1; FALSE_NEG.
DR PROSITE; PS00082; WD_REPEATS.2; FALSE_NEG.
DR PROSITE; PS0294; WD_REPEATS_REGION; 1.
KW Hypothetical protein; Repeat; WD repeat.
FT REPEAT 243 283
FT REPEAT 288 327 WD 2.
FT SEQUENCE 500 AA; 55102 MW; 06B2DFAF842AE933 CRC64;
Query Match 75.5%; Score 37; DB 1; Length 500;
Best Local Similarity 70.0%; Pred. No. 3;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 2 LIRVSSQSSIS 11
Db 378 MIRVSSQKLS 387
:|||||:|
RESULT 3
POLG_PRSVH STANDARD; PRT; 3344 AA.
AC Q01901;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Genome polyprotein [Contains: N-terminal protein (P1); Helper
DE component proteinase (EC 3.4.22.45) (HC-Pro); Protein p3; 6 kDa
DE protein 1 (6k1); Cytoplasmic inclusion protein (CI); 6 kDa protein 2
DE (6k2); Genome-linked protein (VPG); Nuclear inclusion protein A (NI-A)
DE (NIA) (EC 3.4.22.44) (49 kDa proteinase) (49 kDa-Pro); Nuclear
DE inclusion protein B (NI-B) (NIB) (RNA-directed RNA polymerase) (EC
DE 2.7.7.48); Coat protein (CP)].
OS Papaya ringspot virus (strain P / mutant HA).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
OC Potyvirus.
OX NCBI_TaxID=31731;
RN [1]
RP SEQUENCE FROM N.A.
RA Wang C.H., Bau H.J., Yeh S.D.;
RT "Comparison of the nuclear inclusion b protein and coat protein genes

of five papaya ringspot virus strains distinct in geographic origin
and pathogenicity";
Phytopathology 84:1205-1210(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93019006; PubMed=1402799;
RA Yeh S.D., Jan F.J., Chiang C.H., Doong T.J., Chen M.C.,
RA Chung P.H., Bau H.J.;
RT "Complete nucleotide sequence and genetic organization of papaya
RT ringspot virus RNA";
RL J. Gen. Virol. 73:2531-2541(1992).
RN [3]
RP SEQUENCE OF 2561-3344 FROM N.A.
RX MEDLINE=93090098; PubMed=1456896;
RA Wang C.H., Yeh S.D.;
RT "Nucleotide sequence comparison of the 3'-terminal regions of severe,
RT mild, and non-papaya infecting strains of papaya ringspot virus";
RL Arch. Virol. 127:345-354(1992).
CC -1- FUNCTION: HELPER COMPONENT-PROTEINASE IS REQUIRED FOR APHID
CC TRANSMISSION AND ALSO HAS PROTEOLYTIC ACTIVITY.
CC -1- FUNCTION: CYTOPLASMIC INCLUSION PROTEIN HAS HELICASE ACTIVITY. IT
CC MAY BE INVOLVED IN REPLICATION.
CC -1- FUNCTION: NUCLEAR INCLUSION PROTEIN A HAS PROTEOLYTIC ACTIVITY.
CC -1- CATALYTIC ACTIVITY: Hydrolyzes glutamyl bonds, and activity is
CC further restricted by preferences for the amino acids in P6 - P1'
CC that vary with the species of potyvirus, e.g. Glu-Xaa-Xaa-Tyr-Xaa-
CC Gln+(Ser or Gly) for the enzyme from tobacco etch virus. The
CC natural substrate is the viral polyprotein, but other proteins and
CC oligopeptides containing the appropriate consensus sequence are
CC also cleaved.
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC [RNA](N).
CC -1- CATALYTIC ACTIVITY: Hydrolyzes a Gly-I-Gly bond at its own C-
CC terminus, commonly in the sequence -Tyr-Xaa-Val-Gly-I-Gly, in the
CC processing of the potyviral polyprotein.
CC -1- PTM: VPG IS COVALENTLY LINKED TO THE GENOMIC RNA.
CC -1- PTM: THE VIRAL RNA OF POTYVIRUSES IS EXPRESSED AS A SINGLE
CC POLYPROTEIN WHICH UNDERGOES POSTTRANSLATIONAL PROTEOLYTIC
CC PROCESSING RESULTING IN THE PRODUCTION OF AT LEAST EIGHT
CC INDIVIDUAL PROTEINS.
CC -1- SIMILARITY: HC PROTEINASE BELONGS TO PEPTIDASE FAMILY C6.
CC -1- SIMILARITY: NI-A PROTEINASE BELONGS TO PEPTIDASE FAMILY C4.
CC -1- SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPROTEIN FAMILY.
CC -----
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CC -----
DR EMBL; X67673; CAA47905.1; -;
DR EMBL; S46722; AAB23789.1; -;
DR EMBL; X67672; CAA47904.1; -;
DR PIR; S24785; S24785.
DR MEROPS; C04.009; -;
DR MEROPS; C06.001; -;
DR MEROPS; S30.001; -;
DR InterPro; IPR001410; DEAD.
DR InterPro; IPR001650; Helicase_C.
DR InterPro; IPR001730; Peptidase_C4.
DR InterPro; IPR001456; Peptidase_C6.
DR InterPro; IPR002540; Poty_P1.
DR InterPro; IPR001592; Poty_coat.
DR InterPro; IPR001205; RNA_pol_P3D.
DR InterPro; IPR001254; Ser_protease_Try.
DR Pfam; PF00271; helicase_C; 1.
DR Pfam; PF00680; RNA_dep_RNA_pol; 1.
DR Pfam; PF00767; Poty_coat; 1.
DR Pfam; PF00851; Peptidase_C6; 1.
DR Pfam; PF00863; Peptidase_C4; 1.
DR Pfam; PF01577; Poty_P1; 1.

PRINTS; PR00966; NIAPOTYPTASE.
DR SMART; SM00487; DEXDC; 1.
KW SMART; SM00490; HELIC; 1.
KW Hydrolase; Transferase; Thiol protease; RNA-directed RNA polymerase;
KW Coat protein; Polyprotein; Covalent protein-RNA linkage; Helicase;
KW ATP-binding.
FT CHAIN 1 529 N-TERMINAL PROTEIN (BY SIMILARITY).
FT CHAIN 530 1149 HELPER COMPONENT PROTEINASE
(BY SIMILARITY).
FT CHAIN 1150 ? PROTEIN P3 (BY SIMILARITY).
FT CHAIN ? 1401 6 KDA PROTEIN 1 (BY SIMILARITY).
FT CHAIN 1402 2036 CYTOPLASMIC INCLUSION PROTEIN (BY
SIMILARITY).
FT CHAIN 2037 2093 6 KDA PROTEIN 2 (BY SIMILARITY).
FT CHAIN 2094 ? GENOME-LINKED PROTEIN (BY SIMILARITY).
FT CHAIN ? 2520 NUCLEAR INCLUSION PROTEIN A
(BY SIMILARITY).
FT CHAIN 2521 3037 NUCLEAR INCLUSION PROTEIN B
(BY SIMILARITY).
FT CHAIN 3038 3344 COAT PROTEIN (BY SIMILARITY).
FT BINDING 2156 2156 COVALENT LINKAGE OF VIRAL RNA (BY
SIMILARITY).
FT NP_BIND 1486 1493 ATP (POTENTIAL).
FT SEQUENCE 3344 AA; 381040 MW; E90CD7523AC5243D CRC64;
Query Match 73.5%; Score 36; DB 1; Length 3344;
Best Local Similarity 70.0%; Pred. No. 42;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 2 LIRYSSQSIS 11
Db 1737 MIRYSQAIS 1746
:|||||:|
RESULT 4
UL06_EBV STANDARD; PRT; 613 AA.
ID UL06_EBV
AC P03213;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE Virion protein BBRL1.
GN BBRL1.
OS Epstein-barr virus (strain B95-8) (Human herpesvirus 4).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Lymphocryptovirus.
OX NCBI_TaxID=10377;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84270667; PubMed=60871149;
RA Baer R., Bankier A.T., Biggin M.D., Deininger P.L., Farrell P.J.,
RA Gibson T.J., Hatfull G., Hudson G.S., Satchwell S.C., Seguin C.,
RA Tuffnell P.S., Barrell B.G.;
RT "DNA sequence and expression of the B95-8 Epstein-Barr virus genome.";
RL Nature 310:207-211(1984).
CC -!- FUNCTION: PRESUMED VIRION PROTEIN; POSSIBLE ROLE IN DNA
PACKAGING (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL6,
EHV-1 56, EBV BBRL1, HCMV UL104, AND VZV 54.
CC
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CC
CC EMBL; V01555; CAA24820.1; -
DR PIR; A03775; QBBE33.
DR PIR; S33025; S33025.
DR InterPro; IPR002660; Herpes_UL6.
DR Pfam; PF01763; Herpes_UL6; 1.

DR ProDom; PD003210; Herpes_UL6; 1.
KW Late protein.
SQ SEQUENCE 613 AA; 68456 MW; E6E65BB078FBD9AD CRC64;
Query Match 71.4%; Score 35; DB 1; Length 613;
Best Local Similarity 63.6%; Pred. No. 10;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 LLIRYSSQSIS 11
Db 510 LYVRYSSDTIS 520
:|||||:|
RESULT 5
DCHS_DROME STANDARD; PRT; 847 AA.
ID DCHS_DROME
AC Q05733;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Histidine decarboxylase (EC 4.1.1.22) (HDC).
GN HDC.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93209238; PubMed=8096176;
RA Burg M.G., Sarthy P.V., Kollant G., Pak W.L.;
RT "Genetic and molecular identification of a Drosophila histidine
decarboxylase gene required in photoreceptor transmitter synthesis.";
RL EMBO J. 12:911-919(1993).
CC -!- FUNCTION: REQUIRED IN PHOTORECEPTOR TRANSMITTER SYNTHESIS.
CC -!- CATALYTIC ACTIVITY: L-histidine - histamine + CO(2).
CC -!- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND
TYRDC).
CC
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CC
CC EMBL; X70644; CAA49989.1; -
DR PIR; S36337; S36337
DR FlyBase; FBgn0005619; Hdc.
DR InterPro; IPR002129; Pyridoxal_dec.
DR Pfam; PF00282; Pyridoxal_dec; 1.
DR PRINTS; PR00800; YHDCRBOXLASE.
DR PROSITE; PS00392; DDC_GAD_HDC_YDC; 1.
KW Lyase; Decarboxylase; Catecholamine biosynthesis; Pyridoxal phosphate.
FT BINDING 304 304 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
SQ SEQUENCE 847 AA; 94106 MW; 6DFDDE7B9034BC8F CRC64;
Query Match 71.4%; Score 35; DB 1; Length 847;
Best Local Similarity 81.8%; Pred. No. 15;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 LLIRYSSQSIS 11
Db 762 LLERYSSQSQS 772
:|||||:|
RESULT 6
NU4M_CERSI STANDARD; PRT; 459 AA.
ID NU4M_CERSI
AC O03204;

RESULT 9

POLG_PPVNA STANDARD; PRT; 3125 AA.

AC PF17766;

DT 01-AUG-1990 (Rel. 15, Last sequence update)

DT 01-AUG-1990 (Rel. 15, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Genome polyprotein [Contains: N-terminal protein (P1); Helper component proteinase (EC 3.4.22.45) (HC-Pro); Protein P3; 6 kDa protein 1 (6K1); Cytoplasmic inclusion protein (CI); 6 kDa protein 2 (6K2); Genome-linked protein (VPG); Nuclear inclusion protein A (NI-A) (EC 3.4.22.44) (49 kDa proteinase) (49 kDa-Pro); Nuclear inclusion protein B (NI-B) (RNA-directed RNA polymerase) (EC 2.7.7.48); Coat protein (CP)].

OS Plum pox polyvirus (isolate NAT) (PPV).

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae; Potyvirus.

OX NCBI_TaxID=12213;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=89279232; PubMed=2732699;

RA Maiss E., Timpe U., Brisse A., Jekmann W., Casper R., Himmeler G., Mattanovich D., Katinger H.W.D.;

RT "The complete nucleotide sequence of plum pox virus RNA.";

RL J. Gen. Virol. 70:513-524(1989).

CC -!- FUNCTION: HELPER COMPONENT-PROTEINASE IS REQUIRED FOR APHD TRANSMISSION AND ALSO HAS PROTEOLYTIC ACTIVITY.

CC -!- FUNCTION: CYTOPLASMIC INCLUSION PROTEIN HAS HELICASE ACTIVITY. IT MAY BE INVOLVED IN REPLICATION.

CC -!- FUNCTION: NUCLEAR INCLUSION PROTEIN A HAS PROTEOLYTIC ACTIVITY.

CC -!- CATALYTIC ACTIVITY: Hydrolyzes glutamyl bonds, and activity is further restricted by preferences for the amino acids in P6 - P1, that vary with the species of potyvirus, e.g. Glu-Xaa-Xaa-Tyr-Xaa-Gln+(Ser or Gly) for the enzyme from tobacco etch virus. The natural substrate is the viral polyprotein, but other proteins and oligopeptides containing the appropriate consensus sequence are also cleaved.

CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate + (RNA)(N).

CC -!- CATALYTIC ACTIVITY: Hydrolyzes a Gly-I-Gly bond at its own C-terminus, commonly in the sequence -Tyr-Xaa-Val-Gly-I-Gly, in the processing of the polyviral polyprotein.

CC -!- PTM: VPG IS COVALENTLY LINKED TO THE GENOMIC RNA.

CC -!- PTM: THE VIRAL RNA OF POTYVIRUSES IS EXPRESSED AS A SINGLE POLYPEPTIDE WHICH UNDERGOES POSTTRANSLATIONAL PROTEOLYTIC PROCESSING RESULTING IN THE PRODUCTION OF AT LEAST EIGHT INDIVIDUAL PROTEINS.

CC -!- SIMILARITY: HC PROTEINASE BELONGS TO PEPTIDASE FAMILY C6.

CC -!- SIMILARITY: NI-A PROTEINASE BELONGS TO PEPTIDASE FAMILY C4.

CC -!- SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPEPTIDE FAMILY.

CC -----

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CC -----

DR EMBL; D13751; BAA02898.1; -.

DR F01; JQ0003; GNVSP.

DR MEROPS; C04.001; -.

DR MEROPS; C06.001; -.

DR InterPro; IPR001410; DEAD.

DR InterPro; IPR001650; Helicase_C.

DR InterPro; IPR001730; Peptidase_C6.

DR InterPro; IPR001456; Peptidase_C6.

DR InterPro; IPR002540; Poty_P1.

DR InterPro; IPR001592; Poty_coat.

DR InterPro; IPR001205; RNA_pol_P3D.

DR InterPro; IPR001254; Ser_protease_Try.

DR Pfam; PF00271; helicase_C; 1.

DR Pfam; PF00680; RNA_dep_RNA_pol; 1.

DR Pfam; PF00767; Poty_coat; 1.

DR Pfam; PF00851; Peptidase_C6; 1.

DR Pfam; PF00863; Peptidase_C4; 1.

DR Pfam; PF01577; Poty_P1; 1.

DR PRINTS; PR00966; NIAPOTYPPTASE.

DR SMART; SM00487; DEXDC; 1.

DR SMART; SM00490; HELIC; 1.

KW Hydrolase; Transferase; Thiol protease; RNA-directed RNA polymerase; Covalent protein-RNA linkage; Helicase; ATP-binding.

KW Covalent protein-RNA linkage; Helicase; ATP-binding.

FT CHAIN 1 301 N-TERMINAL PROTEIN.

FT CHAIN 302 914 HELPER COMPONENT PROTEINASE.

FT CHAIN 915 ? PROTEIN P3.

FT CHAIN ? 1168 6 KDA PROTEIN 1.

FT CHAIN 1169 1803 CYTOPLASMIC INCLUSION PROTEIN.

FT CHAIN 1804 1856 6 KDA PROTEIN 2.

FT CHAIN 1857 ? GENOME-LINKED PROTEIN.

FT CHAIN ? 2292 NUCLEAR INCLUSION PROTEIN A.

FT CHAIN 2293 2810 NUCLEAR INCLUSION PROTEIN B.

FT CHAIN 2811 3125 COAT PROTEIN.

FT BINDING 1919 1919 COVALENT LINKAGE OF VIRAL RNA (BY SIMILARITY).

FT NP_BIND 1253 1260 ATP (POTENTIAL).

FT SEQUENCE 3125 AA; 354261 MW; ED0DD33C439CB712 CRC64;

Query Match 67.3%; Score 33; DB 1; Length 3125;

Best Local Similarity 60.0%; Pred. No. 1.7e+02;

Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 LIRYSQSIS 11

DB 1504 LVRYTKKSIS 1513

RESULT 10

POLG_PPVRA STANDARD; PRT; 3140 AA.

AC PF17767;

DT 01-AUG-1990 (Rel. 15, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Genome polyprotein [Contains: N-terminal protein (P1); Helper component proteinase (EC 3.4.22.45) (HC-Pro); Protein P3; 6 kDa protein 1 (6K1); Cytoplasmic inclusion protein (CI); 6 kDa protein 2 (6K2); Genome-linked protein (VPG); Nuclear inclusion protein A (NI-A) (EC 3.4.22.44) (49 kDa proteinase) (49 kDa-Pro); Nuclear inclusion protein B (NI-B) (RNA-directed RNA polymerase) (EC 2.7.7.48); Coat protein (CP)].

OS Plum pox polyvirus (strain Rankovic) (PPV).

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae; Potyvirus.

OX NCBI_TaxID=12214;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=89370814; PubMed=2773595;

RA Lain S., Riechmann J.L., Garcia J.A.;

RT "The complete nucleotide sequence of plum pox polyvirus RNA.";

RL Virus Res. 13:157-172(1989).

RN [2]

RP SEQUENCE OF 1778-2342 FROM N.A.

RX MEDLINE=89268456; PubMed=2658302;

RA Garcia J.A., Riechmann J.L., Lain S.;

RT "Proteolytic activity of the plum pox polyvirus Nta-like protein in Escherichia coli.";

RL Virology 170:362-369(1989).

RN [3]

RP SEQUENCE OF 2263-3140 FROM N.A.

RX Lain S., Riechmann J.L., Mendez E., Garcia J.A.;

RT "Nucleotide sequence of the 3' terminal region of plum pox polyvirus RNA.";

RL Virus Res. 10:325-342(1988).

CC -!- FUNCTION: CYTOPLASMIC INCLUSION PROTEIN HAS HELICASE ACTIVITY. IT

CC MAY BE INVOLVED IN REPLICATION.

CC -1- FUNCTION: NUCLEAR INCLUSION PROTEIN A HAS PROTEOLYTIC ACTIVITY.

CC -1- CATALYTIC ACTIVITY: Hydrolyzes glutamyl bonds, and activity is

CC further restricted by preferences for the amino acids in p6 - p1,

CC that vary with the species of potyvirus, e.g. Glu-Xaa-Xaa-Tyr-Xaa-

CC Gln+(Ser or Gly) for the enzyme from tobacco etch virus. The

CC natural substrate is the viral polyprotein, but other proteins and

CC oligopeptides containing the appropriate consensus sequence are

CC also cleaved.

CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +

CC (RNA)(N).

CC -1- CATALYTIC ACTIVITY: Hydrolyzes a Gly-I-Gly bond at its own C-

CC terminus, commonly in the sequence -Tyr-Xaa-Val-Gly-I-Gly, in the

CC processing of the potyviral polyprotein.

CC -1- PTM: VPG IS COVALENTLY LINKED TO THE GENOMIC RNA.

CC -1- PTM: THE VIRAL RNA OF POTYVIRUSES IS EXPRESSED AS A SINGLE

CC POLYPROTEIN WHICH UNDERGOES POSTTRANSLATIONAL PROTEOLYTIC

CC PROCESSING RESULTING IN THE PRODUCTION OF AT LEAST EIGHT

CC INDIVIDUAL PROTEINS.

CC -1- SIMILARITY: HC PROTEINASE BELONGS TO PEPTIDASE FAMILY C6.

CC -1- SIMILARITY: NI-A PROTEINASE BELONGS TO PEPTIDASE FAMILY C4.

CC -1- SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPROTEIN FAMILY.

CC -----

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CC or send an email to license@isb-sib.ch).

CC -----

CC EMBL; M21847; AAA85458.1; -.

CC EMBL; M26965; AAA47085.1; -.

CC PIR; A60009; GNVSRA.

CC MEROPS; C04.001; -.

CC MEROPS; C06.001; -.

CC InterPro: IPR001410; DEAD.

CC InterPro: IPR001650; Helicase_C.

CC InterPro: IPR001730; Peptidase_C4.

CC InterPro: IPR001456; Peptidase_C6.

CC InterPro: IPR002540; Poty_P1.

CC InterPro: IPR001592; Poty_coat.

CC InterPro: IPR001205; RNA_pol_P3D.

CC InterPro: IPR001254; Ser_protease_Try.

CC Pfam; PF00271; helicase_C; 1.

CC Pfam; PF00680; RNA_dep_RNA_pol; 1.

CC Pfam; PF00767; Poty_coat; 1.

CC Pfam; PF00851; Peptidase_C6; 1.

CC Pfam; PF00863; Peptidase_C4; 1.

CC Pfam; PF01577; Poty_P1; 1.

CC PRINTS; PR00966; NIAPOTYPTASE.

CC SMART; SM00487; DEXDC; 1.

CC SMART; SM00490; HELIC; 1.

CC Hydrolyase; Transferase; Thiol protease; RNA-directed RNA polymerase;

CC Coat protein; Polyprotein; Covalent protein-RNA linkage; Helicase;

CC ATP-binding.

CC CHAIN 1 301 N-TERMINAL PROTEIN.

CC CHAIN 302 914 HELPER COMPONENT PROTEINASE.

CC CHAIN 915 ? PROTEIN P3.

CC CHAIN ? 1168 6 KDA PROTEIN 1.

CC CHAIN 1169 1803 CYTOPLASMIC INCLUSION PROTEIN.

CC CHAIN 1804 1856 6 KDA PROTEIN 2.

CC CHAIN 1857 ? GENOME-LINKED PROTEIN.

CC CHAIN ? 2292 NUCLEAR INCLUSION PROTEIN A.

CC CHAIN 2293 2810 NUCLEAR INCLUSION PROTEIN B.

CC CHAIN 2811 3140 COAT PROTEIN.

CC BINDING 1919 1919 COVALENT LINKAGE OF VIRAL RNA (BY

CC SIMILARITY).

CC NP_BIND 1253 1260 ATP (POTENTIAL).

CC SEQUENCE 3140 AA; 355577 MW; 5F3DBB07982CF3F5 CRC64;

CC Query Match 67.3%; Score 33; DB 1; Length 3140;

CC Best Local Similarity 60.0%; Pred. No. 1.7e+02;

Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LIRYSSQSIS 11

Db 1504 LVRYTKKSIS 1513

RESULT 11

ID POLG_PPVSK STANDARD; PRT; 3140 AA.

AC O84934;

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Genome polyprotein [Contains: N-terminal protein (P1); Helper

DE component proteinase (EC 3.4.22.45) (HC-Pro); Protein P3; 6 kDa

DE protein 1 (6K1); Cytoplasmic inclusion protein (CI); 6 kDa protein 2

DE (6K2); Genome-linked protein (VPG); Nuclear inclusion protein A (NI-A)

DE (NIA) (EC 3.4.22.44) (49 kDa proteinase) (49 kDa-Pro); Nuclear

DE inclusion protein B (NI-B) (NIB) (RNA-directed RNA polymerase) (EC

DE 2.7.7.48); Coat protein (CP)].

OS Plum pox potyvirus (strain SK 68) (PPV).

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;

OC Potyvirus.

OX NCBI_TaxID=103927;

OX [1]

RP SEQUENCE FROM N.A.

RN MEDLINE=94167908; Pubmed=8122394;

RX Palkovics L., Burgyan J., Balazs E.;

RA "Comparative sequence analysis of four complete primary structures of

RT plum pox virus strains.";

RL Virus Genes 7:339-347(1993).

CC -1- FUNCTION: HELPER COMPONENT-PROTEINASE IS REQUIRED FOR APHID

CC TRANSMISSION AND ALSO HAS PROTEOLYTIC ACTIVITY.

CC -1- FUNCTION: CYTOPLASMIC INCLUSION PROTEIN HAS HELICASE ACTIVITY. IT

CC MAY BE INVOLVED IN REPLICATION.

CC -1- FUNCTION: NUCLEAR INCLUSION PROTEIN A HAS PROTEOLYTIC ACTIVITY.

CC -1- CATALYTIC ACTIVITY: Hydrolyzes glutamyl bonds, and activity is

CC further restricted by preferences for the amino acids in p6 - p1,

CC that vary with the species of potyvirus, e.g. Glu-Xaa-Xaa-Tyr-Xaa-

CC Gln+(Ser or Gly) for the enzyme from tobacco etch virus. The

CC natural substrate is the viral polyprotein, but other proteins and

CC oligopeptides containing the appropriate consensus sequence are

CC also cleaved.

CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +

CC (RNA)(N).

CC -1- CATALYTIC ACTIVITY: Hydrolyzes a Gly-I-Gly bond at its own C-

CC terminus, commonly in the sequence -Tyr-Xaa-Val-Gly-I-Gly, in the

CC processing of the potyviral polyprotein.

CC -1- PTM: VPG IS COVALENTLY LINKED TO THE GENOMIC RNA.

CC -1- PTM: THE VIRAL RNA OF POTYVIRUSES IS EXPRESSED AS A SINGLE

CC POLYPROTEIN WHICH UNDERGOES POSTTRANSLATIONAL PROTEOLYTIC

CC PROCESSING RESULTING IN THE PRODUCTION OF AT LEAST EIGHT

CC INDIVIDUAL PROTEINS.

CC -1- SIMILARITY: HC PROTEINASE BELONGS TO PEPTIDASE FAMILY C6.

CC -1- SIMILARITY: NI-A PROTEINASE BELONGS TO PEPTIDASE FAMILY C4.

CC -1- SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPROTEIN FAMILY.

CC -----

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CC or send an email to license@isb-sib.ch).

CC -----

CC EMBL; M92280; AAB05823.1; -.

CC InterPro: IPR001410; DEAD.

CC InterPro: IPR001650; Helicase_C.

CC InterPro: IPR001730; Peptidase_C4.

CC InterPro: IPR001456; Peptidase_C6.

CC InterPro: IPR002540; Poty_P1.

CC InterPro: IPR001592; Poty_coat.

```

DR InterPro: IPR001205; RNA_pol_P3D.
DR InterPro: IPR001254; Ser_protease_Try.
DR Pfam: PF00271; helicase_C; 1.
DR Pfam: PF00680; RNA_dep_RNA_pol; 1.
DR Pfam: PF00767; Poty_coat; 1.
DR Pfam: PF00851; Peptidase_C6; 1.
DR Pfam: PF00863; Peptidase_C4; 1.
DR Pfam: PF01577; Poty_P1; 1.
DR PRINTS: PR00966; NIAPOTYPASE.
DR SMART: SM00487; DEXDC; 1.
DR SMART: SM00490; HELICC; 1.
KW Hydrolase; Transferase; Thiol protease; RNA-directed RNA polymerase;
KW Coat protein; Polyprotein; Covalent protein-RNA linkage; Helicase;
KW ATP-binding.
FT CHAIN 1 301 N-TERMINAL PROTEIN.
FT CHAIN 302 914 HELPER COMPONENT PROTEINASE.
FT CHAIN 915 ? PROTEIN P3.
FT CHAIN ? 1169 6 KDA PROTEIN 1.
FT CHAIN 1169 1803 CYTOPLASMIC INCLUSION PROTEIN.
FT CHAIN 1804 1856 6 KDA PROTEIN 2.
FT CHAIN 1857 ? GENOME-LINKED PROTEIN.
FT CHAIN ? 2292 NUCLEAR INCLUSION PROTEIN A.
FT CHAIN 2293 2810 NUCLEAR INCLUSION PROTEIN B.
FT CHAIN 2811 3140 COAT PROTEIN.
FT BINDING 1919 1919 COVALENT LINKAGE OF VIRAL RNA (BY SIMILARITY).
FT NP_BIND 1253 1260 ATP (POTENTIAL).
FT SEQUENCE 3140 AA; 355992 MW; 837A5A692B56436A CRC64;

Query Match 67.3%; Score 33; DB 1; Length 3140;
Best Local Similarity 60.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 LIRYSQSIS 11
|:|:|:|:|
Db 1504 LVRYTKKSIS 1513

RESULT 12
ID POLG_PPVD STANDARD; PRT; 3141 AA.
AC P13529; Q84929; P89038;
DT 01-JAN-1990 (Rel. 13, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Genome polyprotein [Contains: N-terminal protein (P1); Helper
DE component proteinase (EC 3.4.22.45) (HC-Pro); Protein P3; 6 kDa
DE protein 1 (6K1); Cytoplasmic inclusion protein (CI); 6 kDa protein 2
DE (6K2); Genome-linked protein (VPG); Nuclear inclusion protein A (NI-A)
DE (NIA) (EC 3.4.22.44) (49 kDa proteinase) (49 kDa-Pro); Nuclear
DE inclusion protein B (NI-B) (NIB) (RNA-directed RNA polymerase) (EC
DE 2.7.7.48); Coat protein (CP)].
OS Plum pox potyvirus (strain D) (PPV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
OC Potyvirus.
OC NCBI_Taxid=12212;
OX [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90098790; PubMed=2602121;
RA Teycheney P.Y., Tavert G., Delbos R., Ravelonandro M., Dunez J.;
RT "The complete nucleotide sequence of plum pox virus RNA (strain D).";
RL Nucleic Acids Res. 17:10115-10116(1989).
RN [2]
RP SEQUENCE OF 2810-3141 FROM N.A., AND SEQUENCE OF 2812-2828.
RA Ravelonandro M., Varveri C., Delbos R., Dunez J.;
RT "Nucleotide sequence of the capsid protein gene of plum pox
RT potyvirus.";
RL J. Gen. Virol. 69:1509-1516(1988).
RN [3]
RP REVISIONS TO C-TERMINUS.
RA Le Gall O.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: HELPER COMPONENT-PROTEINASE IS REQUIRED FOR APHID

```

```

CC -!- TRANSMISSION AND ALSO HAS PROTEOLYTIC ACTIVITY.
CC -!- MAY BE INVOLVED IN REPLICATION.
CC -!- FUNCTION: NUCLEAR INCLUSION PROTEIN A HAS PROTEOLYTIC ACTIVITY.
CC -!- CATALYTIC ACTIVITY: Hydrolyzes glutamyl bonds, and activity is
CC further restricted by preferences for the amino acids in P6 - P1'
CC that vary with the species of potyvirus, e.g. Glu-Xaa-Xaa-Tyr-Xaa-
CC Gln+(Ser or Gly) for the enzyme from tobacco etch virus. The
CC natural substrate is the viral polyprotein, but other proteins and
CC oligopeptides containing the appropriate consensus sequence are
CC also cleaved.
CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC {RNA}(N).
CC -!- CATALYTIC ACTIVITY: Hydrolyzes a Gly-I-Gly bond at its own C-
CC terminus, commonly in the sequence -Tyr-xaa-val-Gly-I-Gly, in the
CC processing of the potyviral polyprotein.
CC -!- PFM: VPG IS COVALENTLY LINKED TO THE GENOMIC RNA.
CC -!- PFM: THE VIRAL RNA OF POTYVIRUSES IS EXPRESSED AS A SINGLE
CC POLYPROTEIN WHICH UNDERGOES POSTTRANSLATIONAL PROTEOLYTIC
CC PROCESSING RESULTING IN THE PRODUCTION OF AT LEAST EIGHT
CC INDIVIDUAL PROTEINS.
CC -!- SIMILARITY: HC PROTEINASE BELONGS TO PEPTIDASE FAMILY C6.
CC -!- SIMILARITY: NI-A PROTEINASE BELONGS TO PEPTIDASE FAMILY C4.
CC -!- SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPROTEIN FAMILY.
CC -----
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X16415; CAA34437.1; -.
CC EMBL: D00298; BAA00210.1; -.
CC PIR: S06929; GNVSPD.
CC PIR: JAO078; JAO078.
CC MEROPS: C04.001; -.
CC MEROPS: C06.001; -.
CC MEROPS: S30.001; -.
CC InterPro: IPR001410; DEAD.
CC InterPro: IPR001650; Helicase_C.
CC InterPro: IPR001730; Peptidase_C4.
CC InterPro: IPR001456; Peptidase_C6.
CC InterPro: IPR002540; Poty_P1.
CC InterPro: IPR001592; Poty_coat.
CC InterPro: IPR001205; RNA_pol_P3D.
CC InterPro: IPR001254; Ser_protease_Try.
CC Pfam: PF00271; helicase_C; 1.
CC Pfam: PF00680; RNA_dep_RNA_pol; 1.
CC Pfam: PF00767; Poty_coat; 1.
CC Pfam: PF00851; Peptidase_C6; 1.
CC Pfam: PF00863; Peptidase_C4; 1.
CC Pfam: PF01577; Poty_P1; 1.
CC PRINTS: PR00966; NIAPOTYPASE.
CC SMART: SM00487; DEXDC; 1.
CC SMART: SM00490; HELICC; 1.
KW Hydrolase; Transferase; Thiol protease; RNA-directed RNA polymerase;
KW Coat protein; Polyprotein; Covalent protein-RNA linkage; Helicase;
KW ATP-binding.
FT CHAIN 1 301 N-TERMINAL PROTEIN.
FT CHAIN 302 915 HELPER COMPONENT PROTEINASE.
FT CHAIN 916 ? 6 KDA PROTEIN 1.
FT CHAIN ? 1169 PROTEIN P3.
FT CHAIN 1170 1804 CYTOPLASMIC INCLUSION PROTEIN.
FT CHAIN 1805 1857 6 KDA PROTEIN 2.
FT CHAIN 1858 ? GENOME-LINKED PROTEIN.
FT CHAIN ? 2293 GENOME-LINKED PROTEIN.
FT CHAIN 2294 2811 NUCLEAR INCLUSION PROTEIN A.
FT CHAIN 2812 3141 NUCLEAR INCLUSION PROTEIN B.
FT BINDING 1920 1920 COAT PROTEIN.
FT BINDING 1920 1920 COVALENT LINKAGE OF VIRAL RNA (BY SIMILARITY).
FT NP_BIND 1254 1261 ATP (POTENTIAL).

```

SQ SEQUENCE 3141 AA; 355569 MW; 6C3641C404414DBB CRC64;

Query Match 67.3%; Score 33; DB 1; Length 3141;
Best Local Similarity 60.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 LLRYSSQSI 11

||:|:|:|

Db 1505 LVRYTKKSI 1514

RESULT 13

Y447_MYCGE

ID Y447_MYCGE STANDARD; PRT; 547 AA.

AC P47685;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Hypothetical protein MG447.

GN MG447.

OS Mycoplasma genitalium.

OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.

OX NCBI_TaxID=2097;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 33530 / G-37;

RX MEDLINE=96026346; PubMed=7569993;

RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,

RA Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,

RA Fritchmann J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,

RA Nguyen D.T., Dougherty T.R., Saudek D.M., Phillips C.A., Merrick J.M.,

RA Tomb J.-F., Dutterback T.A., Brott K.F., Hu P.-C., Lucier T.S.,

RA Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;

RT "The minimal gene complement of Mycoplasma genitalium.";

RL Science 270:397-403(1995).

RN [2]

RP SEQUENCE OF 107-215 FROM N.A.

RC STRAIN=ATCC 33530 / G-37;

RX MEDLINE=94075230; PubMed=8253680;

RA Peterson S.N., Hu P.-C., Bott K.F., Hutchison C.A. III;

RT "A survey of the Mycoplasma genitalium genome by using random

sequencing.";

RL J. Bacteriol. 175:7918-7930(1993).

CC -I- SUBCELLULAR LOCATION: Integral membrane protein (Potential).

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CC or send an email to license@isb-sib.ch).

CC -----

CC EMBL; U39726; AAC72467.1; -.

CC EMBL; U01788; AAD10610.1; -.

CC TIGR; MG447; -.

KW Hypothetical protein; Transmembrane; Complete proteome.

FT TRANSMEM 33 53 POTENTIAL.

FT TRANSMEM 107 127 POTENTIAL.

FT TRANSMEM 145 165 POTENTIAL.

FT TRANSMEM 203 223 POTENTIAL.

FT TRANSMEM 231 251 POTENTIAL.

FT TRANSMEM 263 283 POTENTIAL.

FT TRANSMEM 298 318 POTENTIAL.

FT TRANSMEM 351 371 POTENTIAL.

FT TRANSMEM 397 417 POTENTIAL.

FT TRANSMEM 432 452 POTENTIAL.

FT TRANSMEM 470 490 POTENTIAL.

FT TRANSMEM 499 519 POTENTIAL.

SQ SEQUENCE 547 AA; 62052 MW; E6D115C419A2E81B CRC64;

Query Match,

Best Local Similarity 65.3%; Score 32; DB 1; Length 547;

Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LLIRYSSQSI 10

||:|:|:|

Db 249 LLVRYSSILGV 258

RESULT 14

MTLL_LACLA

ID MTLL_LACLA STANDARD; PRT; 622 AA.

AC P35516;

DT 01-JUN-1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Modification methylase LlaI (EC 2.1.1.72) (Adenine-specific

DE methyltransferase LlaI) (M.LlaI).

GN LLAIM.

OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).

OG Plasmid pTR2030.

OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.

OX NCBI_TaxID=1360;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ME2;

RX MEDLINE=91294179; PubMed=1906061;

RA Hill C., Miller L.A., Klaenhammer T.R.;

RT "In vivo genetic exchange of a functional domain from a type II A

RT methylase between lactococcal plasmid pTR2030 and a virulent

RT bacteriophage.";

RL J. Bacteriol. 173:4363-4370(1991).

CC -I- FUNCTION: METHYLATION OF SPECIFIC ADENINE RESIDUES; REQUIRED FOR

CC BOTH RESTRICTION AND MODIFICATION ACTIVITIES. MAY RECOGNIZE A

CC NONPALINDROMIC SEQUENCE.

CC -I- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + DNA adenine = S-

CC adenosyl-L-homocysteine + DNA 6-methylaminopurine.

CC -I- SIMILARITY: CONTAINS TWO COPIES OF A SEGMENT OF FOUR AMINO ACIDS

CC WHICH IS CHARACTERISTIC OF ADENINE-SPECIFIC METHYLASES.

CC -----

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CC -----

CC EMBL; U17233; AAA65073.1; -.

CC PIR; A47029; A47029.

CC REBASE; 3437; M.LlaI.

CC InterPro; IPR002294; D12N6_mtfrase.

CC InterPro; IPR002052; N6_Mtase

CC Pfam; PF02086; MethyltransfD12; 2.

CC PRINTS; PR00505; D12N6MTFRASE.

CC TIGRFAMS; TIGR00571; dam; 1.

CC PROSITE; PS00092; N6_MTASE; 1.

KW Transferase; Methyltransferase; Restriction system; Repeat; Plasmid.

SQ SEQUENCE 622 AA; 72512 MW; 69A817F46B9C772 CRC64;

Query Match 65.3%; Score 32; DB 1; Length 622;

Best Local Similarity 60.0%; Pred. No. 47;

Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLIRYSSQSI 10

||:|:|:|

Db 281 VLVYSNQSI 290

RESULT 15

POLG_SBMVG

ID POLG_SBMVG STANDARD; PRT; 3066 AA.

AC Q90069;

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

15-JUL-2002 (Rel. 41, Last annotation update)
 Genome polyprotein [Contains: N-terminal protein (P1); Helper component proteinase (EC 3.4.22.45) (HC-Pro); Protein P3; 6 kDa protein 1 (6K1); Cytoplasmic inclusion protein (CI); 6 kDa protein 2 (6K2); Genome-linked protein (VP6); Nuclear inclusion protein A (NI-A) (NIA) (EC 3.4.22.44) (49 kDa-proteinase) (49 kDa-Pro); Nuclear inclusion protein B (NI-B) (NIB) (RNA-directed RNA polymerase) (EC 2.7.7.48); Coat protein (CP)].
 Soybean mosaic virus (strain G2) (SMV).
 Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae; Potyvirus.
 NCBI_TaxID=103931;
 [1]
 SEQUENCE FROM N.A.
 MEDLINE=92356085; PubMed=1645142;
 Jayaram C., Hill J.H., Miller W.A.;
 "Complete nucleotide sequences of two soybean mosaic virus strains differentiated by response of soybean containing the Rsv resistance gene.";
 J. Gen. Virol. 73:2067-2077(1992).
 CC -!- FUNCTION: Helper component-proteinase is required for aphid transmission and also has proteolytic activity.
 CC -!- FUNCTION: Cytoplasmic inclusion protein has helicase activity. It may be involved in replication.
 CC -!- FUNCTION: Nuclear inclusion protein A has proteolytic activity.
 CC -!- CATALYTIC ACTIVITY: Hydrolyzes a Gly-I-Gly bond at its own C-terminus, commonly in the sequence -Tyr-Xaa-Val-Gly-I-Gly, in the processing of the potyviral polyprotein.
 CC -!- CATALYTIC ACTIVITY: Hydrolyzes glutamyl bonds, and activity is further restricted by preferences for the amino acids in P6 - P1, that vary with the species of potyvirus, e.g. Glu-Xaa-Xaa-Tyr-Xaa-Gln-(Ser or Gly) for the enzyme from tobacco etch virus. The natural substrate is the viral polyprotein, but other proteins and oligopeptides containing the appropriate consensus sequence are also cleaved.
 CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate - N diphosphate + (RNA)(N).
 CC -!- PTM: VP6 IS COVALENTLY LINKED TO THE GENOMIC RNA.
 CC -!- PTM: THE VIRAL RNA OF POTYVIRUSES IS EXPRESSED AS A SINGLE POLYPEPTIDE WHICH UNDERGOES POSTTRANSLATIONAL PROTEOLYTIC PROCESSING RESULTING IN THE PRODUCTION OF AT LEAST EIGHT INDIVIDUAL PROTEINS.
 CC -!- SIMILARITY: HC PROTEINASE BELONGS TO PEPTIDASE FAMILY C6.
 CC -!- SIMILARITY: NI-A PROTEINASE BELONGS TO PEPTIDASE FAMILY C4.
 CC -!- SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPEPTIDE FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: S42280; AAB22819.2; -;
 DR MEROPS: C04.003; -;
 DR MEROPS: C06.001; -;
 DR InterPro: IPR001410; DEAD.
 DR InterPro: IPR001650; Helicase_C.
 DR InterPro: IPR001730; Peptidase_C4.
 DR InterPro: IPR001456; Peptidase_C6.
 DR InterPro: IPR002540; Poty_P1.
 DR InterPro: IPR001592; Poty_coat.
 DR InterPro: IPR001205; RNA_pol_P3D.
 DR InterPro: IPR001254; Ser_protease_Try.
 DR Pfam: PF00271; helicase_C; 1.
 DR Pfam: PF00680; RNA_dep_RNA_pol; 1.
 DR Pfam: PF00767; Poty_coat; 1.
 DR Pfam: PF00851; Peptidase_C6; 1.
 DR Pfam: PF00863; Peptidase_C4; 1.
 DR Pfam: PF01377; Poty_P1; 1.
 DR PRINTS: PR00966; NIAPOPTYASE.
 DR SMART: SM00487; DEXDC; 1.

DR SMART: SM00490; HELICC; 1.
 KW Hydrolase; Transferase; RNA-directed RNA polymerase;
 KW Coat protein; Polyprotein; Covalent protein-RNA linkage; Helicase;
 KW ATP-binding.
 FT CHAIN 1 ? N-TERMINAL PROTEIN.
 FT CHAIN ? ? HELPER COMPONENT PROTEINASE.
 FT CHAIN ? ? PROTEIN P3.
 FT CHAIN ? ? 6 KDA PROTEIN 1.
 FT CHAIN ? ? CYTOPLASMIC INCLUSION PROTEIN.
 FT CHAIN ? ? 6 KDA PROTEIN 2.
 FT CHAIN ? ? GENOME-LINKED PROTEIN.
 FT CHAIN ? ? NUCLEAR INCLUSION PROTEIN A.
 FT CHAIN ? ? NUCLEAR INCLUSION PROTEIN B.
 FT CHAIN ? 3066 COAT PROTEIN.
 FT NP_BIND 1249 1256 ATP (POTENTIAL).
 SQ SEQUENCE 3066 AA; 349538 MW; 218BA79DBD155399 CRC64;
 Query Match 65.3%; Score 32; DB 1; Length 3066;
 Best Local Similarity 55.6%; Pred. No. 2.8e+02;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 Oy 3 TRYSSQSIS 11
 :||: ||:
 Db 1501 VRYNKQSVS 1509

Search completed: November 18, 2002, 17:33:31
 Job time : 3.69608 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:01 ; Search time 11.4853 Seconds
(without alignments)
197.341 Million cell updates/sec

Title: US-09-016-061-84
Perfect score: 49
Sequence: 1 LLIRYSSQSIS 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	73.5	210	8 Q8W9Q9	Q8W9Q9 mesostigma
2	36	73.5	3343	12 Q91HK6	Q91HK6 papaya ring
3	35	71.4	284	17 Q97UT0	Q97UT0 sulfobolus
4	35	71.4	598	12 Q993H6	Q993H6 callitrichi
5	35	71.4	614	12 Q8UZG6	Q8UZG6 cercopithec
6	35	71.4	675	10 Q9M0X5	Q9M0X5 arabidopsis
7	35	71.4	847	5 Q9V5I3	Q9V5I3 drosophila
8	35	71.4	3344	12 P902I3	P902I3 papaya ring
9	34	69.4	141	16 Q9REA6	Q9REA6 bacillus ha
10	34	69.4	3036	12 Q65892	Q65892 bean yellow
11	33	67.3	132	10 Q9SMA8	Q9SMA8 oryza sativ
12	33	67.3	161	8 Q9BAG2	Q9BAG2 ranunculus
13	33	67.3	162	8 Q9BAG3	Q9BAG3 ranunculus
14	33	67.3	164	8 Q9B1C4	Q9B1C4 ranunculus
15	33	67.3	167	8 Q9B1T1	Q9B1T1 ranunculus
16	33	67.3	167	8 Q9B1E6	Q9B1E6 ranunculus

17	33	67.3	167	8 Q9B1E5	Q9B1E5 ranunculus
18	33	67.3	167	8 Q9B0X4	Q9B0X4 ranunculus
19	33	67.3	167	8 Q9B0X3	Q9B0X3 ranunculus
20	33	67.3	167	8 Q9B0T6	Q9B0T6 ranunculus
21	33	67.3	167	8 Q9BAG4	Q9BAG4 ranunculus
22	33	67.3	167	8 Q9BAG1	Q9BAG1 ranunculus
23	33	67.3	167	8 Q9BAG0	Q9BAG0 ranunculus
24	33	67.3	167	8 Q9BAF9	Q9BAF9 ranunculus
25	33	67.3	167	8 Q9BAF8	Q9BAF8 ranunculus
26	33	67.3	167	8 Q9BAF7	Q9BAF7 ranunculus
27	33	67.3	167	8 Q9BAF2	Q9BAF2 ranunculus
28	33	67.3	167	8 Q9BAF1	Q9BAF1 ranunculus
29	33	67.3	167	8 Q9BAF0	Q9BAF0 ranunculus
30	33	67.3	167	8 Q9BAE9	Q9BAE9 ranunculus
31	33	67.3	167	8 Q9BAE8	Q9BAE8 ranunculus
32	33	67.3	167	8 Q9BAE7	Q9BAE7 ranunculus
33	33	67.3	167	8 Q9BAE6	Q9BAE6 ranunculus
34	33	67.3	167	8 Q9BAE3	Q9BAE3 ranunculus
35	33	67.3	173	8 Q9BAF3	Q9BAF3 ranunculus
36	33	67.3	194	2 Q93G05	Q93G05 lactobacill
37	33	67.3	399	16 Q8Z8Z4	Q8Z8Z4 salmonella
38	33	67.3	403	16 Q8ZRF1	Q8ZRF1 salmonella
39	33	67.3	406	16 Q9KQW4	Q9KQW4 vibrio chol
40	33	67.3	422	9 Q9XJL2	Q9XJL2 bacterioph
41	33	67.3	422	16 Q9KXB5	Q9KXB5 escherichia
42	33	67.3	598	12 Q9YWL5	Q9YWL5 melanoplus
43	33	67.3	684	10 Q9SBC6	Q9SBC6 arabidopsis
44	33	67.3	998	10 Q9SVG2	Q9SVG2 arabidopsis
45	33	67.3	3140	12 Q9PYF0	Q9PYF0 plum pox vi

ALIGNMENTS

RESULT 1

Q8W9Q9 PRELIMINARY; PRT; 210 AA.
ID Q8W9Q9;
AC Q8W9Q9;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Ribosomal protein S3.
GN RPS3.
OS Mesostigma viride.
OG Mitochondrion.
OC Eukaryota; Viridiplantae; Streptophyta; Mesostigmataphyceae;
OC Mesostigmatales; Mesostigmataceae; Mesostigma.
OX NCBI_TaxID=41882;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NIES-296;
RX MEDLINE=21624446; PubMed=11752187;
RA Turmel M., Otis C., Lemieux C.;
RT "The Complete Mitochondrial DNA Sequence of Mesostigma viride
RT Identifies This Green Alga as the Earliest Green Plant Divergence and
RT Predicts a Highly Compact Mitochondrial Genome in the Ancestor of All
RT Green Plants.";
RL Mol. Biol. Evol. 19:24-38(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NIES-296;
RX Turmel M., Otis C., Lemieux C.;
RT Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL: AF353999; AAL36749.1;
DR InterPro: IPR001351; Ribosomal_S3.
DR Pfam: PF00189; Ribosomal_S3_C; 1.
DR Pfam: PF00417; Ribosomal_S3_N; 1.
DR PROSITE: PS00548; RIBOSOMAL_S3; UNKNOWN_1.
KW Mitochondrion.
SQ SEQUENCE 210 AA; 24399 MW; FFE89050D59B0590 CRC64;
Query Match 73.5%; Score 36; DB 8; Length 210;
Best Local Similarity 88.9%; Pred. No. 13;

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Matches      8;  Conservative      0;  Mismatches      1;  Indels      0;  Gaps      0;

QY  3 IRYSSQSIS 11
    I | | | | |
Db  187 IRYSSQSIS 195

RESULT 2
Q91HK6
ID  Q91HK6      PRELIMINARY;      PRT;      3343 AA.
AC  Q91HK6;
DT  01-DEC-2001 (TrEMBLrel. 19, Created)
DT  01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT  01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE  Polyprotein.
OS  Papaya ringspot virus (strain W).
OC  Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
OC  Potyvirus.
OX  NCBI_TaxID=12207;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=W;
RA  Attasart P., Kertbundit S., Panyim S., Juricek M.;
RT  "Cloning and sequencing of papaya ringspot virus (strain W) from
RT  Thailand.";
RL  EMBL: AY010722; AAG47346.1; -.
DR  MEROPS: C04.009; -.
DR  MEROPS: C06.001; -.
DR  MEROPS: S30.001; -.
DR  InterPro: IPR001410; DEAD.
DR  InterPro: IPR001650; Helicase_C.
DR  InterPro: IPR001730; Peptidase_C4.
DR  InterPro: IPR001456; Peptidase_C6.
DR  InterPro: IPR001592; Poty_coat.
DR  InterPro: IPR002540; Poty_PI.
DR  InterPro: IPR001205; RNA_pol_P3D.
DR  Pfam: PF00271; helicase_C; 1.
DR  Pfam: PF00863; Peptidase_C4; 1.
DR  Pfam: PF00851; Peptidase_C6; 1.
DR  Pfam: PF00767; Poty_coat; 1.
DR  Pfam: PF01577; Poty_PI; 1.
DR  Pfam: PF00680; RNA_dep_RNA_pol; 1.
SQ  SEQUENCE 3343 AA; 380344 MW; 06BE74CE2CD8F669 CRC64;

Query Match      73.5%; Score 36; DB 12; Length 3343;
Best Local Similarity 70.0%; Pred. No. 2.3e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY  2 LIRYSSQSIS 11
    : | | | | |
Db  1737 MIRYSQAIS 1746

RESULT 3
Q97UT0
ID  Q97UT0      PRELIMINARY;      PRT;      284 AA.
AC  Q97UT0;
DT  01-OCT-2001 (TrEMBLrel. 18, Created)
DT  01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT  01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE  Hypothetical protein SS02914.
GN  SS02914.
OS  Sulfolobus solfataricus.
OC  Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC  Sulfolobus.
OX  NCBI_TaxID=2287;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=ATCC 35092 / DSM 1617 / P2;
RX  MEDLINE=21332296; PubMed=11427726;
RA  She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
RA  Awayez M.J., Chan-Welher C.C.-Y., Clausen I.G., Curtis B.A.,

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RA  De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,
RA  Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
RA  Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
RA  Charlebois R.L., Doolittle W.F., Duquet M., Gaasterland T.,
RA  Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;
RT  "The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";
RL  Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
DR  EMBL: AE006883; AAK43022.1; -.
KW  Hypothetical protein; Complete proteome.
SQ  SEQUENCE 284 AA; 31759 MW; 331D46FE534428F7 CRC64;

Query Match      71.4%; Score 35; DB 17; Length 284;
Best Local Similarity 63.6%; Pred. No. 28;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY  1 LLIRYSSQSIS 11
    I | | | | |
Db  34 LLIRYTNKQIS 44

RESULT 4
Q993H6
ID  Q993H6      PRELIMINARY;      PRT;      598 AA.
AC  Q993H6;
DT  01-JUN-2001 (TrEMBLrel. 17, Created)
DT  01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT  01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE  ORE34.
OS  calitricine herpesvirus 3.
OC  Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC  Gammaherpesvirinae; Lymphocryptovirus.
OX  NCBI_TaxID=106331;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=CJ0149;
RX  MEDLINE=21107697; PubMed=11158621;
RA  Cho Y., Ramer J., Rivaller P., Quink C., Garber R.L., Beier D.R.,
RA  Wang F.;
RT  "An Epstein-Barr-related herpesvirus from marmoset lymphomas.";
RL  Proc. Natl. Acad. Sci. U.S.A. 98:1224-1229(2001).
DR  EMBL: AF319782; AAK38242.1; -.
DR  InterPro: IPR002660; Herpes_UL6.
DR  Pfam: PF01763; Herpes_UL6; 1.
DR  ProDom: PD003210; Herpes_UL6; 1.
SQ  SEQUENCE 598 AA; 68553 MW; 43681BE38912A4BC CRC64;

Query Match      71.4%; Score 35; DB 12; Length 598;
Best Local Similarity 63.6%; Pred. No. 62;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY  1 LLIRYSSQSIS 11
    I : | | | | |
Db  501 LYVRYSDTIS 511

RESULT 5
Q8UZG6
ID  Q8UZG6      PRELIMINARY;      PRT;      614 AA.
AC  Q8UZG6;
DT  01-MAR-2002 (TrEMBLrel. 20, Created)
DT  01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT  01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE  BBRF1.
OS  cercopithecine herpesvirus 15.
OC  Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC  Gammaherpesvirinae; Lymphocryptovirus.
OX  NCBI_TaxID=104228;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=LCL8664;
RX  MEDLINE=97048062; PubMed=8892903;
RA  Franken M., Devergne O., Rosenzweig M., Annis B., Kieff E., Wang F.;
RT  "Comparative analysis identifies conserved tumor necrosis factor

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OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY.
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Anantides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan J.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abrial J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Folsler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houch J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacieb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000)
 CC -1- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND TYRDC).
 CC EMBL; AF003830; AAF58823.1; -;
 DR FlyBase; FBgn0005619; Hdc.
 DR InterPro; IPR002129; Pyridoxal_deC.
 DR Pfam; PF00282; Pyridoxal_deC; 1.
 DR PRINTS; PR00800; YHDCRBOXLASE.
 DR PROSITE; PS00392; DDC_GAD_HDC_YDC; 1.
 DR Decarboxylase; Lysase; Pyridoxal phosphate.
 SQ SEQUENCE 847 AA; 94035 MW; C04F32F01C176951 CRC64;
 Query Match 71.4%; Score 35; DB 5; Length 847;
 Best Local Similarity 81.8%; Pred. No. 89;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 LLIRYSQSIS 11
 DB 762 LLIRYSQSQS 772
 RESULT 8
 P90213
 ID P90213 PRELIMINARY; PRT; 3344 AA.
 AC P90213
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)

DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE PRSV_YK polyprotein.
 OS Papaya ringspot virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
 OC Potyvirus.
 OX NCBI_TaxID=12205;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=YK;
 RA Wang C.H., Yeh S.D.;
 RT "Divergence and conservation of the genomic RNAs of Taiwan and Hawaii strains of papaya ringspot potyvirus.";
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; X97251; CAA65886.1; -;
 DR MEROPS; C04.009; -;
 DR MEROPS; C06.001; -;
 DR MEROPS; S30.001; -;
 DR InterPro; IPR001410; DEAD.
 DR InterPro; IPR001650; Helicase_C.
 DR InterPro; IPR001730; Peptidase_C4.
 DR InterPro; IPR001456; Peptidase_C6.
 DR InterPro; IPR001592; Poty_coat.
 DR InterPro; IPR002540; Poty_P1.
 DR InterPro; IPR001205; RNA_pol_P3D.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR Pfam; PF00271; helicase_C; 1.
 DR Pfam; PF00863; Peptidase_C4; 1.
 DR Pfam; PF00851; Peptidase_C6; 1.
 DR Pfam; PF00767; Poty_coat; 1.
 DR Pfam; PF01577; Poty_P1; 1.
 DR Pfam; PF00680; RNA_dep_RNA_pol; 1.
 DR PRINTS; PR00966; NIAPOTYPTASE.
 DR SMART; SM00487; DEXDC; 1.
 DR SMART; SM00490; HELIC_C; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR KW ATP-binding; Helicase; Hydrolase; Polyprotein; Serine protease.
 SQ SEQUENCE 3344 AA; 380581 MW; 7BFF421E092C4E85 CRC64;
 Query Match 71.4%; Score 35; DB 12; Length 3344;
 Best Local Similarity 60.0%; Pred. No. 3.7e+02;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 2 LIRYSQSIS 11
 DB 1737 MIRYSKQVS 1746
 RESULT 9
 ID Q9KEA6 PRELIMINARY; PRT; 141 AA.
 AC Q9KEA6;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Hypothetical protein BH0947.
 GN BH0947.
 OS Bacillus halodurans.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Bacillaceae; Bacillus.
 OX NCBI_TaxID=86665;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C-125 / JCM 9153;
 RX MEDLINE=20512582; PubMed=11058132;
 RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
 RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
 RA Horikoshi K.;
 RT "Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and genomic sequence comparison with *Bacillus subtilis*.";
 RL Nucleic Acids Res. 28:4317-4331(2000).
 DR EMBL; AP001510; BAB04666.1; -;
 DR InterPro; IPR001622; K+channel_pore.
 DR Hypothetical protein; Complete proteome.


```

SQ SEQUENCE 141 AA; 15618 MW; 58C490C4A57D201A CRC64;
Query Match 69.4%; Score 34; DB 16; Length 141;
Best Local Similarity 77.8%; Pred. No. 22;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLIRYSQS 9
Db 23 LLVRFQS 31

RESULT 10
ID Q65892 PRELIMINARY; PRT; 3056 AA.
AC Q65892;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Polyprotein.
OS Bean yellow mosaic virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
OC Potyvirus.
OX NCBI_TaxID=12197;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MB4;
RA Nakamura S.;
RN [2]
RN [3]
RT "Nucleotide sequence of the 3'-terminal region of bean yellow mosaic
virus RNA and resistance to viral infection in transgenic Nicotiana
benthiana expressing its coat protein gene.";
RT Ann. Phytopathol. Soc. Jpn. 60:295-304 (1994).
RP SEQUENCE FROM N.A.
RC STRAIN=MB4;
RA Nakamura S.;
RN [2]
RN [3]
RT "The complete nucleotide sequence of bean yellow mosaic virus genomic
RNA.";
RN Ann. Phytopathol. Soc. Jpn. 62:472-477 (1996).
DR EMBL; D83749; BAAL2099.1; -.
DR MEROPS; C04.008; -.
DR MEROPS; C06.001; -.
DR MEROPS; S30.001; -.
DR InterPro; IPR001410; DEAD.
DR InterPro; IPR001650; Helicase_C.
DR InterPro; IPR001730; Peptidase_C4.
DR InterPro; IPR001456; Peptidase_C6.
DR InterPro; IPR001592; Poty_coat.
DR InterPro; IPR002540; Poty_P1.
DR InterPro; IPR001205; RNA_pol_P3D.
DR Pfam; PF00271; helicase_C; 1.
DR Pfam; PF00863; Peptidase_C4; 1.
DR Pfam; PF00851; Peptidase_C6; 1.
DR Pfam; PF00767; Poty_coat; 1.
DR Pfam; PF01577; Poty_P1; 1.
DR Pfam; PF00680; RNA_dep_RNA_pol; 1.
DR PRINTS; PR00966; NIAPOTYPTASE.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELICC; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
KW ATP-binding; Helicase; Hydrolase; Serine protease.
SQ SEQUENCE 3056 AA; 347572 MW; AFFBE0B50F12D9CF CRC64;

Query Match 69.4%; Score 34; DB 12; Length 3056;
Best Local Similarity 60.8%; Pred. No. 5.5e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 LLIRYSQS 11

```

```

Db 1478 LMRYTKQSVS 1487
I::I::I::I

RESULT 11
ID Q9SMA8 PRELIMINARY; PRT; 132 AA.
AC Q9SMA8;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TRENBLrel. 13, Last annotation update)
DE zwh0001.1 (Fragment).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. INDICA;
RA Hong G.; Zhao W.;
RT "Oryza sativa genomic DNA, chromosome 4, clone: b6015.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL117264; CAB55385.1; -.
FT NON_TER 1
SQ SEQUENCE 132 AA; 14829 MW; 480E20C36B16AD0C CRC64;

Query Match 67.3%; Score 33; DB 10; Length 132;
Best Local Similarity 54.5%; Pred. No. 34;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 LLIRYSQS 11
Db 101 LLFYQSRVS 111
I::I::I::I

RESULT 12
ID Q9BAG2 PRELIMINARY; PRT; 161 AA.
AC Q9BAG2;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
DE Hypothetical 19.3 kDa protein (Fragment).
OS Ranunculus lyallii.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales;
OC Ranunculaceae; Ranunculus.
OX NCBI_TaxID=147630; .
RN [1]
RP SEQUENCE FROM N.A.
RA Lockhart P.J.; McLenahan P.A.; Havell D.; Glenn D.; Huson D.;
RA Jensen U.;
RT "Phylogeny, radiation and transoceanic dispersal of New Zealand alpine
buttercups: Molecular evidence under split decomposition.";
RL Ann. Mo. Bot. Gard. 0:0-0 (2001).
DR EMBL; AF323332; AAK16113.1; -.
KW Chloroplast; Hypothetical protein.
FT NON_TER 1
FT NON_TER 161
SQ SEQUENCE 161 AA; 19312 MW; 75B91CAAC7FC70BB CRC64;

Query Match 67.3%; Score 33; DB 8; Length 161;
Best Local Similarity 87.5%; Pred. No. 42;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LLIRYSQS 9
Db 52 LLIRYSQS 59
I::I::I::I

RESULT 13

```

Q9BAG3 PRELIMINARY: PRT; 162 AA.

AC Q9BAG3; 01-JUN-2001 (TREMBlrel. 17, Created)

DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)

DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)

DE Hypothetical 19.5 kDa protein (Fragment).

OS Ranunculus lyallii.

OG Chloroplast.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales;

OC Ranunculaceae; Ranunculus.

OX NCBI_TaxID=147630;

[1]

RN SEQUENCE FROM N.A.

RA Lockhart P.J., McLenachan P.A., Havell D., Glenn D., Huson D.,

RA Jensen U.;

RT "Phylogeny, radiation and transoceanic dispersal of New Zealand alpine

RT buttercups: Molecular evidence under split decomposition.";

RL Ann. Mo. Bot. Gard. 0:0-0(2001).

DR EMBL; AF323328; AAK16109.1; -

KW Chloroplast; Hypothetical protein.

FT NON_TER 1 1

FT NON_TER 162 162

SQ SEQUENCE 162 AA; 19531 MW; 4645BFD38F3E68CF CRC64;

Query Match 67.3%; Score 33; DB 8; Length 162;

Best Local Similarity 87.5%; Pred. No. 42;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LIRYSQS 9

Db 53 LIRYSQS 60

RESULT 14

Q9B1C4 PRELIMINARY: PRT; 164 AA.

AC Q9B1C4; 01-JUN-2001 (TREMBlrel. 17, Created)

DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)

DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)

DE Hypothetical 19.7 kDa protein (Fragment).

OS Ranunculus buchanani.

OG Chloroplast.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales;

OC Ranunculaceae; Ranunculus.

OX NCBI_TaxID=147621;

[1]

RN SEQUENCE FROM N.A.

RA Lockhart P.J., McLenachan P.A., Havell D., Glenn D., Huson D.,

RA Jensen U.;

RT "Phylogeny, radiation and transoceanic dispersal of New Zealand alpine

RT buttercups: Molecular evidence under split decomposition.";

RL Ann. Mo. Bot. Gard. 0:0-0(2001).

DR EMBL; AF323329; AAK16110.1; -

DR EMBL; AF323330; AAK16111.1; -

DR EMBL; AF323331; AAK16112.1; -

KW Chloroplast; Hypothetical protein.

FT NON_TER 1 1

FT NON_TER 164 164

SQ SEQUENCE 164 AA; 19739 MW; 6A0A4CDDA7DCB36C CRC64;

Query Match 67.3%; Score 33; DB 8; Length 164;

Best Local Similarity 87.5%; Pred. No. 43;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LIRYSQS 9

Db 55 LIRYSQS 62

RESULT 15

Q9B1T1 PRELIMINARY: PRT; 167 AA.

AC Q9B1T1; 01-JUN-2001 (TREMBlrel. 17, Created)

DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)

DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)

DE Hypothetical 20.0 kDa protein (Fragment).

OS Ranunculus crithmifolius subsp. crithmifolius.

OG Chloroplast.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales;

OC Ranunculaceae; Ranunculus.

OX NCBI_TaxID=147686;

[1]

RN SEQUENCE FROM N.A.

RA Lockhart P.J., McLenachan P.A., Havell D., Glenn D., Huson D.,

RA Jensen U.;

RT "Phylogeny, radiation and transoceanic dispersal of New Zealand alpine

RT buttercups: Molecular evidence under split decomposition.";

RL Ann. Mo. Bot. Gard. 0:0-0(2001).

DR EMBL; AF323361; AAK16142.1; -

DR EMBL; AF323363; AAK16144.1; -

KW Chloroplast; Hypothetical protein.

FT NON_TER 1 1

FT NON_TER 167 167

SQ SEQUENCE 167 AA; 19952 MW; 1176A5A16C499B38 CRC64;

Query Match 67.3%; Score 33; DB 8; Length 167;

Best Local Similarity 87.5%; Pred. No. 44;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LIRYSQS 9

Db 58 LIRYSQS 65

Search completed: November 18, 2002, 17:40:51

Job time : 12.5353 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:21:57 ; Search time 15.2059 Seconds
(without alignments)
96.394 Million cell updates/sec

Title: US-09-016-061-84
Perfect score: 49
Sequence: 1 LLIRYSSQSIS 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
- 23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	49	100.0	11	AAW76032	LM609 grafted anti
2	49	100.0	11	AAW61390	Mutant VL CDR2 pep
3	44	89.8	11	AAW76012	LM609 grafted anti
4	44	89.8	11	AAW61370	LM609 VL CDR2 pept
5	43	87.8	88	AAV56653	Partial peptide fr
6	43	87.8	102	AAW77337	Human bone marrow
7	43	87.8	105	AAW87456	Jk gene product.
8	43	87.8	105	AAW87458	Humanised anti-alp
9	43	87.8	106	AAW41234	Monoclonal antibod
10	43	87.8	107	AAW25729	Humanised VL regio

11	43	87.8	107	14	AAW38601	HYH light chain.
12	43	87.8	107	19	AAW58482	Murine HYH antibod
13	43	87.8	107	20	AAW84098	Humanised anti-alp
14	43	87.8	107	21	AAW71238	Humanised antibody
15	43	87.8	107	21	AAW71240	Humanised antibody
16	43	87.8	107	21	AAW71472	Mouse monoclonal a
17	43	87.8	107	22	AAW69677	Murine CMV5 antio
18	43	87.8	107	22	AAW69678	Humanised CMV5 ant
19	43	87.8	107	22	AAW69690	Human WOI antibody
20	43	87.8	108	17	AAW04333	Light chain of mon
21	43	87.8	108	20	AAW84094	Murine vitronectin
22	43	87.8	109	15	AAW52033	Light chain variab
23	43	87.8	109	20	AAW06380	Murine monoclonal
24	43	87.8	112	20	AAW84100	Vitronectin alpha-
25	43	87.8	114	22	AAW98665	Murine protein #2.
26	43	87.8	127	15	AAW54093	Sequence of mouse
27	43	87.8	127	22	AAW69687	Murine CMV5 antio
28	43	87.8	128	21	AAW56718	Amino acid sequenc
29	43	87.8	259	21	AAW09775	TMV 30K movement p
30	41	83.7	107	19	AAW76002	Vitaxin antibody 1
31	41	83.7	107	19	AAW76004	LM609 antibody lig
32	41	83.7	107	22	AAW63590	A light chain vari
33	41	83.7	107	22	AAW61360	Vitaxin light chal
34	41	83.7	107	22	AAW61362	Antibody LM609 lig
35	40	81.6	104	19	AAW26795	Antibody LM609 lig
36	40	81.6	106	19	AAW71241	Anti-gp54 Mab 48-1
37	40	81.6	107	14	AAW32129	Light chain variab
38	40	81.6	107	14	AAW37612	Anti-IL2R beta ant
39	40	81.6	107	14	AAW37610	hIL2R Ab L chain v
40	40	81.6	107	15	AAW50190	B-B10 Mab L chain
41	40	81.6	107	15	AAW50190	Light chain variab
42	40	81.6	107	18	AAW08948	Kappa light chain
43	40	81.6	107	20	AAW26979	Light chain variab
44	40	81.6	107	21	AAW70604	Vkappa region of h
45	40	81.6	107	23	AAW72842	Anti-NKG2D hybrido
			107	23	AAW72850	Anti-NKG2D hybrido

ALIGNMENTS

RESULT 1
AAW76032
ID AAW76032 standard; Protein; 11 AA.
XX
AC AAW76032;
XX
DT 02-NOV-1998 (first entry)
XX
DE LM609 grafted antibody V-L region CDR2 protein fragment #2.
XX
KW Vitaxin; antibody; variable region; heavy chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-L region; CDR;
KW complementarity determining region.
XX
OS Mus sp.
XX
PN WO9833919-A2.
XX
PD 06-AUG-1998.
XX
PF 30-JAN-1998; 98WO-US01826.
XX
PR 30-JAN-1997; 97US-0791391.
XX
PA (IXSY-) IXSYS INC.
XX
PI Glaser SM, Huse WD;
XX
DR WPI; 1998-437472/37.
DR N-PSDB; AAW49869.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
XX Claim 62; Page 41; 129pp; English.
XX
XX AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
CC antibodies contain non-murine framework regions so are suitable for use
CC in humans. Enhanced types of LM609 have affinity more than 90 times
CC greater than that of parent the parent antibody.
XX
XX Sequence 11 AA;
XX
XX Query Match 100.0%; Score 49; DB 19; Length 11;
XX Best Local Similarity 100.0%; Pred. No. 0.0011;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 LLIRYSSQSIS 11
XX | | | | | | | | | |
XX Db 1 LLIRYSSQSIS 11
XX
XX RESULT 2
XX AAB61390
XX ID AAB61390 standard; peptide; 11 AA.
XX AC AAB61390;
XX
XX DT 03-APR-2001 (first entry)
XX
XX DE Mutant VL CDR2 peptide.
XX
XX LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
KW inflammatory; cancer; retina; restenosis; osteoporosis.
KW
XX Unidentified.
XX
XX WO200078815-A1.
XX
XX 28-DEC-2000.
XX
XX 23-JUN-2000; 2000WO-US17454.
XX
XX 24-JUN-1999; 99US-0339922.
XX
XX (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX
XX Huse WD, Wu H;
XX
XX WPI; 2001-050110/06.
XX
XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
PT osteoporosis -
XX
XX Disclosure; Page 41; 132pp; English.
XX
XX The present invention relates to enhanced LM609 grafted antibodies
CC exhibiting selective binding affinity to alphavbeta_3 integrin or
CC their functional fragments. The antibodies or their functional
CC fragments can be used in the diagnosis and treatment of
CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory

CC diseases (such as psoriasis and chronic articular rheumatism),
CC disorders associated with inappropriate or inopportune invasion of
CC vessels (such as diabetic retinopathy, neovascular glaucoma and
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
CC diseases (such as macular degeneration), restenosis and
CC osteoporosis.
XX
XX Sequence 11 AA;
XX
XX Query Match 100.0%; Score 49; DB 22; Length 11;
XX Best Local Similarity 100.0%; Pred. No. 0.0011;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 LLIRYSSQSIS 11
XX | | | | | | | | | |
XX Db 1 LLIRYSSQSIS 11
XX
XX RESULT 3
XX AAW76012
XX ID AAW76012 standard; Protein; 11 AA.
XX AC AAW76012;
XX
XX DT 02-NOV-1998 (first entry)
XX
XX DE LM609 grafted antibody V-L region CDR2 protein fragment #1.
XX
XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-L region; CDR;
KW complementarity determining region.
XX
XX Mus sp.
XX
XX WO9833919-A2.
XX
XX PD 06-AUG-1998.
XX
XX 30-JAN-1998; 98WO-US01826.
XX
XX 30-JAN-1997; 97US-0791391.
XX
XX (IXSY-) IXSYS INC.
XX
XX Glaser SM, Huse WD;
XX
XX WPI; 1998-437472/37.
XX
XX N-PSDB; AAV49849.
XX
XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
XX Disclosure; Page 40; 129pp; English.
XX
XX AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
CC antibodies contain non-murine framework regions so are suitable for use
CC in humans. Enhanced types of LM609 have affinity more than 90 times
CC greater than that of parent the parent antibody.
XX
XX Sequence 11 AA;
XX

Query Match 89.8%; Score 44; DB 19; Length 11;
 Best Local Similarity 90.9%; Pred. No. 0.012; Mismatches 0; Indels 1; Gaps 0;

QY 1 LLIRYSQSIS 11
 DB 1 LLIRYSQSIS 11

RESULT 4
 AAB61370
 ID AAB61370 standard; peptide; 11 AA.
 XX
 AC AAB61370;
 XX
 DT 03-APR-2001 (first entry)
 XX
 DE LM609 VL CDR2 peptide.
 XX
 KW LM609; grafted antibody; alphaVbeta3 integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis.
 XX
 OS Unidentified.
 XX
 PN WO200078815-A1.
 XX
 PD 28-DEC-2000.
 XX
 PF 23-JUN-2000; 2000WO-US17454.
 XX
 PR 24-JUN-1999; 99US-0339922.
 XX
 PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
 XX
 PI Huse WD, Wu H;
 XX
 DR WPI; 2001-050110/06.
 XX
 PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -

XX
 PS Disclosure; Page 39; 132pp; English.
 XX
 CC The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphaVbeta3 integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphaVbeta3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.

XX
 XX Sequence 11 AA;
 XX
 XX Query Match 89.8%; Score 44; DB 22; Length 11;
 XX Best Local Similarity 90.9%; Pred. No. 0.012;
 XX Mismatches 0; Indels 1; Gaps 0;

QY 1 LLIRYSQSIS 11
 DB 1 LLIRYSQSIS 11

RESULT 5
 AAY56653
 ID AAY56653 standard; protein; 88 AA.
 XX

AC AAY56653;
 XX
 DT 15-FEB-2000 (first entry)
 XX
 DE Partial peptide fragment of chimpanzee V kappa cDNA clone 46-4.
 XX
 KW Complementarity determining region; antibody; primate; immunogenicity;
 KW Old World ape; Old World monkey; antigen-binding affinity.
 XX
 OS Pan troglodytes.
 XX
 PN WO995369-A1.
 XX
 PD 04-NOV-1999.
 XX
 PF 28-APR-1999; 99WO-US09131.
 XX
 PR 28-APR-1998; 98US-0083367.
 XX
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 XX
 PI Taylor AH;
 XX
 DR WPI; 2000-023265/02.
 DR N-PSDB; AAZ39321.
 XX
 PT Antibodies containing donor complementarity determining regions and
 PT non-human primate acceptor frameworks, having reduced immunogenicity in
 PT humans -

PS Claim 22; Page 70; 123pp; English.
 XX
 CC The invention provides an antibody (Ab) comprising donor CDRs
 CC (complementarity determining regions) derived from a non-human antigen-
 CC specific donor antibody, and an acceptor framework from a non-human
 CC primate. The Abs are prepared by grafting CDRs from a non-human antigen-
 CC specific donor antibody onto homologous Old World ape or monkey acceptor
 CC frameworks. The Abs have reduced immunogenicity and are better tolerated
 CC in humans (because of the close similarity between the human and primate
 CC proteins), but retain the full antigen-binding affinity of the donor
 CC antibody.

XX
 XX Sequence 88 AA;
 XX
 XX Query Match 87.8%; Score 43; DB 21; Length 88;
 XX Best Local Similarity 81.8%; Pred. No. 0.23;
 XX Mismatches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIRYSQSIS 11
 DB 46 LLIRYSQSIS 56

RESULT 6
 AAM77337
 ID AAM77337 standard; protein; 102 AA.
 XX
 AC AAM77337;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human bone marrow expressed probe encoded protein SEQ ID NO: 37643.
 XX
 KW Human; bone marrow expressed exon; gene expression analysis; probe;
 KW microarray; cancer; leukaemia; lymphoma; myeloma.
 XX
 OS Homo sapiens.
 XX
 PN WO200157276-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US00668.

XX 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-0234687.
 PR 27-SEP-2000; 2000US-0236359.
 PR 04-OCT-2000; 2000GB-0024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-488900/53.
 XX human genome-derived single exon nucleic acid probes useful for
 PT analyzing gene expression in human bone marrow -
 XX
 XX Example 4; SEQ ID NO: 37643; 658pp + Sequence Listing; English.
 XX
 XX The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC bone marrow. They can be used to measure gene expression in bone marrow
 CC samples, which may enable the improved diagnosis and treatment of cancers
 CC such as lymphoma, leukaemia and myeloma. The present sequence is a
 CC protein encoded by one of the probes of the invention.
 XX
 XX Sequence 102 AA;
 SQ
 Query Match 87.8%; Score 43; DB 22; Length 102;
 Best Local Similarity 81.8%; Pred. No. 0.28;
 Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LLIRYSSQSIS 11
 DB 30 LLIRYSSQSIS 40
 III:|:|:|:|:|
 RESULT 7
 AAW87456
 ID AAW87456 standard; Protein; 105 AA.
 AC AAW87456;
 XX 15-MAR-1999 (first entry)
 DT Jk gene product.
 XX
 XX Humanised antibody; monoclonal antibody; MAB; antibody engineering;
 KW mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;
 KW cancer; metastasis; rheumatoid arthritis; atherosclerosis;
 KW angiogenesis; diabetic retinopathy; inflammation;
 KW macular degeneration; osteoporosis; Paget's disease;
 KW hyperparathyroidism; hypercalcaemia; therapy; immunotherapy;
 KW D12H2LCREI; Jk protein.
 XX
 XX Mus sp.
 OS
 XX WO9840488-A1.
 PN 17-SEP-1998.
 PD 12-MAR-1998; 98WO-US04987.
 PF 12-MAR-1997; 97US-0039609.
 PR (SMIK) SMITHKLINE BEECHAM CORP.
 XX
 XX Johanson KO, Jonak ZL, Taylor AH;
 PI WPI; 1999-034590/03.
 XX N-PSDB; AAV71803.
 DR
 XX

PT New anti alpha_v beta_3 vitronectin receptor antibodies - used for
 PT immunotherapeutic treatment of e.g. diabetic retinopathy,
 PT inflammatory disorders, atherosclerosis, restenosis, cancers or
 PT osteoporosis
 XX
 XX Example 14; Page 66; 97pp; English.
 XX
 XX This polypeptide is encoded by a Jk synthetic gene segment (see
 CC AAV71803). It was utilising in novel D12H2REI humanised light chain
 CC variable region (see AAW87458), which comprises a human REI framework
 CC and complementarity determining regions from the anti-human alpha-v
 CC beta-3 vitronectin receptor monoclonal antibody D12. Humanised D12
 CC antibodies can be used for passive immunotherapy of disorders
 CC mediated by the alpha-v beta-3 vitronectin receptor, e.g. restenosis
 CC and angiogenic associated diseases.
 XX
 XX Sequence 105 AA;
 SQ
 Query Match 87.8%; Score 43; DB 20; Length 105;
 Best Local Similarity 81.8%; Pred. No. 0.28;
 Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LLIRYSSQSIS 11
 DB 46 LLIRYSSQSIS 56
 III:|:|:|:|:|
 RESULT 8
 AAW87458
 ID AAW87458 standard; Protein; 105 AA.
 AC AAW87458;
 XX 15-MAR-1999 (first entry)
 DT Humanised anti-alpha-v beta-3 MAB D12H2LCREI VL.
 XX
 XX Humanised antibody; monoclonal antibody; MAB; antibody engineering;
 KW mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;
 KW cancer; metastasis; rheumatoid arthritis; atherosclerosis;
 KW angiogenesis; diabetic retinopathy; inflammation;
 KW macular degeneration; osteoporosis; Paget's disease;
 KW hyperparathyroidism; hypercalcaemia; therapy; immunotherapy;
 KW D12H2LCREI.
 XX
 XX Homo sapiens.
 OS
 XX Synthetic.
 OS
 XX WO9840488-A1.
 PN 17-SEP-1998.
 PD 12-MAR-1998; 98WO-US04987.
 PF 12-MAR-1997; 97US-0039609.
 PR (SMIK) SMITHKLINE BEECHAM CORP.
 XX
 XX Johanson KO, Jonak ZL, Taylor AH;
 PI WPI; 1999-034590/03.
 XX N-PSDB; AAV71805.
 DR
 XX New anti alpha_v beta_3 vitronectin receptor antibodies - used for
 PT immunotherapeutic treatment of e.g. diabetic retinopathy,
 PT inflammatory disorders, atherosclerosis, restenosis, cancers or
 PT osteoporosis
 XX
 XX Example 14; Page 68-69; 97pp; English.
 PS
 XX This is the amino acid sequence of the light chain variable region
 CC (VL) of humanised anti-alpha-v beta-3 vitronectin receptor
 CC monoclonal antibody D12H2LCREI. It is based on a synthetic

CC humanised kappa chain based on a modified human REI kappa
 CC framework and complementarity determining regions from the murine
 CC anti-human alpha-v beta-3 vitronectin receptor monoclonal antibody
 CC D12 (see AAW84094). Humanised antibodies of the invention can be used
 CC for passive immunotherapy of a disorder mediated by the alpha-v
 CC beta-3 receptor, e.g. cardiovascular disorders or angiogenic-
 CC related disorders, such as angiogenesis associated with diabetic
 CC retinopathy, atherosclerosis and restenosis, chronic inflammatory
 CC disorders, macular degeneration, rheumatoid arthritis and cancer,
 CC e.g. solid tumour metastasis, and diseases where bone resorption is
 CC associated with pathology such as osteoporosis, hyperparathyroidism,
 CC Paget's disease, hypercalcaemia of malignancy, osteolytic lesions
 CC produced by bone metastasis, bone loss due to immobilisation or sex
 CC hormone deficiency. They can also be used for targeted drug
 CC therapy, and for detection and diagnosis.

SQ Sequence 105 AA;

Query Match 87.8%; Score 43; DB 20; Length 105;
 Best Local Similarity 81.8%; Pred. No. 0.29;
 Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLIRYSSQSIS 11
 Db 46 LLIKYASQSIS 56
 III:IIIIII

RESULT 9
 AAR41234
 ID AAR41234 standard; Protein; 106 AA.

XX AAR41234;
 XX 18-MAR-1994 (first entry)
 DE Monoclonal antibody BW2121 V-gene light chain coding region.
 XX Monoclonal antibody; tumour; melanoma; ss.

OS Mus musculus.

PN EP561183-A.

XX 22-SEP-1993.

XX 25-FEB-1993; 93EP-0102895.

XX 19-MAR-1992; 92DE-4208795.

XX (BEHW) BEHRINGWERKE AG.

XX Bosslet K, Dippold W, Seemann G;

XX WPI; 1993-296513/38.

DR N-PSDB; AAQ48766.

XX Hybridoma 2121 (dsm acc 2036) and monoclonal antibody BW 2121 -
 PT specifically bind to gangliosides GD3 and GD1b, useful for prodn.
 PT and diagnosis of melanoma or tumours expressing GD3 and GD1b

XX Claim 2; Page 6; 9pp; German.

XX The monoclonal antibody BW2121 can be used for the detection of
 CC melanomas and other tumours expressing GD3 and GD1b. The monoclonal
 CC antibody may also be used as part of a pharmaceutical composition or
 CC diagnostic kit.

SQ Sequence 106 AA;

Query Match 87.8%; Score 43; DB 14; Length 106;
 Best Local Similarity 81.8%; Pred. No. 0.29;
 Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLIRYSSQSIS 11
 Db 46 LLIKYSSSESIS 56
 III:IIIIII

RESULT 10

AAR25729
 ID AAR25729 standard; Protein; 107 AA.

XX AAR25729;

XX 13-JAN-1993 (first entry)

XX Humanised VL region of the mouse CMV5 antibody.

XX Murine; immunoglobulin; CDR; non immunogenic; cytomegalovirus;
 KW gH; light chain; variable region; framework; human; Wol.

XX Mus musculus.

XX Key Location/Qualifiers
 FT Region 24..34
 FT /note= "CDR"

FT Region 50..56
 FT /note= "CDR"

FT Region 89..97
 FT /note= "CDR"

FT Misc-difference 49
 FT /note= "mutated residue"

XX WO9211018-A.

XX 09-JUL-1992.

XX 19-DEC-1991; 91WO-US09711.

XX 19-DEC-1990; 90US-0634278.

XX (PROT-) PROTEIN DESIGN LABS INC.

XX Co MS, Coeltingh KL, Landolfi NF, Queen CL, Schneider WP;

XX WPI; 1992-249842/30.

XX New immunoglobulin(s) having murine CDRs in human framework
 PT regions - have lower antigenicity; useful for treating e.g. HSV,
 PT CMV, T-cell disorders, myeloid disorders and auto-immune
 PT conditions

XX Claim 40; Fig 27A; 141pp; English.

XX The sequence shows the humanised mature light chain variable
 CC region of the mouse CMV5 antibody. Murine CDRs were used
 CC in a human Wol framework to produce a pure humanised immunoglobulin
 CC (Ig) which is capable of binding to the gH glycoprotein of
 CC cytomegalovirus. The Ig is non immunogenic, due to the human
 CC framework, and has a strong affinity for its predetermined
 CC antigen. They can be produced in large quantities via recombinant
 CC DNA and monoclonal antibody technology. The humanised Igs may be
 CC used alone or in combination with chemotherapeutic agents such as
 CC non-steroidal anti-inflammatory drugs or immunosuppressants.
 CC See also AAR25721-32.

XX Sequence 107 AA;

Query Match 87.8%; Score 43; DB 13; Length 107;
 Best Local Similarity 81.8%; Pred. No. 0.29;
 Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLIRYSSQSIS 11
 Db 46 LLIKYASQSIS 56
 III:IIIIII

```

RESULT 11
AAW38601
ID AAR38601 standard; peptide; 107 AA.
AC AAR38601;
XX
XX 28-OCT-1993 (first entry)
DT
DE
DE HYH light chain.
XX
XX Antibody; variable domain; light; L; heavy; H; consensus;
KW affinity; antigen; immunogenicity; humanisation; framework.
KW
XX Homo sapiens.
OS
XX WO9311794-A.
PN
XX 24-JUN-1993.
PD
XX 14-DEC-1992; 92WO-US10906.
PF
XX 13-DEC-1991; 91US-0808464.
PR
XX (XOMA ) XOMA CORP.
PA
XX Fishwild DM, Kohn FR, Little RG, Studnicka GM;
PI
XX WPI; 1993-213827/26.
DR
XX
XX Antibodies prepn. used for treatment of auto-immune diseases - by
PT replacement of critical residues to reduce immunogenicity but
PT retain binding affinity, etc.
PT
XX
XX Disclosure; Page 84; 160pp; English.
PS
XX
XX The amino acid sequences of the light and heavy chains of the
CC variable domains from antibodies HYH [HYHEL-10 Fab-lysosyme complex]
CC (AAR38601 and AAR38608, respectively), MCPC [IgA Fab
CC MCPC603-phosphocholine complex] (AAR38602-03 and AAR38609-10,
CC respectively), NEWM [Ig Fab' NEW] (AAR38604-05 and AAR38611,
CC respectively), and KOL [IgG1 KOL] (AAR38606-07 and AAR38612, respectively)
CC may be used to determine an alignment from which appropriate changes may
CC be made. Unlike other methods of humanisation, which advocate the
CC replacement of entire antibody framework regions with those of human
CC antibodies, this method involves only the introduction of human
CC residues into those positions not critical for antigen binding.
CC This ensures that the binding properties of the modified antibody
CC are not diminished.
XX
XX Sequence 107 AA;
QY
Query Match 87.8%; Score 43; DB 14; Length 107;
Best Local Similarity 81.8%; Pred. No. 0.29;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Db 46 LLIRYSSQSIS 11
1111111111
46 LLIKYASQSIS 56
QY 1 LLIRYSSQSIS 11
Db 46 LLIKYASQSIS 56
RESULT 12
AAW58482
ID AAW58482 standard; protein; 107 AA.
XX
XX AAW58482;
AC
XX 18-AUG-1998 (first entry)
DT
XX Murine HYH antibody light chain variable domain.
DE
XX Humanised; human; mouse; CD5; anti-CD5 antibody; immunoglobulin;
KW depletion; cytotoxic; immunoconjugate; fusion protein; psoriasis;
KW

```

```

KW autoimmune disease; rheumatoid arthritis; type I diabetes.
XX
OS Mus sp..
XX
XX US5770196-A.
PN
XX
XX 23-JUN-1998.
PD
XX
XX 07-JUN-1995; 95US-0472788.
PF
XX
XX 23-JUN-1993; 93US-0082842.
PR
XX 13-DEC-1991; 91US-0808464.
PR
XX 14-DEC-1992; 92WO-US10906.
PR
XX 07-JUN-1995; 95US-0472788.
XX
XX (XOMA ) XOMA CORP.
PA
XX Studnicka GM;
XX
XX WPI; 1998-376744/32.
DR
XX
XX Depletion of CD5-positive cells in vivo - using anti-CD5 antibodies
PT with humanised variable regions
PT
XX
XX Disclosure; Column 43-44; 77pp; English.
PS
XX
XX A method has been developed of depleting CD5+ cells in an animal. The
CC method comprises administering a cytotoxic protein containing a modified
CC immunoglobulin (Ig) variable domain, where the protein is an anti-CD5 Ig
CC molecule or an immunoconjugate or fusion protein containing an anti-CD5
CC Ig molecule, and where the modified Ig variable domain comprises at
CC least one of (a) a modified light chain variable region (see AAW58478 or
CC AAW58480), and (b) a modified heavy chain variable region (see AAW58479
CC or AAW58481), where AAW58478 and AAW58479 are humanised forms of the H65
CC light and heavy chain variable domains with low risk amino acid
CC substitutions [i.e. low risk of reducing antigen-binding specificity.]
CC and AAW58480 and AAW58481 are humanised forms of the H65 light and heavy
CC chain variable domains with moderate risk amino acid substitutions and
CC are present in humanised H65 antibody he3 (ATCC HB 11206). The method is
CC useful for treating autoimmune diseases, especially systemic lupus
CC erythematosus, rheumatoid arthritis, psoriasis or type I diabetes. The
CC present sequence represents the murine HYH antibody light chain variable
CC domain.
XX
XX Sequence 107 AA;
QY
Query Match 87.8%; Score 43; DB 19; Length 107;
Best Local Similarity 81.8%; Pred. No. 0.29;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 LLIRYSSQSIS 11
1111111111
46 LLIKYASQSIS 56
Db 46 LLIKYASQSIS 56
RESULT 13
AAW84098
ID AAW84098 standard; protein; 107 AA.
XX
XX AAW84098;
AC
XX
XX 15-MAR-1999 (first entry)
DT
XX
XX Humanised anti-alpha-v beta-3 MAb D12HZHC 1-0 VL.
DE
XX
XX Humanised antibody; monoclonal antibody; MAB; antibody engineering;
KW mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;
KW cancer; metastasis; rheumatoid arthritis; atherosclerosis;
KW angiogenesis; diabetic retinopathy; inflammation;
KW macular degeneration; osteoporosis; Paget's disease;
KW hyperparathyroidism; hypercalcaemia; therapy; immunotherapy;
KW D12HZHC-10.
XX

```


OS Homo sapiens.
 XX Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Region 24..34
 FT /label= CDR1
 FT Region 50..56
 FT /label= CDR2
 FT Region 89..97
 FT /label= CDR3
 XX
 PN WO9840488-A1.
 XX
 XX 17-SEP-1998.
 XX
 XX 12-MAR-1998; 98WO-US04987.
 XX
 XX 12-MAR-1997; 97US-0039609.
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 XX
 PI Johanson KO, Jonak ZL, Taylor AH;
 XX
 XX WPI; 1999-034590/03.
 DR N-PSDB; AAV71800.
 XX
 XX New anti alpha_v beta_3 vitronectin receptor antibodies - used for
 PT immunotherapeutic treatment of e.g. diabetic retinopathy,
 PT inflammatory disorders, atherosclerosis, restenosis, cancers or
 PT osteoporosis
 XX
 PS Claim 2; Page 61-62; 97pp; English.
 XX
 CC This is the amino acid sequence of the light chain variable region
 CC (VL) of humanised anti-alpha-v beta-3 vitronectin receptor
 CC monoclonal antibody D12H2HC 1-0. It is based on the VL sequence
 CC (see AAW84096) of human Kabat subgroup III kappa chain, with
 CC complementarity determining regions (CDRs) from the murine
 CC anti-human alpha-v beta-3 vitronectin receptor monoclonal antibody
 CC D12 (see AAW84093). 3 Murine framework residues (1, 49 and 50)
 CC are retained. The humanised light chain can be expressed in host
 CC cells using nucleic acid molecules (see AAV71800) of the invention.
 CC Humanised D12 VH is also provided (see AAW84097). The humanised
 CC antibodies can be used for passive immunotherapy of disorders
 CC mediated by the alpha-v beta-3 receptor, e.g. cardiovascular or
 CC angiogenic-related disorders, such as angiogenesis associated
 CC with diabetic retinopathy, atherosclerosis and restenosis, chronic
 CC inflammatory disorders, macular degeneration, rheumatoid arthritis
 CC and cancer, e.g. solid tumour metastasis, and diseases where bone
 CC resorption is associated with pathology such as osteoporosis,
 CC hyperparathyroidism, Paget's disease, hypercalcaemia of malignancy,
 CC osteolytic lesions produced by bone metastasis, bone loss due to
 CC immobilisation or sex hormone deficiency. They can also be used for
 CC targeted drug therapy, and for detection and diagnosis.
 XX
 SQ Sequence 107 AA;
 Query Match 87.8%; Score 43; DB 20; Length 107;
 Best Local Similarity 81.8%; Pred. No. 0.29;
 Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LLIRYSQSIS 11
 Db 46 LLIRYASQSI 56
 RESULT 14
 ID AAV71238
 XX AAV71238 standard; Protein; 107 AA.
 AC AAV71238;
 XX
 DT 04-OCT-2000 (first entry)

XX
 DE Humanised antibody H24B4k-1 light chain variable (VL) region.
 XX
 KW Humanised antibody; H24B4k-1; human 4-LBB receptor protein; mouse;
 KW light chain variable region; VL; heavy chain variable region; VH; MAb;
 KW monoclonal antibody 4B4-1-1; complementarity determining region; CDR;
 KW FR; framework region; treat; transplant rejection; rheumatoid arthritis;
 KW autoimmune disease; immunosuppressant; antirheumatic; antiarthritic.
 XX
 OS Chimeric - Homo sapiens.
 OS Chimeric - Mus sp.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 8 /note= "This residue is substituted for Gln in murine
 FT monoclonal antibody 4B4-1-1 VL (AAV71472)."
 FT Misc-difference 14 /note= "This residue is substituted for Thr in murine
 FT monoclonal antibody 4B4-1-1 VL (AAV71472)."
 FT Misc-difference 17 /note= "This residue is substituted for Asp in murine
 FT monoclonal antibody 4B4-1-1 VL (AAV71472)."
 FT Misc-difference 20 /note= "This residue is substituted for Ser in murine
 FT monoclonal antibody 4B4-1-1 VL (AAV71472)."
 FT Region 24..34 /label= CDR 1
 FT /note= "Complementarity determining region"
 FT Misc-difference 40 /note= "This residue is substituted for Ser in murine
 FT monoclonal antibody 4B4-1-1 VL (AAV71472)."
 FT Misc-difference 41 /note= "This residue is substituted for His in murine
 FT monoclonal antibody 4B4-1-1 VL (AAV71472)."
 FT Misc-difference 42 /note= "This residue is substituted for Glu in murine
 FT monoclonal antibody 4B4-1-1 VL (AAV71472)."
 FT Region 50..56 /label= CDR 2
 FT /note= "Complementarity determining region"
 FT Misc-difference 74 /note= "This residue is substituted for Ser in murine
 FT monoclonal antibody 4B4-1-1 VL (AAV71472)."
 FT Misc-difference 76 /note= "This residue is substituted for Asn in murine
 FT monoclonal antibody 4B4-1-1 VL (AAV71472)."
 FT Misc-difference 83 /note= "This residue is substituted for Val in murine
 FT monoclonal antibody 4B4-1-1 VL (AAV71472)."
 FT Region 89..97 /label= CDR 3
 FT /note= "Complementarity determining region"
 XX WO200029445-A1.
 XX
 XX 25-MAY-2000.
 XX
 XX 17-NOV-1999; 99WO-KR00689.
 XX
 XX 17-NOV-1998; 98KR-0049177.
 PR 11-MAY-1999; 99KR-0016750.
 XX
 XX (GLDS) LG CHEM LTD.
 XX
 XX Hong HJ, Park SS, Kang YJ, Kang CY, Yoon SK;
 PI WPI; 2000-387750/33.
 DR N-PSDB; AAD00904.
 XX
 XX Humanized antibody specific for human 4-1BB, the composition comprising
 PT the antibody useful for treating autoimmune diseases e.g. rheumatoid
 PT arthritis or as an immuno suppressant to prevent graft rejection .
 XX

PS Claim 14a; Fig 2; 83pp; English.

XX The present sequence is the humanised antibody H24B4k-1, kappa light
CC chain variable region (VL), specific to human 4-LBB receptor protein.
CC It comprises of the complementarity determining region (CDR) of mouse
CC monoclonal antibody (Mab) 4B4-1-1, grafted on to a human antibody. In
CC order to increase the antigen binding affinity of the humanised antibody,
CC about 10 critical amino acid substitutions are made in the framework
CC region (FR) of humanised VL, to resemble the mouse antibody. It functions
CC to block human 4-LBB protein receptor. The humanised antibody can be used
CC to treat autoimmune diseases, especially rheumatoid arthritis and for
CC immune suppression in transplant rejection. It acts as an effective
CC immunosuppressant, by inhibiting T cell activation, without any adverse
CC side effects.

XX
SQ Sequence 107 AA;

Query Match 87.8%; Score 43; DB 21; Length 107;
Best Local Similarity 81.8%; Pred. No. 0.29;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIRYSSQSSIS 11
|||:|||||

Db 46 LLIKYASQSSIS 56

RESULT 15
AAV71240
ID AAV71240 standard; Protein; 107 AA.

XX
AC AAV71240;

XX
DT 04-OCT-2000 (first entry)

XX
DE Humanised antibody H24B4k-2 light chain variable (VL) region.

XX
KW Humanised antibody; H24B4k-2; human 4-LBB receptor protein; mouse;
KW light chain variable region; VL; heavy chain variable region; VH; Mab;
KW monoclonal antibody 4B4-1-1; complementarity determining region; CDR;
KW FR; framework region; treat; transplant rejection; rheumatoid arthritis;
KW autoimmune disease; immunosuppressant; antirheumatic; antiarthritic.

XX
OS Chimeric - Homo sapiens.

OS Chimeric - Mus sp.

XX
FH Key Location/Qualifiers

FT Misc-difference 9
FT /note= "This residue is substituted for Ala in humanised
FT antibody H24B4-1 VL (AAV71238)"

FT Misc-difference 11
FT /note= "This residue is substituted for Gln in humanised
FT antibody H24B4-1 VL (AAV71238)"

FT Misc-difference 13
FT /note= "This residue is substituted for Val in humanised
FT antibody H24B4-1 VL (AAV71238)"

FT Region 24..34
FT /label= CDR 1

FT /note= "Complementarity determining region"

FT Misc-difference 28
FT /note= "This residue is substituted for Thr in humanised
FT antibody H24B4-1 VL (AAV71238)"

FT Region 50..56
FT /label= CDR 2

FT /note= "Complementarity determining region"

FT Misc-difference 60
FT /note= "This residue is substituted for Ser in humanised
FT antibody H24B4-1 VL (AAV71238)"

FT Misc-difference 69
FT /note= "This residue is substituted for Ser in humanised
FT antibody H24B4-1 VL (AAV71238)"

FT Misc-difference 78
FT /note= "This residue is substituted for Val in humanised
FT antibody H24B4-1 VL (AAV71238)"

FT Misc-difference 84
FT /note= "This residue is substituted for Gly in humanised
FT antibody H24B4-1 VL (AAV71238)"

FT Region 89..97
FT /label= CDR 3

FT /note= "Complementarity determining region"

FT Misc-difference 104
FT /note= "This residue is substituted for Leu in humanised
FT antibody H24B4-1 VL (AAV71238)"

XX WO200029445-A1.

XX 25-MAY-2000.

XX 17-NOV-1999; 99WO-KR00689.

XX 17-NOV-1998; 98KR-0049177.

PR 11-MAY-1999; 99RR-0016750.

XX (GLDS) LG CHEM LTD.

XX Hong HJ, Park SS, Kang YJ, Kang CY, Yoon SK;

PI WPI; 2000-387750/33.

XX N-PSDB; AAD00906.

DR Humanized antibody specific for human 4-LBB, the composition comprising
the antibody useful for treating autoimmune diseases e.g. rheumatoid
arthritis or as an immuno suppressant to prevent graft rejection -

XX Claim 16a; Fig 5; 83pp; English.

XX The present sequence is the humanised antibody H24B4k-2, kappa light
CC chain variable region (VL), specific to human 4-LBB receptor protein. It
CC comprises of the complementarity determining region (CDR) of mouse
CC monoclonal antibody (Mab) 4B4-1-1, grafted on to a human antibody.
CC In order to increase the antigen binding affinity of this humanised
CC antibody, 1 residue in the CDR1 and 8 residues in the framework region
CC (FR) of the humanised H24B4-1 light chain (VL) are substituted, to
CC resemble the mouse antibody. It functions to block human 4-LBB protein
CC receptor. The humanised antibody can be used to treat autoimmune
CC diseases, especially rheumatoid arthritis and for immune suppression in
CC transplant rejection. It acts as an effective immunosuppressant, by
CC inhibiting T cell activation, without any adverse side effects.

XX
SQ Sequence 107 AA;

Query Match 87.8%; Score 43; DB 21; Length 107;
Best Local Similarity 81.8%; Pred. No. 0.29;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIRYSSQSSIS 11
|||:|||||

Db 46 LLIKYASQSSIS 56

Search completed: November 18, 2002, 17:31:40
Job time : 16.2059 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:54:45 ; Search time 2.15686 Seconds
(without alignments)
76.811 Million cell updates/sec

Title: US-09-016-061-84
Perfect score: 49
Sequence: 1 LLIRYSQSIS 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 97044 seqs, 15060890 residues

Total number of hits satisfying chosen parameters: 97044

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_AA:*
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13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43	87.8	88	10	US-09-905-243-30
2	43	87.8	102	10	US-09-864-761-48570
3	43	87.8	128	12	US-10-006-773-6
4	41	83.7	107	8	US-08-790-540A-8
5	41	83.7	107	8	US-08-791-391A-4
6	41	83.7	107	8	US-08-791-391A-8
7	39	79.6	244	10	US-09-940-391-1
8	38	77.6	107	8	US-08-790-540A-4
9	38	77.6	107	8	US-08-791-391A-32
10	37	75.5	107	10	US-09-756-301A-3
11	37	75.5	107	10	US-09-927-703-3
12	37	75.5	107	10	US-09-766-535A-3
13	37	75.5	107	10	US-09-756-161A-3
14	37	75.5	107	12	US-10-010-229-3
15	37	75.5	107	12	US-10-043-450-3
16	37	75.5	107	12	US-10-044-534-3
17	32	65.3	1150	9	US-10-108-605-301
18	31	63.3	154	10	US-09-764-877-1878
19	31	63.3	255	10	US-09-925-302-455

20	31	63.3	453	10	US-09-815-242-12035	Sequence 12035, A
21	31	63.3	2785	10	US-09-801-574-8	Sequence 8, Appli
22	30	61.2	61	10	US-09-908-322-21	Sequence 21, Appli
23	30	61.2	81	10	US-09-864-761-44504	Sequence 44504, A
24	30	61.2	297	10	US-09-815-242-5206	Sequence 5206, Ap
25	30	61.2	674	10	US-09-925-299-979	Sequence 979, App
26	29	59.2	33	9	US-09-956-206A-12	Sequence 12, Appli
27	29	59.2	126	10	US-09-734-569-86	Sequence 86, Appli
28	29	59.2	207	10	US-09-731-872-386	Sequence 386, App
29	29	59.2	238	10	US-09-815-242-5463	Sequence 5463, Ap
30	29	59.2	242	10	US-09-815-242-12164	Sequence 12164, A
31	29	59.2	437	10	US-09-815-242-11187	Sequence 11187, A
32	29	59.2	624	10	US-09-815-242-5391	Sequence 5391, Ap
33	29	59.2	627	10	US-09-815-242-12305	Sequence 12305, A
34	29	59.2	1224	10	US-09-801-368-222	Sequence 222, App
35	29	59.2	2448	10	US-09-815-242-11870	Sequence 11870, A
36	28	57.1	69	10	US-09-205-658-81	Sequence 81, Appli
37	28	57.1	69	10	US-09-844-353A-81	Sequence 81, Appli
38	28	57.1	322	10	US-09-767-041-35	Sequence 35, Appli
39	28	57.1	333	10	US-09-895-686-3	Sequence 3, Appli
40	28	57.1	365	10	US-09-925-300-1391	Sequence 1391, Ap
41	28	57.1	381	10	US-09-205-658-106	Sequence 106, App
42	28	57.1	381	10	US-09-844-353A-106	Sequence 106, App
43	28	57.1	406	10	US-09-215-450-26	Sequence 26, Appli
44	28	57.1	443	9	US-09-895-913A-150	Sequence 150, App
45	28	57.1	458	10	US-09-801-368-168	Sequence 168, App

ALIGNMENTS

RESULT 1
US-09-905-243-30
; Sequence 30, Application US/09905243
; Patent No. US20020062009A1
; GENERAL INFORMATION:
; APPLICANT: Taylor, Alexander H
; TITLE OF INVENTION: Monoclonal Antibodies with Reduced
; IMMUNOGENICITY
; FILE REFERENCE: P50770
; CURRENT APPLICATION NUMBER: US/09/905,243
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/300,970
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Pan troglodytes
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (24)...(34)
; OTHER INFORMATION: CDRI
; NAME/KEY: DOMAIN
; LOCATION: (50)...(66)
; OTHER INFORMATION: CDRII
; OTHER INFORMATION: CDRII
US-09-905-243-30

Query Match 87.8%; Score 43; DB 10; Length 88;
Best Local Similarity 81.8%; Pred. No. 0.025;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIRYSQSIS 11
|||:|:|||||
Db 46 LLIKYASQSIS 56

RESULT 2
US-09-864-761-48570
; Sequence 48570, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:

; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aecmca-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
; SEQ ID NO 48570
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AP001242.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.4
; OTHER INFORMATION: EST_HUMAN HIT: AW378342.1, EVALUE 1.00e-27
; OTHER INFORMATION: SWISSPROT HIT: P01605, EVALUE 2.00e-27
US-09-864-761-48570

Query Match 87.8%; Score 43; DB 10; Length 102;
Best Local Similarity 81.8%; Pred. No. 0.029; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 2;

Qy 1 LLIRYSQSIS 11
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Db 30 LLIKYASQSIS 40

RESULT 3
US-10-006-773-6
; Sequence 6, Application US/10006773
; Patent No.: US20020132983A1
; GENERAL INFORMATION:
; APPLICANT: Jüngmans, Richard P.

; TITLE OF INVENTION: Antibodies as Chimeric Effector Cell Receptors Against Tumor A
; FILE REFERENCE: 003
; CURRENT APPLICATION NUMBER: US/10/006,773
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: 60/250,089
; PRIOR FILING DATE: 2000-11-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-006-773-6

Query Match 87.8%; Score 43; DB 12; Length 128;
Best Local Similarity 81.8%; Pred. No. 0.038;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLIRYSQSIS 11
|||:|||||

Db 66 LLIKYASQSIS 76

RESULT 4
US-08-790-540A-8
; Sequence 8, Application US/08790540A
; Patent No. US20010011125A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,540A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-790-540A-8

Query Match 83.7%; Score 41; DB 8; Length 107;
Best Local Similarity 81.8%; Pred. No. 0.081;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LLIRYSQSIS 11
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Db 46 LLIKYRSQSIS 56

RESULT 5

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US-08-791-391A-4
; Sequence 4, Application US/08791391A
; Patent No. US20010016645A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791.391A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-791-391A-4

Query Match 83.7%; Score 41; DB 8; Length 107;
Best Local Similarity 81.8%; Pred. No. 0.081;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLIRYSQSIS 11
Db 46 LLIKYRSQSIS 56

RESULT 6
US-08-791-391A-8
; Sequence 8, Application US/08791391A
; Patent No. US20010016645A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791.391A

Query Match 83.7%; Score 41; DB 8; Length 107;
Best Local Similarity 81.8%; Pred. No. 0.081;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLIRYSQSIS 11
Db 46 LLIKYRSQSIS 56

RESULT 6
US-08-791-391A-8
; Sequence 8, Application US/08791391A
; Patent No. US20010016645A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791.391A

US-08-791-391A-4
; Sequence 4, Application US/08791391A
; Patent No. US20010016645A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791.391A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-791-391A-4

Query Match 83.7%; Score 41; DB 8; Length 107;
Best Local Similarity 81.8%; Pred. No. 0.081;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLIRYSQSIS 11
Db 46 LLIKYRSQSIS 56

RESULT 7
US-09-940-391-1
; Sequence 1, Application US/09940391
; Patent No. US20020035325A1
; GENERAL INFORMATION:
; APPLICANT: Barbera-Guillem, Emilio
; TITLE OF INVENTION: Method for detecting lymphoid tissue involved in tumor progres
; FILE REFERENCE: Phy-03
; CURRENT APPLICATION NUMBER: US/09/940,391
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: 09/244,369
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 60/077,970
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: 60/073,882
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Mus sp.
; US-09-940-391-1

Query Match 79.6%; Score 39; DB 10; Length 244;
Best Local Similarity 63.6%; Pred. No. 0.56;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIRYSQSIS 11
Db 180 LLIKYASESVS 190

RESULT 8
US-08-790-540A-4
; Sequence 4, Application US/08790540A
; Patent No. US2001001125A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
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; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,540A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-790-540A-4

Query Match 77.6%; Score 38; DB 8; Length 107;
Best Local Similarity 81.8%; Pred. No. 0.34;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LLIRYSQSIS 11
| | | | |
Db 46 LLIXRSQSIS 56

RESULT 9
US-08-791-391A-32
; Sequence 32, Application US/08791391A
; Patent No. US20010016645A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,391A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

; MOLECULE TYPE: protein
; US-08-791-391A-32

Query Match 77.6%; Score 38; DB 8; Length 107;
Best Local Similarity 81.8%; Pred. No. 0.34;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LLIRYSQSIS 11
| | | | |
Db 46 LLIXRSQSIS 56

RESULT 10
US-09-756-301A-3
; Sequence 3, Application US/09756301A
; Patent No. US20010027249A1
; GENERAL INFORMATION:
; APPLICANT: Le, Junming
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Grayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
; TITLE OF INVENTION: Human Tumor Necrosis Factor
; FILE REFERENCE: 0975.1005-008
; CURRENT APPLICATION NUMBER: US/09/756,301A
; CURRENT FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: U.S. 09/133,119
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1994-10-18
; PRIOR APPLICATION NUMBER: U.S. 08/192,102
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,861
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,093
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/010,406
; PRIOR FILING DATE: 1993-01-29
; PRIOR APPLICATION NUMBER: U.S. 08/013,413
; PRIOR FILING DATE: 1993-02-02
; PRIOR APPLICATION NUMBER: U.S. 07/943,852
; PRIOR FILING DATE: 1992-09-11
; PRIOR APPLICATION NUMBER: U.S. 07/853,606
; PRIOR FILING DATE: 1992-03-18
; PRIOR APPLICATION NUMBER: U.S. 07/670,827
; PRIOR FILING DATE: 1991-03-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus Balb/c
; US-09-756-301A-3

Query Match 75.5%; Score 37; DB 10; Length 107;
Best Local Similarity 63.6%; Pred. No. 0.55;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIRYSQSIS 11
| | | | |
Db 46 LLIKYSESMS 56

RESULT 11
US-09-927-703-3
; Sequence 3, Application US/09927703
; Patent No. US20020022720A1
; GENERAL INFORMATION:
; APPLICANT: Le, Junming

```
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Ghayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
; FILE REFERENCE: 0975.1005-013
; CURRENT APPLICATION NUMBER: US/09/927,703
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: U.S. 09/756,398
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: U.S. 09/133,119
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1994-10-18
; PRIOR APPLICATION NUMBER: U.S. 08/192,102
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,861
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,093
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/010,406
; PRIOR FILING DATE: 1993-01-29
; PRIOR APPLICATION NUMBER: U.S. 08/013,413
; PRIOR FILING DATE: 1993-02-02
; PRIOR APPLICATION NUMBER: U.S. 07/943,852
; PRIOR FILING DATE: 1992-09-11
; PRIOR APPLICATION NUMBER: U.S. 07/853,606
; PRIOR FILING DATE: 1992-03-18
; PRIOR APPLICATION NUMBER: U.S. 07/670,827
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus Balb/c
US-09-927-703-3

Query Match 75.5%; Score 37; DB 10; Length 107;
Best Local Similarity 63.6%; Pred. No. 0.55;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIRYSQSIS 11
Db 46 LLIRYSESMS 56

RESULT 12
US-09-766-535A-3
; Sequence 3, Application US/09766535A
; Patent No. US20020106372A1
; GENERAL INFORMATION:
; APPLICANT: Le, Junming
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Ghayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
; FILE REFERENCE: 0975.1005-010
; CURRENT APPLICATION NUMBER: US/09/766,535A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: U.S. 09/133,119
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1994-10-18
; PRIOR APPLICATION NUMBER: U.S. 08/192,861
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,093
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/010,406
; PRIOR FILING DATE: 1993-01-29
; PRIOR APPLICATION NUMBER: U.S. 08/013,413
; PRIOR FILING DATE: 1993-02-02
; PRIOR APPLICATION NUMBER: U.S. 07/943,852
; PRIOR FILING DATE: 1992-09-11
; PRIOR APPLICATION NUMBER: U.S. 07/853,606
; PRIOR FILING DATE: 1992-03-18
; PRIOR APPLICATION NUMBER: U.S. 07/670,827
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus Balb/c
US-09-927-703-3
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Query Match 75.5%; Score 37; DB 10; Length 107;
Best Local Similarity 63.6%; Pred. No. 0.55;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
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QY 1 LLIRYSQSIS 11
Db 46 LLIRYSESMS 56
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RESULT 13
US-09-756-161A-3
; Sequence 3, Application US/09756161A
; Patent No. US20020132307A1
; GENERAL INFORMATION:
; APPLICANT: Le, Junming
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Ghayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
; FILE REFERENCE: 0975.1005-007
; CURRENT APPLICATION NUMBER: US/09/756,161A
; CURRENT FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: U.S. 09/133,119
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1994-10-18
; PRIOR APPLICATION NUMBER: U.S. 08/192,102
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,861
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,093
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/010,406
; PRIOR FILING DATE: 1993-01-29
; PRIOR APPLICATION NUMBER: U.S. 08/013,413
; PRIOR FILING DATE: 1993-02-02
; PRIOR APPLICATION NUMBER: U.S. 07/943,852
; PRIOR FILING DATE: 1992-09-11
; PRIOR APPLICATION NUMBER: U.S. 07/853,606
; PRIOR FILING DATE: 1992-03-18
; PRIOR APPLICATION NUMBER: U.S. 07/670,827
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSEQ for Windows Version 4.0
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; SEQ ID NO 3
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus Balb/c
US-09-756-161A-3

Query Match 75.5%; Score 37; DB 10; Length 107;
Best Local Similarity 63.6%; Pred. No. 0.55;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLIRYSSQIS 11
Db 46 LLIKYASESMS 56

RESULT 14

US-10-010-229-3

; Sequence 3, Application US/10010229
; Patent No. US20020114805A1
; GENERAL INFORMATION:
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Grayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
; FILE REFERENCE: 0975.1005-013
; CURRENT APPLICATION NUMBER: US/10/010.229
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US/09/927,703
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus Balb/c
US-10-010-229-3

Query Match 75.5%; Score 37; DB 12; Length 107;
Best Local Similarity 63.6%; Pred. No. 0.55;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLIRYSSQIS 11
Db 46 LLIKYASESMS 56

RESULT 15

US-10-043-450-3

; Sequence 3, Application US/10043450
; Patent No. US20020141996A1
; GENERAL INFORMATION:
; APPLICANT: Le, Junming
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Grayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
; FILE REFERENCE: 0975.1005-013
; CURRENT APPLICATION NUMBER: US/10/043.450
; CURRENT FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: 09/927,703
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: U.S. 09/756,398
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: U.S. 09/133,119
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674

; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1994-10-18
; PRIOR APPLICATION NUMBER: U.S. 08/192,102
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,861
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,093
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/010,406
; PRIOR FILING DATE: 1993-01-29
; PRIOR APPLICATION NUMBER: U.S. 08/013,413
; PRIOR FILING DATE: 1993-02-02
; PRIOR APPLICATION NUMBER: U.S. 07/943,852
; PRIOR FILING DATE: 1992-09-11
; PRIOR APPLICATION NUMBER: U.S. 07/853,606
; PRIOR FILING DATE: 1992-03-18
; PRIOR APPLICATION NUMBER: U.S. 07/670,827
; PRIOR FILING DATE: 1991-03-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus Balb/c
US-10-043-450-3

Query Match 75.5%; Score 37; DB 12; Length 107;
Best Local Similarity 63.6%; Pred. No. 0.55;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLIRYSSQIS 11
Db 46 LLIKYASESMS 56

Search completed: November 18, 2002, 18:45:18
Job time : 2.15686 secs

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QM protein - protein search, using sw model

Run on: November 18, 2002, 17:22:01 ; Search time 4.66422 Seconds
(without alignments)
69.390 Million cell updates/sec

Title: US-09-016-061-84
Perfect score: 49
Sequence: 1 LLIRYSQSIS 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43	87.8	96	2	US-08-737-560A-9
2	43	87.8	100	1	US-08-436-463-19
3	43	87.8	106	1	US-08-326-362-4
4	43	87.8	107	1	US-07-634-278-62
5	43	87.8	107	1	US-07-634-278-63
6	43	87.8	107	1	US-07-634-278-87
7	43	87.8	107	1	US-08-477-728-62
8	43	87.8	107	1	US-08-477-728-63
9	43	87.8	107	1	US-08-477-728-87
10	43	87.8	107	1	US-08-474-040-62
11	43	87.8	107	1	US-08-474-040-63
12	43	87.8	107	1	US-08-474-040-87
13	43	87.8	107	1	US-08-487-200-62
14	43	87.8	107	1	US-08-487-200-63
15	43	87.8	107	1	US-08-487-200-87
16	43	87.8	107	1	US-08-436-463-20
17	43	87.8	107	1	US-08-107-669D-1
18	43	87.8	107	1	US-08-472-788A-1
19	43	87.8	107	2	US-08-477-531B-1
20	43	87.8	107	2	US-08-082-842A-1
21	43	87.8	107	4	US-08-484-537-62
22	43	87.8	107	4	US-08-484-537-63
23	43	87.8	107	4	US-08-484-537-87
24	43	87.8	107	4	US-08-438-954-1
25	43	87.8	107	4	US-09-438-954-3
26	43	87.8	107	4	US-09-438-954-38
27	43	87.8	108	2	US-08-737-560A-11

28	43	87.8	109	1	US-07-942-245-4	Sequence 4, Appl
29	43	87.8	127	1	US-07-634-278-83	Sequence 83, Appl
30	43	87.8	127	1	US-08-477-728-83	Sequence 83, Appl
31	43	87.8	127	1	US-08-474-040-83	Sequence 83, Appl
32	43	87.8	127	1	US-08-487-200-83	Sequence 4, Appl
33	43	87.8	127	1	US-08-436-463-4	Sequence 18, Appl
34	43	87.8	127	1	US-08-436-463-18	Sequence 83, Appl
35	43	87.8	127	4	US-08-484-537-83	Sequence 21, Appl
36	41	83.7	103	1	US-08-436-463-21	Sequence 4, Appl
37	40	81.6	106	2	US-08-800-198-4	Sequence 9, Appl
38	40	81.6	106	3	US-09-296-595-4	Sequence 4, Appl
39	40	81.6	107	2	US-08-232-081B-9	Sequence 40, Appl
40	40	81.6	107	2	US-08-232-081B-40	Sequence 4, Appl
41	40	81.6	107	2	US-08-476-176B-4	Sequence 4, Appl
42	40	81.6	107	3	US-08-127-721A-4	Sequence 4, Appl
43	40	81.6	107	3	US-08-485-246A-4	Sequence 6, Appl
44	40	81.6	127	2	US-08-476-176B-6	Sequence 8, Appl
45	40	81.6	127	2	US-08-476-176B-8	

ALIGNMENTS

RESULT 1
US-08-737-560A-9
; Sequence 9, Application US/08737560A
; Patent No. 5928893
; GENERAL INFORMATION:
; APPLICANT: KANG, Chang-Yuill
; APPLICANT: KIM, Joong-Gon
; TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC FOR HUMAN
; TITLE OF INVENTION: 4-1BB AND CELL LINE PRODUCING SAME
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KANG, Chang-Yuill
; STREET: Professor Apt. Ka-302, #244-2, Bongchun 7-dong,
; STREET: Kwanak-gu
; CITY: Seoul
; STATE: Seoul
; COUNTRY: Republic of Korea
; ZIP: 151-057
; ADDRESSEE: KIM, Joong-Gon
; STREET: Hanyang Apt. 72-1213, Apgujung-dong, Kangnam-gu
; CITY: Seoul
; STATE: Seoul
; COUNTRY: Republic of Korea
; ZIP: 135-110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5inch, 1.44MB storage
; COMPUTER: IBM PC/AT
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/737,560A
; FILING DATE: 13-NOV-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: KR 95-8176
; FILING DATE: 08-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 96 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:

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;
; OTHER INFORMATION: VK23.32'CL
US-08-737-560A-9

Query Match      87.8%; Score 43; DB 2; Length 96;
Best Local Similarity 81.8%; Pred. No. 0.16;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIRYSSQIS 11
Db 46 LLIKYSSQIS 56

RESULT 2
US-08-436-463-19
; Sequence 19, Application US/08436463
; Patent No. 5760185
; GENERAL INFORMATION:
; APPLICANT: KIMACHI, Kazuhiko
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: NISHIYAMA, Kiyoto
; APPLICANT: TOKIYOSHI, Sachio
; TITLE OF INVENTION: ANTI-PELVINE HERPES VIRUS-1 RECOMBINANT
; TITLE OF INVENTION: ANTIBODY AND GENE FRAGMENT CODING FOR SAID ANTIBODY
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436.463
; FILING DATE: 26-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 341255/1992
; FILING DATE: 28-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: KIMACHI-1
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 100 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-436-463-19

Query Match      87.8%; Score 43; DB 1; Length 100;
Best Local Similarity 81.8%; Pred. No. 0.17;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIRYSSQIS 11
Db 46 LLIKYSSQIS 56

RESULT 3
US-08-326-362-4
; Sequence 4, Application US/08326362
; Patent No. 5730981
; GENERAL INFORMATION:
; APPLICANT: Bosslet, Klaus
; APPLICANT: Seeman, Gerhard
; APPLICANT: Dippold, Wolfgang
; TITLE OF INVENTION: Monoclonal Anti-Ganglioside Antibody,
; TITLE OF INVENTION: Its Preparation and Use as a Tumortherapeutic Agent
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/326,362
; FILING DATE: 19-MAR-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/032,863
; FILING DATE: 17-MAR-1993
; APPLICATION NUMBER: DE P 42 08 795.3
; FILING DATE: 19-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Einaudi, Carol P.
; REGISTRATION NUMBER: 32,220
; REFERENCE/DOCKET NUMBER: 02481-1276-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 106 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-326-362-4

Query Match      87.8%; Score 43; DB 1; Length 106;
Best Local Similarity 81.8%; Pred. No. 0.18;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIRYSSQIS 11
Db 46 LLIKYSSQIS 56

RESULT 4
US-07-634-278-62
; Sequence 62, Application US/07634278
; Patent No. 5530101
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
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;
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/634,278
; FILING DATE: 19-DEC-1990
; CLASSIFICATION: 424
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
;
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-07-634-278-62

Query Match 87.8%; Score 43; DB 1; Length 107;
Best Local Similarity 81.8%; Pred. No. 0.19;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIRYSSQSI 11
Db 46 LLIKYASQSI 56

RESULT 5
US-07-634-278-63
; Sequence 63, Application US/07634278
; Patent No. 5530101
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/634,278
; FILING DATE: 19-DEC-1990
; CLASSIFICATION: 424
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274

;
; FILING DATE: 28-SEP-1990
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
;
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-07-634-278-63

Query Match 87.8%; Score 43; DB 1; Length 107;
Best Local Similarity 81.8%; Pred. No. 0.19;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIRYSSQSI 11
Db 46 LLIKYASQSI 56

RESULT 6
US-07-634-278-87
; Sequence 87, Application US/07634278
; Patent No. 5530101
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/634,278
; FILING DATE: 19-DEC-1990
; CLASSIFICATION: 424
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223

; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 87:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-634-278-87

Query Match 87.8%; Score 43; DB 1; Length 107;
Best Local Similarity 81.8%; Pred. No. 0.19;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIRYSQSIS 11
Db 46 LLIKVASQSIS 56

RESULT 7

US-08-477-728-62
; Sequence 62, Application US/08477728
; Patent No. 5585089
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,728
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; MOLECULE TYPE: peptide
US-08-477-728-62

Query Match 87.8%; Score 43; DB 1; Length 107;
Best Local Similarity 81.8%; Pred. No. 0.19;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIRYSQSIS 11
Db 46 LLIKVASQSIS 56

RESULT 8

US-08-477-728-63
; Sequence 63, Application US/08477728
; Patent No. 5585089
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,728
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; FILING DATE: 19-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-477-728-63

Query Match 87.8%; Score 43; DB 1; Length 107;
Best Local Similarity 81.8%; Pred. No. 0.19;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIRYSQSIS 11
Db 46 LLIKVASQSIS 56

RESULT 9
US-08-477-728-87
; Sequence 87, Application US/08477728
; Patent No. 5585089
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,728
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 87:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-477-728-87

Query Match 87.8%; Score 43; DB 1; Length 107;
Best Local Similarity 81.8%; Pred. No. 0.19;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLIRYSSQSSIS 11
Db 46 LLIKYASQSSIS 56

RESULT 10
US-08-474-040-62
; Sequence 62, Application US/08474040
; Patent No. 5693761
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.

; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,040
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US/07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-474-040-62

Query Match 87.8%; Score 43; DB 1; Length 107;
Best Local Similarity 81.8%; Pred. No. 0.19;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLIRYSSQSSIS 11
Db 46 LLIKYASQSSIS 56

RESULT 11
US-08-474-040-63
; Sequence 63, Application US/08474040
; Patent No. 5693761
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue

; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,040
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-474-040-63

Query Match 87.8%; Score 43; DB 1; Length 107;
Best Local Similarity 81.8%; Pred. No. 0.19;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIRYSQSIS 11
Db 46 LLIKYASQSIS 56

RESULT 12
; US-08-474-040-87
; Sequence 87, Application US/08474040
; Patent No. 5693761
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLET, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourile and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,200
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990

; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,040
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 87:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-474-040-87

Query Match 87.8%; Score 43; DB 1; Length 107;
Best Local Similarity 81.8%; Pred. No. 0.19;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIRYSQSIS 11
Db 46 LLIKYASQSIS 56

RESULT 13
; US-08-487-200-62
; Sequence 62, Application US/08487200
; Patent No. 5693762
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLET, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,200
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/590,274
;; FILING DATE: 28-SEP-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/310,252
;; FILING DATE: 13-FEB-1989
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/290,975
;; FILING DATE: 28-DEC-1988
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Smith, William M
;; REGISTRATION NUMBER: 30,223
;; REFERENCE/DOCKET NUMBER: 11823-002610
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 326-2400
;; TELEFAX: (415) 326-2422
;; INFORMATION FOR SEQ ID NO: 62:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 107 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-08-487-200-62

Query Match 87.8%; Score 43; DB 1; Length 107;
Best Local Similarity 81.8%; Pred. No. 0.19;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIRYSQSIS 11
Db 46 LLIKYASQSIS 56
|||:|:|||||

RESULT 14
US-08-487-200-63
; Sequence 63, Application US/08487200
; Patent No. 5693762
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,200
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 07/290,975
;; FILING DATE: 28-DEC-1988
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Smith, William M
;; REGISTRATION NUMBER: 30,223
;; REFERENCE/DOCKET NUMBER: 11823-002610
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 326-2400
;; TELEFAX: (415) 326-2422
;; INFORMATION FOR SEQ ID NO: 63:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 107 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-08-487-200-63

Query Match 87.8%; Score 43; DB 1; Length 107;
Best Local Similarity 81.8%; Pred. No. 0.19;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIRYSQSIS 11
Db 46 LLIKYASQSIS 56
|||:|:|||||

RESULT 15
US-08-487-200-87
; Sequence 87, Application US/08487200
; Patent No. 5693762
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,200
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002610
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 87:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-487-200-87

Query Match 87.8%; Score 43; DB 1; Length 107;
Best Local Similarity 81.8%; Pred. No. 0.19;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLIRYSQSIS 11
|||:||||
Db 46 LLIRYSQSIS 56

Search completed: November 18, 2002, 17:43:39
Job time : 4.66422 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:47:14 ; Search time 9.5921 Seconds
(without alignments)
90.200 Million cell updates/sec

Title: US-09-016-061-86

Perfect score: 55

Sequence: 1 QQNSNPHT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_73.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%	Query Match	Length	DB ID	Description
1	55	100.0	107	2	A45722	anti-glycoprotein
2	55	100.0	123	2	S35479	Ig kappa chain pre
3	52	94.5	107	2	B45722	anti-glycoprotein
4	49	89.1	106	2	PL0267	Ig kappa chain v r
5	47	85.5	67	2	PH1081	Ig light chain v r
6	47	85.5	69	2	PH1080	Ig light chain v r
7	46	83.6	102	2	S26346	Ig kappa' chain v r
8	44	80.0	104	2	B43413	Ig kappa chain v r
9	44	80.0	108	2	C30502	Ig kappa chain v r
10	44	80.0	138	2	A26471	Ig kappa chain pre
11	42	76.4	87	2	PH1082	Ig light chain v r
12	42	76.4	115	1	KVMSU7	Ig kappa chain pre
13	42	76.4	128	2	PN0445	Ig kappa chain pre
14	40	72.7	128	2	S40343	Ig kappa chain v-J
15	40	72.7	613	4	C40201	artifact-warning s
16	39	70.9	581	2	G96811	unknown protein T1
17	38	69.1	91	2	S37527	Ig kappa chain v r
18	38	69.1	242	2	H64824	arginine transport
19	38	69.1	242	2	AH0607	arginine transport
20	38	69.1	242	2	C90747	arginine transport
21	38	69.1	242	2	G85597	arginine transport
22	38	69.1	271	2	AB3266	asparagine transpo
23	38	69.1	278	2	S60619	homeotic protein c
24	38	69.1	1109	2	C84545	probable disease r
25	36	65.5	86	2	C28195	Ig kappa chain v r
26	36	65.5	96	2	JC5945	regulatory protein
27	36	65.5	107	2	C45722	anti-glycoprotein
28	36	65.5	108	1	K1HULY	Ig kappa chain V-I
29	36	65.5				

30 36 65.5 109 1 K3HUPM
31 36 65.5 118 2 S69461
32 36 65.5 226 1 KCUF
33 36 65.5 400 1 JC1428
34 36 65.5 458 2 AD0068
35 36 65.5 467 2 AG0546
36 36 65.5 534 2 AB0392
37 36 65.5 640 2 T28820
38 36 65.5 1185 2 A42404
39 36 65.5 1581 2 T30832
40 36 65.5 1776 1 RRWPM
41 35 63.6 91 2 S37525
42 35 63.6 117 2 S40362
43 35 63.6 145 2 S77537
44 35 63.6 428 2 AB2215
45 35 63.6 750 2 T10864

Ig kappa chain V-I
hypothetical prote
brachyurin (EC 3.4
ketol-acid reducto
UDP-N-acetylmuramo
probable terminal
probable carbohydr
hypothetical prote
collagen adhesin -
pentafunctional en
genome polyprotein
Ig kappa chain v r
Ig kappa chain - h
hypothetical prote
probable alanine r
transcription acti

ALIGNMENTS

RESULT 1

A45722
anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 5) - mouse (C:Species: Mus musculus (house mouse)
C:Date: 03-Mar-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: A45722
R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdaloovic, N.; Yuan, S.; Au, D.; Co, M.S.; Va

J. Virol. 67, 489-496, 1993
A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on
A:Reference number: A45722; MUID:93100833; PMID:7677958
A:Accession: A45722

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-107 <SIM>

A:Note: sequence extracted from NCBI backbone (NCBIP:120589)

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: glycoprotein

F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 55; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.0062;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQNSNPHT 9

Db 89 QQNSNPHT 97

RESULT 2

S35479

Ig kappa chain precursor V region - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 19-Mar-1997 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000

C:Accession: S35479

R:Takeda, Y.; Wise, K.S.; Hoffman, R.W.

Nucleic Acids Res. 20, 4099, 1992

A:Title: Nucleotide sequences of immunoglobulin heavy and light chain V-regions from

A:Reference number: S35479; MUID:92375706; PMID:1387203

A:Accession: S35479

A:Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-123 <TAK>

A:Cross-references: EMBL:M93959; NID:g197572; PIDN:AAA39079.1; PID:g554148

C:Genetics:

A:Map position: 6

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-12/Domain: signal sequence (fragment) #status predicted <STG>

F:13-123/Product: Ig kappa chain V region (fragment) #status predicted <MAT>

F:28-102/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 55; DB 2; Length 123;

Best Local Similarity 100.0%; Pred. No. 0.0072;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQSNSWPHT 9
|||||||

Db 101 QQSNSWPHT 109

RESULT 3

B45722 anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 33) - mouse (fr

C:Species: Mus musculus (house mouse)

C>Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000

C:Accession: B45722

R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Vasqu

J. Virol. 67, 489-496, 1993

A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on hu

A:Reference number: A45722; MUID:93100833; PMID:7677958

A:Accession: B45722

A>Status: preliminary: not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-107 <SIM>

A>Note: sequence extracted from NCBI backbone (NCBIP:120590)

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: glycoprotein

F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 94.5%; Score 52; DB 2; Length 107;

Best Local Similarity 88.9%; Pred. No. 0.021;

Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQSNSWPHT 9

|||||||

Db 89 QQTNSWPHT 97

RESULT 4

PL0267 Ig kappa chain V region (anti-DNA, DP12VK) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000

C:Accession: PL0267

R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A

J. Exp. Med. 171, 265-297, 1990

A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic

A:Reference number: PL0231; MUID:90111618; PMID:2104919

A:Accession: PL0267

A:Molecule type: mRNA

A:Residues: 1-106 <SHL>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-23/Region: framework 1

F:16-90/Domain: immunoglobulin homology <IMM>

F:24-34/Region: complementarity-determining 1

F:35-49/Region: framework 2

F:50-56/Region: complementarity-determining 2

F:57-88/Region: framework 3

F:89-97/Region: complementarity-determining 3

F:98-106/Region: framework 4

Query Match 89.1%; Score 49; DB 2; Length 106;

Best Local Similarity 88.9%; Pred. No. 0.073;

Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQSNSWPHT 9

|||||||

Db 89 QQSNSWPHT 97

RESULT 5

PH1081 Ig light chain V region (clone 165.6) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 15-Jun-1996

C:Accession: PH1081

R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective

A:Reference number: PH0971; MUID:92381444; PMID:1512540

A:Accession: PH1081

A>Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-67 <TIL>

A:Experimental source: B cell, strain [NZB x NZW]F1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

Query Match 85.5%; Score 47; DB 2; Length 67;

Best Local Similarity 88.9%; Pred. No. 0.1;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSNSWPHT 9

|||||||

Db 58 QQSNSWPQT 66

RESULT 6

PH1080

Ig light chain V region (clone 165.60) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 15-Jun-1996

C:Accession: PH1080

R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective

A:Reference number: PH0971; MUID:92381444; PMID:1512540

A:Accession: PH1080

A>Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-69 <TIL>

A:Experimental source: B cell, strain [NZB x NZW]F1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

Query Match 85.5%; Score 47; DB 2; Length 69;

Best Local Similarity 88.9%; Pred. No. 0.11;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSNSWPHT 9

|||||||

Db 60 QQSNSWPQT 68

RESULT 7

S26346

Ig kappa chain V region - mouse

C:Species: Mus musculus (house mouse)

C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000

C:Accession: S26346

R:Stark, S.E.; Caton, A.J.

J. Exp. Med. 174, 613-624, 1991

A:Title: Antibodies that are specific for a single amino acid interchange in a protei

A:Reference number: S26309; MUID:91341421; PMID:1908510

A:Accession: S26346

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-102 <STA>

A:Cross-references: EMBL:X59211; NID:952338; PIDN:CAA41921.1; PID:g1334075

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:14-88/Domain: immunoglobulin homology <IMM>

Query Match 83.6%; Score 46; DB 2; Length 102;

Best Local Similarity 77.8%; Pred. No. 0.24;

Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQSNSWPHT 9
|||||:||||

Db 87 QQSNTWPYT 95

RESULT 8

B43413

Ig kappa chain V region - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000

C:Accession: B43413

R:Tomiya, Y.; Brojer, E.; Ruggeri, Z.M.; Shattil, S.J.; Smiltneck, J.; Gorski, J.; Kum

J. Biol. Chem. 267, 18085-18092, 1992

A>Title: A molecular model of RGD ligands. Antibody D gene segments that direct specific

A:Reference number: A43413; MUID:92388177; PMID:1517241

A:Accession: B43413

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-104 <TOM>

A>Note: sequence extracted from NCBI backbone (NCBIP:112818)

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:13-87/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 80.0%; Score 44; DB 2; Length 104;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSNSWPHT 9

|||||:||||

Db 86 QQSNSWPLT 94

RESULT 9

C30502

Ig kappa chain V region (D444) - mouse

C:Species: Mus musculus (house mouse)

C>Date: 03-Nov-1988 #sequence_revision 03-Nov-1988 #text_change 21-Jan-2000

C:Accession: C30502

R:Eilat, D.; Webster, D.M.; Rees, A.R.

J. Immunol. 141, 1745-1753, 1988

A>Title: V region sequences of anti-DNA and anti-RNA autoantibodies from NZB/NZW F-1 mice

A:Reference number: A30502; MUID:88315787; PMID:2457627

A:Accession: C30502

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-108 <EIL>

A:Cross-references: GB:M21907; NID:gl97071; PIDN:AAA38907.1; PID:gl97072

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-90/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 80.0%; Score 44; DB 2; Length 108;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSNSWPHT 9

|||||:||||

Db 89 QQTNSWPRT 97

RESULT 10

A26471

Ig kappa chain precursor V region (MAK33) - mouse

C:Species: Mus musculus (house mouse)

C>Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 23-Jul-1999

C:Accession: A26471

R:Buckel, P.; Hubner-Parajsz, C.; Mattes, R.; Lenz, H.; Haug, H.; Beaucamp, K.

Gene 51, 13-19, 1987

A>Title: Cloning and nucleotide sequence of heavy- and light-chain cDNAs from a creatine

A:Reference number: A91572; MUID:87248058; PMID:3110009

A:Accession: A26471

A:Molecule type: mRNA

A:Residues: 1-138 <BUC>

A:Cross-references: GB:M16162; NID:gl96893; PIDN:AAA38823.1; PID:gl96894

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-138/Product: Ig kappa chain V region #status predicted <MAT>

Query Match

Best Local Similarity 80.0%; Score 44; DB 2; Length 138;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSNSWPHT 9

|||||:||||

Db 109 QQSNSWPLT 117

RESULT 11

PHI082

Ig light chain V region (clone 165.54) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000

C:Accession: PHI082

R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A>Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective

A:Reference number: PH0971; MUID:92381444; PMID:1512540

A:Accession: PHI082

A>Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-87 <TIL>

A:Experimental source: B cell, strain [NZB x NZW]F1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

F:6-80/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 76.4%; Score 42; DB 2; Length 87;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQSNSWP 7

|||||:||||

Db 79 QQSNSWP 85

RESULT 12

KVMSL7

Ig kappa chain precursor V region (L7) - mouse

C:Species: Mus musculus (house mouse)

C>Date: 18-Dec-1981 #sequence_revision 18-Dec-1981 #text_change 22-Jun-1999

C:Accession: A01925

R:Pech, M.; Hochtl, J.; Schnell, H.; Zachau, H.G.

Nature 291, 668-670, 1981

A>Title: Differences between germ-line and rearranged immunoglobulin V-kappa coding s

A:Reference number: A93259; MUID:81220975; PMID:6264318

A:Accession: A01925

A:Molecule type: DNA

A:Residues: 1-115 <PEC>

A:Cross-references: GB:V01564; GB:J00574; NID:951718; PIDN:CAA24884.1; PID:g758153

A>Note: the sequence was determined from the germline gene

A>Note: there appear to be two possible splice junctions at the 3' end of the intron;

C:Genetics:

A:Introns: 17/1

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (

chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-115/Product: Ig kappa chain V region (L7) #status predicted <MAT>

F:36-110/Domain: immunoglobulin homology <IMM>

F:43-108/Disulfide bonds: #status predicted

Query Match

Best Local Similarity 76.4%; Score 42; DB 1; Length 115;

Matches 7; Conservative 0; Mismatches 0; Indels 1; Gaps 1.4;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QOSNSWP 7

||||||

Db 109 QOSNSWP 115

RESULT 13

PN0445

Ig kappa chain precursor V-I region - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000

C:Accession: PN0445

R:Kaluza, B.; Betzi, G.; Shao, H.; Diamantstein, T.; Weidle, U.H.

Gene 122, 321-328, 1992

A:Title: A general method for chimerization of monoclonal antibodies by inverse polymera

A:Reference number: PN0444; MUID:93138402; PMID:1339379

A:Accession: PN0445

A:Molecule type: mRNA

A:Residues: 1-128 <KAL>

A:Cross-references: GB:L02347

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-10/Domain: signal sequence #status predicted <SIG>

F:11-128/Product: Ig light chain kappa-1 V region #status predicted <MAT>

F:26-100/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 76.4%; Score 42; DB 2; Length 128;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOSNSWPHT 9

|||||

Db 99 QOTNSWPTT 107

RESULT 14

S40343

Ig kappa chain V-J region - human

C:Species: Homo sapiens (man)

C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C:Accession: S40343

R:Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A:Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; MUID:94080891; PMID:8258341

A:Accession: S40343

A:Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-128 <KLE>

A:Cross-references: EMBL:X72453; NID:g441374; PIDN:CAA51121.1; PID:g441375

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:36-110/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 72.7%; Score 40; DB 2; Length 128;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOSNSWPHT 9

|||||

Db 109 QQYNNWPTT 117

RESULT 15

C40201

artifact-warning sequence (translated ALU class C) - human

C:Species: Homo sapiens (man)

C:Date: 31-Mar-1992 #sequence_revision 11-Aug-1995 #text_change 19-May-2000

C:Accession: C40201

R:Claverie, J.M.

personal communication, 1992

A:Reference number: A40201

A:Accession: C40201

A:Molecule type: DNA

A:Residues: 1-613 <CIA>

R:Claverie, J.M.

Genomics 12, 838-841, 1992

A:Title: Identifying coding exons by similarity search: Alu-derived and other potenti

A:Reference number: A40200; MUID:92241891; PMID:1572661

A:Contents: annotation

C:Comment: This "warning" entry is a conceptual translation in all 6 reading frames o

in-frame stop codons are shown as 'x'.

C:Comment: Any significant similarity of a predicted protein sequence to a portion of

Query Match

Best Local Similarity 72.7%; Score 40; DB 4; Length 613;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SNSWPH 8

|||||

Db 588 SNSWPH 593

Search completed: November 18, 2002, 17:57:19

Job time : 10.5921 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:33:36 ; Search time 4.95526 Seconds
(without alignments)
76.883 Million cell updates/sec

Title: US-09-016-061-86
Perfect score: 55
Sequence: 1 QQNSNSWPH 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match %	Score	Length	ID	Description
1	42	76.4	115	1 KV5L_MOUSE	P01642 mus musculus
2	38	69.1	242	1 ARTP_ECOLI	P30858 escherichia
3	36	65.5	96	1 CTCL_ACILW	O33947 acinetobact
4	36	65.5	108	1 KV1M_HUMAN	P01605 homo sapien
5	36	65.5	109	1 KV3F_HUMAN	P01624 homo sapien
6	36	65.5	226	1 COGS_UCAPU	P00771 uca pugilat
7	36	65.5	400	1 ILV5_NEUCR	P38674 neurospora
8	36	65.5	975	1 KIT_CANFA	O97799 canis faml
9	36	65.5	1183	1 CNA_STAAR	Q53654 staphylococ
10	36	65.5	1581	1 ARO1_PNECA	Q12659 p pentafunc
11	36	65.5	1776	1 POLR_OYVY	P20127 ononis yell
12	35	63.6	392	1 ALR2_VIRCH	Q9kse5 vibrio chol
13	34	61.8	108	1 KVIV_HUMAN	P04430 homo sapien
14	34	61.8	459	1 NU4M_PELSU	O79677 pelomedusa
15	34	61.8	492	1 TYTR_TRYCR	P28593 trypanosoma
16	34	61.8	519	1 GAG_SIVAT	P05892 simian immu
17	34	61.8	520	1 GAG_SIVAL	P27972 simian immu
18	34	61.8	774	1 L0L2_HUMAN	Q9y4k0 homo sapien
19	33	60.0	87	1 YIMC_BPPH1	P10435 bacterioph
20	33	60.0	127	1 ACPS_THETN	Q8r857 thermoanaer
21	33	60.0	129	1 KV3H_HUMAN	P27978 simian immu
22	33	60.0	235	1 PSP_MOUSE	P07743 mus musculus
23	33	60.0	243	1 ARTP_HAETN	P45092 haemophilus
24	33	60.0	254	1 VG12_BPMLS	Q05328 mycobacteri
25	33	60.0	513	1 BMP6_HUMAN	P22004 homo sapien
26	33	60.0	521	1 GAG_SIVAG	P27978 simian immu
27	33	60.0	632	1 2179_HUMAN	Q9ulx5 homo sapien
28	33	60.0	675	1 COP1_ARATH	P43254 arabidopsis
29	33	60.0	762	1 AOCX_BOVIN	Q29437 bos taurus
30	33	60.0	762	1 AOCY_BOVIN	O46406 bos taurus
31	33	60.0	766	1 METE_PSEAE	P57703 pseudomonas
32	33	60.0	822	1 DEXT_STRSL	Q59979 streptococc
33	32	58.2	192	1 Y3_SOCMV	P15633 soybean chl

ALIGNMENTS

RESULT 1

KV5L_MOUSE STANDARD; PRT; 115 AA.
AC P01642;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1993 (Rel. 38, Last annotation update)
DE Ig kappa chain V-V region L7 precursor (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81220375; Pubmed=6264318;
RA Pech M., Hochtl J., Schnell H., Zachau H.G.;
RT "Differences between germ-line and rearranged immunoglobulin V kappa
RT coding sequences suggest a localized mutation mechanism.";
RL Nature 291:668-670(1981).
CC -!- MISCELLANEOUS: THERE APPEAR TO BE TWO POSSIBLE SPLICE JUNCTIONS AT
CC THE 3' END OF THE INTRON. THE ALTERNATE WOULD CODE FOR A PROTEIN
CC LACKING RESIDUES 17-19.
DR PIR: A01925; KVM5L7.
DR HSSP: P80362; 1WTL.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IgV_1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 >115
FT DOMAIN 21 43
FT DOMAIN 44 54
FT DOMAIN 55 69
FT DOMAIN 70 76
FT DOMAIN 77 108
FT DOMAIN 109 >115
FT DISULFID 43 108
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12615 MW; C17BEC758C577E00 CRC64;
Query Match 76.4%; Score 42; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 0.85;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQNSNSWP 7

|||||
DB 109 QQNSNSWP 115

RESULT 2

ARTP_ECOLI STANDARD; PRT; 242 AA.
ID ARTP_ECOLI
AC P30858; P77355;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)

16-OCT-2001 (Rel. 40, Last annotation update)
DE Arginine transport ATP-binding protein artp.
GN ARTP OR B0864 OR Z1094 OR ECS0947.
OS Escherichia coli, and
OC Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OX Escherichia.
RN NCBI_TaxID=562, 83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / AN387;
RX MEDLINE=93273744; PubMed=8501075;
RA Wissenbach U., Unden G.;
RT "Physical map location of the new artPIOMJ genes of Escherichia coli,
RT encoding a periplasmic arginine transport system.";
RL J. Bacteriol. 175:3687-3688(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97061202; PubMed=8905232;
RA Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A.,
RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
RA Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saifu N.,
RA Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
RA Yano M., Horiuchi T.;
RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 12.7-28.0 min region on the linkage map.";
RL DNA Res. 3:137-155(1996).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533(2001).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RMD 050952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
RN [6]
RP FUNCTION: PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM
CC FOR ARGININE. PROBABLY RESPONSIBLE FOR ENERGY COUPLING TO
CC THE TRANSPORT SYSTEM.
CC -!- SUBCELLULAR LOCATION: Inner membrane-associated (Potential).
CC -!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
CC -----
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DR EMBL; X86160; CAA60101.1; -;
DR EMBL; AE000188; AAC73951.1; -;
DR EMBL; D90724; BAA35578.1; -;
DR EMBL; AE005267; AAG55243.1; -;
DR EMBL; AP002553; BAB34370.1; -;
DR PIR; S31694; S31694.
DR EcoGene; EGI1624; artp.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003439; ABC_transportr.
DR Pfam; PF00005; ABC_tran; 1.
DR ProDom; PD000006; ABC_transportr; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER; 1.
KW Amino-acid transport; Transport; ATP-binding; Inner membrane;
FT Complete proteome. 42 ATP (POTENTIAL).
FT NP_BIND 35 95 WP -> CA (IN REF. 1).
FT CONFLICT 94 121 R -> S (IN REF. 1).
FT CONFLICT 121 121
SQ SEQUENCE 242 AA; 27022 MW; D5B50062E523413A CRC64;
Query Match 69.1%; Score 38; DB 1; Length 242;
Best Local Similarity 75.0%; Pred. No. 8.8;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 QQSNSWPH 8
DB 89 QQYNLWPH 96
ID CTCL ACILW STANDARD; PRT; 96 AA.
AC O33947;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Muconolactone delta-isomerase 1 (EC 5.3.3.4) (Miase 1).
GN CATC1.
OS Acinetobacter lwoffii.
OC Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;
OC Acinetobacter.
OX NCBI_TaxID=28090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K24;
RX MEDLINE=97405925; PubMed=9260969;
RA Kim S.I., Leem S.-H., Choi J.-S., Chung Y.H., Kim S., Park Y.-M.,
RA Park Y.K., Lee Y.N., Ha K.-S.;
RT "Cloning and characterization of two catA genes in Acinetobacter
RT lwoffii K24.";
RL J. Bacteriol. 179:5226-5231(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K24;
RX MEDLINE=98139907; PubMed=9473520;
RA Kim S.I., Leem S.-H., Choi J.-S., Ha K.-S.;
RT "Organization and transcriptional characterization of the catI gene
RT cluster in Acinetobacter lwoffii K24.";
RL Biochem. Biophys. Res. Commun. 243:289-294(1998).
CC -!- CATALYTIC ACTIVITY: 2,5-dihydro-5-oxofuran-2-acetate = 3,4-
CC dihydro-5-oxofuran-2-acetate.
CC -!- PATHWAY: THIRD STEP IN THE CATABOLISM OF CATECHOL TO SUCCINATE-
CC AND ACETYL-COA IN THE BETA-KETOADIPATE PATHWAY.
CC -!- SUBUNIT: HOMODECAMER (BY SIMILARITY).
CC -----
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CC -----
 DR EMBL; U77658; AAC46227.1; -.
 DR InterPro; IPR003464; Mfase.
 DR Pfam; PF02426; Mfase; 1.
 KW Aromatic hydrocarbons catabolism; Isomerase.
 SQ SEQUENCE 96 AA; 11048 MW; 6955AC14A5DDDEFA CRC64;

Query Match 65.5%; Score 36; DB 1; Length 96;
 Best Local Similarity 62.5%; Pred. No. 7.7;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QOSNSWPH 8
 I:| |||
 Db 35 QKSGKWP 42

RESULT 4
 KVIW_HUMAN STANDARD; PRT; 108 AA.
 AC P01605;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-I region Lay.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.

RX MEDLINE=77038198; PubMed=824717;
 RA Capra J.D., Klapper D.G.;
 RT "Complete amino acid sequence of the variable domains of two human
 RT Ig anti-gamma globulins (Lay/Pom) with shared idiotypic
 RT specificities.";
 RL Scand. J. Immunol. 5:677-684(1976).
 CC -1- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS
 CC CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN,
 CC WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA

CC GLOBULIN ACTIVITY.
 DR PIR; A01871; KIHULY.
 DR HSSP; P01607; IREI.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 34
 FT DOMAIN 35 49
 FT DOMAIN 50 56
 FT DOMAIN 57 88
 FT DOMAIN 89 97
 FT DOMAIN 98 107
 FT DISULFID 23 88
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11834 MW; 739993A95431434A CRC64;

Query Match 65.5%; Score 36; DB 1; Length 108;
 Best Local Similarity 66.7%; Pred. No. 8.6;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QOSNSWPH 9
 I:| |||
 Db 89 QOYNWPT 97

RESULT 5
 KV3F_HUMAN STANDARD; PRT; 109 AA.
 ID KV3F_HUMAN

AC P01624;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ig kappa chain V-III region POM.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=76276460; PubMed=60899;
 RA Klapper D.G., Capra J.D.;
 RT "The amino acid sequence of the variable regions of the light chains
 RT from two idiotypically cross reactive IgM anti-gamma globulins.";
 RL Ann. Immunol. (Paris) 127C:261-271(1976).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
 CC GLOBULIN ACTIVITY.
 DR PIR; A01897; K3HUPM.
 DR HSSP; P80362; LWTL.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 KW Immunoglobulin V region.
 FT DISULFID 23 89
 FT NON_TER 109 109
 FT BY SIMILARITY.
 SQ SEQUENCE 109 AA; 11922 MW; 62821DDC6A8ABA86 CRC64;

Query Match 65.5%; Score 36; DB 1; Length 109;
 Best Local Similarity 66.7%; Pred. No. 8.7;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QOSNSWPH 9
 I:| |||
 Db 90 QOYNWPT 98

RESULT 6
 COGS_UCAPU STANDARD; PRT; 226 AA.
 ID COGS_UCAPU
 AC P00771;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Brachyurin (EC 3.4.21.32) (Collagenolytic protease).
 OS Uca pugnator (Atlantic sand fiddler crab) (Celuca pugnator).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;
 OC Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata;
 OC Brachyura; Eubrachyura; Ocypodidae; Ocypodinae;
 OC Uca complex; Celuca.
 OX NCBI_TaxID=6772;
 RN [1]
 RP SEQUENCE.
 RX TISSUE=Hepatopancreas;
 RX MEDLINE=81040004; PubMed=6252953;
 RA Grant G.A., Henderson K.O., Eisen A.Z., Bradshaw R.A.;
 RT "Amino acid sequence of a collagenolytic protease from the
 RT hepatopancreas of the fiddler crab, Uca pugnator.";
 RL Biochemistry 19:4653-4659(1980).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS), AND REVISIONS.
 RC TISSUE=Hepatopancreas;
 RX MEDLINE=97299771; PubMed=9154920;
 RA Perona J.J., Tsu C.A., Craik C.S., Fletterick R.J.;
 RT "Crystal structure of an ecotin-collagenase complex suggests a model
 RT for recognition and cleavage of the collagen triple helix.";
 RL Biochemistry 36:5381-5392(1997).
 CC -1- FUNCTION: THIS ENZYME IS A SERINE PROTEASE CAPABLE OF DEGRADING
 CC THE NATIVE TRIPLE HELIX OF COLLAGEN.
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of proteins, with broad specificity
 CC for peptide bonds. Degrades native collagen at about 75% of the
 CC length of the molecule from the N-terminus. Low activity on small

CC molecule substrates of both trypsin and chymotrypsin.
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC PIR: A00958; KCUF.
 CC PDB: 1AZ2; 25-FEB-98.

DR MEROPS; S01.122;
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR001254; Ser_protease_Try.
 DR Pfam: PF00089; trypsin; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR SMART: SM00020; Tryp_Spc; 1.
 DR PROSITE; PS0240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Hydrolase: Serine protease: Collagen degradation; 3D-structure.

FT ACT_SITE 41 CHARGE RELAY SYSTEM.
 FT ACT_SITE 87 CHARGE RELAY SYSTEM.
 FT ACT_SITE 178 CHARGE RELAY SYSTEM.
 FT DISULFID 26 42
 FT DISULFID 151 164
 FT DISULFID 174 200
 FT CONFLICT 91 91
 FT CONFLICT 147 148 SN -> NS (IN REF. 1).
 FT CONFLICT 175 175 N -> D (IN REF. 1).
 FT CONFLICT 185 185 N -> D (IN REF. 1).
 SQ SEQUENCE 226 AA; E45591CAF332CE8C CRC64;

Query Match 65.5%; Score 36; DB 1; Length 226;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NSWPH 8
 |||||
 DB 10 NSWPH 14

RESULT 7

ILV5_NEUCR STANDARD; PRT; 400 AA.
 AC P38674;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Ketol-acid reductoisomerase, mitochondrial precursor (EC 1.1.1.86)
 DE (Acetylhydroxy-acid reductoisomerase) (Alpha-keto-beta-hydroxylacil
 reductoisomerase).
 GN ILV-2.
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariales; Sordariaceae; Neurospora.
 OX NCBI_TaxID=5141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93013010; PubMed=1398116;
 RA Sista H., Bowman B.;
 RT "Characterization of the ilv-2 gene from Neurospora crassa encoding
 alpha-keto-beta-hydroxylacil reductoisomerase.";
 RL Gene 120:115-118(1992).
 CC -!- CATALYTIC ACTIVITY: (R)-2,3-dihydroxy-3-methylbutanoate + NADP(+)
 CC -!- (S)-2-hydroxy-2-methyl-3-oxobutanoate + NADPH.
 CC -!- COFACTOR: REQUIRES MAGNESIUM.
 CC -!- PATHWAY: Valine and isoleucine biosynthesis; second step.
 CC -!- SUBCELLULAR LOCATION: Mitochondrial.
 CC -!- SIMILARITY: BELONGS TO THE KETOL-ACID REDUCTOISOMERASE FAMILY.
 CC -----
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 CC -----
 CC EMBL; M84189; AAB00797.1; -.

DR PIR: JCI428; JCI428.
 DR HSP; Q01292; LQMG.
 DR InterPro: IPR000506; Ach_isomrdctse.
 DR Pfam: PF01450; Ilvc; 1.
 DR TIGRFAMS; TIGR00465; ilvc; 1.
 KW Oxidoreductase; Branched-chain amino acid biosynthesis; Magnesium;
 KW NADP; Mitochondrion; Transist peptide.
 FT TRANSIT 1 26 MITOCHONDRION (POTENTIAL).
 FT CHAIN 27 400 KETOL-ACID REDUCTOISOMERASE.
 FT NP_BIND 90 99 NADPH (POTENTIAL).
 FT ACT_SITE 177 177 POTENTIAL.
 SQ SEQUENCE 400 AA; 44508 MW; D8AA4C0A3F4BD7CB CRC64;
 Query Match 65.5%; Score 36; DB 1; Length 400;
 Best Local Similarity 71.4%; Pred. No. 33;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QSNWPH 8

DB 156 QSETWPH 162

RESULT 8

KIT_CANFA STANDARD; PRT; 975 AA.
 AC O97799;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Mast/stem cell growth factor receptor precursor (EC 2.7.1.112) (SCFR)
 DE (Proto-oncogene tyrosine-protein kinase Kit) (c-kit).
 GN KIT.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99142897; PubMed=989791;
 RA Ma Y., Longley B.J., Wang X., Blount J.L., Langley K., Caughey G.H.;
 RT "Clustering of activating mutations in c-kit's juxtamembrane coding
 RT region in canine mast cell neoplasms.";
 RL J. Invest. Dermatol. 112:165-170(1999).
 CC -!- FUNCTION: THIS IS THE RECEPTOR FOR STEM CELL FACTOR (MAST CELL
 CC GROWTH FACTOR). IT HAS A TYROSINE-PROTEIN KINASE ACTIVITY.
 CC BINDING OF THE LIGANDS LEADS TO THE AUTOPHOSPHORYLATION KIT AND
 CC ITS ASSOCIATION WITH SUBSTRATES SUCH AS PHOSPHATIDYLINOSITOL
 CC 3-KINASE (PI3K).
 CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
 CC PROTEIN KINASES.
 CC -!- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
 CC -----
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 CC -----
 CC EMBL; AF044249; AAD02327.1; -.
 DR HSP; P11362; IFGK.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR003599; Ig.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003600; Ig_Like.
 DR InterPro: IPR001824; RTkinaseIII.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam; PF00047; Ig; 2.
 DR Pfam; PF00069; pkinase; 1.


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DR PRODom: PD000001; Euk_pkinase; 2.
DR SMART: SM00409; IG; 2.
DR SMART: SM00410; IG-like; 1.
DR SMART: SM00219; TyKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS00240; RECEPTOR_TYR_KIN_III; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
KW Proto-oncogene; Tyrosine-protein kinase; Receptor; Transmembrane;
KW Transferase; Glycoprotein; Phosphorylation; ATP-binding; Signal;
KW Immunoglobulin domain.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 975 MAST/STEM CELL GROWTH FACTOR RECEPTOR.
FT DOMAIN 25 519 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 520 542 POTENTIAL.
FT DOMAIN 543 975 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 588 936 PROTEIN KINASE.
FT NP_BIND 594 602 ATP (BY SIMILARITY).
FT BINDING 622 622 ATP (BY SIMILARITY).
FT ACT_SITE 791 791 BY SIMILARITY.
FT MOD_RES 822 822 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT CARBOHYD 96 96 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 132 132 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 147 147 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 286 286 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 296 296 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 303 303 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 355 355 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 370 370 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 403 403 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 466 466 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 489 489 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 975 AA; 109335 MW; 8F570BDB9F05B1CB CRC64;

Query Match 65.5%; Score 36; DB 1; Length 975;
Best Local Similarity 85.7%; Pred. No. 80;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QSN5WPH 8
Db 261 QSN5WHH 267
|||||

RESULT 9
ID CNA_STAAU STANDARD; PRT; 1183 AA.
AC Q53654;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Collagen adhesin precursor.
GN CNA.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FDA 574.
RX MEDLINE=92165839; PubMed=1311320;
RA Patti J.M., Jonsson H., Guss B., Switalski L.M., Wiberg K.,
RA Lindberg M., Hoeoek M.;
RT "Molecular characterization and expression of a gene encoding a
RT Staphylococcus aureus collagen adhesin.";
RL J. Biol. Chem. 267:4766-4772(1992).
RN [2]
RP ERRATUM.
RP Patti J.M., Jonsson H., Guss B., Switalski L.M., Wiberg K.,
RA Lindberg M., Hoeoek M.;
RL J. Biol. Chem. 269:11672-11672(1994).
RN [3]
RP COLLAGEN-BINDING DOMAIN.
RC STRAIN=FDA 574;
RX MEDLINE=94032261; PubMed=8218209;

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RA Patti J.M., Boles J.O., Hoeoek M.;
RT "Identification and biochemical characterization of the ligand
RT binding domain of the collagen adhesin from Staphylococcus aureus.";
RL Biochemistry 32:11428-11435(1993).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 169-318.
RX MEDLINE=97475225; PubMed=9334749;
RA Symersky J., Patti J.M., Carson M., House-Pompeo K., Teale M.,
RA Moore D., Jin L., Schneider A., Delucas L.J., Hoeoek M.,
RA Narayana S.V.L.;
RT "Structure of the collagen-binding domain from a Staphylococcus
RT aureus adhesin";
RL Nat. Struct. Biol. 4:833-838(1997).
CC -!- FUNCTION: MEDIATES ATTACHMENT OF STAPHYLOCOCCAL CELLS TO
CC COLLAGEN-CONTAINING SUBSTRATA.
CC -!- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (Potential).
CC -----
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CC -----
CC EMBL; M81736; AAA20874.1; -.
CC PDB; 1AMX; 24-JUN-98.
DR InterPro; IPR001899; Gram_pos_anchor.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR PROSITE; PS00847; GRAM_POS_ANCHORING; FALSE_NEG.
KW Cell wall; Peptidoglycan-anchor; Repeat; Signal; 3D-structure.
FT SIGNAL 1 29 POTENTIAL.
FT CHAIN 30 1154 COLLAGEN ADHESIN.
FT PROPEP 1155 1183 REMOVED BY SORTASE (POTENTIAL).
FT DOMAIN 151 318 COLLAGEN-BINDING.
FT DOMAIN 533 1093 3 X 187 AA APPROXIMATE TANDEM REPEATS.
FT DOMAIN 1093 1157 LYS/PRO-RICH (CELL WALL-SPANNING).
FT REPEAT 533 719 B1.
FT REPEAT 720 906 B2.
FT REPEAT 907 1093 B3.
FT SITE 1151 1155 LPXTG SORTING SIGNAL (POTENTIAL).
FT MOD_RES 1154 1154 AMIDE-LINKED TO CELL WALL (POTENTIAL).
SQ SEQUENCE 1183 AA; 133066 MW; B6A1CC072E575D76 CRC64;

Query Match 65.5%; Score 36; DB 1; Length 1183;
Best Local Similarity 62.5%; Pred. No. 98;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 QSN5WPH 9
Db 1040 ESNNTHT 1047
|||||

RESULT 10
AROL_PNECA STANDARD; PRT; 1581 AA.
ID AROL_PNECA
AC Q12659;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Pentafunctional AROM polypeptide [Includes: 3-dehydroquininate synthase
DE (EC 4.2.3.4); 3-dehydroquininate dehydratase (EC 4.2.1.10) (3-
DE dehydroquinase); Shikimate 5-dehydrogenase (EC 1.1.1.25); Shikimate
DE kinase (EC 2.7.1.71); 3-phosphoshikimate 1-carboxyvinyltransferase
DE (EC 2.5.1.19) (5-enolpyruvylshikimate-3-phosphate synthase) (EPSP
DE synthase) (EPSPS)].
GN AROM.
OS Pneumocystis carinii.
OC Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes; Pneumocystidaceae;
OC Pneumocystis.
OX NCBI_TaxID=4754;
RN [1]

```

SEQUENCE FROM N.A.
MEDLINE=94172285; PubMed=8126418;
Banerji S., Wakefield A.E., Allen A.G., Maskell D.J., Peters S.E.,
Hopkin J.M.;
"The cloning and characterization of the arom gene of Pneumocystis
carinii";
J. Gen. Microbiol. 139:2901-2914(1993).
CC -!- FUNCTION: THE AROM POLYPEPTIDE CATALYSES 5 CONSECUTIVE ENZYMATIC
CC REACTIONS IN PRECHORISMATE POLYAROMATIC AMINO ACID BIOSYNTHESIS.
CC -!- CATALYTIC ACTIVITY: 3-deoxy-arabino-heptulosonate 7-phosphate = 3-
CC dehydroquininate + phosphate.
CC -!- CATALYTIC ACTIVITY: 3-dehydroquininate = 3-dehydroshikimate + H(2)O.
CC -!- CATALYTIC ACTIVITY: Shikimate + NADP(+) = 5-dehydroshikimate +
CC NADPH.
CC -!- CATALYTIC ACTIVITY: ATP + shikimate = ADP + shikimate 3-phosphate.
CC -!- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate =
CC phosphate + 5-O-(1-carboxyvinyl)-3-phosphoshikimate.
CC -!- PATHWAY: SECOND TO SIXTH STEPS IN THE BIOSYNTHESIS OF CHORISMATE
CC WITHIN THE BIOSYNTHESIS OF AROMATIC AMINO ACIDS (THE SHIKIMATE
CC PATHWAY).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE
CC DEHYDROQUINATE SYNTHASE FAMILY.
CC -!- SIMILARITY: IN THE 3RD SECTION; BELONGS TO THE SHIKIMATE KINASE
CC FAMILY.
CC -!- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE SHIKIMATE
CC DEHYDROGENASE FAMILY.
CC -----
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CC -----
DR EMBL; L18918; AAA17839.1; -
DR HSPG; P07547; IDOS.
DR InterPro; IPR002658; DHQ_synthase.
DR InterPro; IPR001381; DHQsinase I.
DR InterPro; IPR001986; EPSP_synthase.
DR InterPro; IPR000623; Shik_kinase.
DR InterPro; IPR002907; Shikimate_DH.
DR Pfam; PF00275; EPSP_synthase; 1.
DR Pfam; PF01202; SKI; 1.
DR Pfam; PF01487; DHQsinase I; 1.
DR Pfam; PF01488; Shikimate_DH; 1.
DR Pfam; PF01761; DHQ_synthase; 1.
DR PRINTS; P01100; SHIKIMTKINASE.
DR PRODOM; PD001867; EPSP_synthase; 1.
DR TIGRFAMS; TIGR01093; arod; 1.
DR PROSITE; PS00104; EPSP_SYNTHASE_1; 1.
DR PROSITE; PS00885; EPSP_SYNTHASE_2; 1.
DR PROSITE; PS01028; DEHYDROQUINASE_I; 1.
DR PROSITE; PS01128; SHIKIMATE_KINASE; 1.
KW Aromatic amino acid biosynthesis; Multifunctional enzyme;
KW Oxidoreductase; Lyase; Transferase; Kinase; NADP; ATP-binding.
FT DOMAIN 1 383 3-DEHYDROQUINATE SYNTHASE.
FT DOMAIN 395 840 EPSP SYNTHASE.
FT DOMAIN 867 1042 SHIKIMATE KINASE.
FT DOMAIN 1043 1284 3-DEHYDROQUINASE.
FT DOMAIN 1297 1581 SHIKIMATE DEHYDROGENASE.
FT ACT_SITE 827 827 POTENTIAL.
FT ACT_SITE 875 882 ATP (POTENTIAL).
FT NP_BIND 1189 1189 BY SIMILARITY.
FT ACT_SITE 1217 1217 FORMS A SCHIFF-BASE INTERMEDIATE
FT ACT_SITE 1217 1217 (BY SIMILARITY).
CC SEQUENCE 1581 AA; 178043 MW; 417A84356061170F CRC64;
Query Match 65.5%; Score 36; DB 1; Length 1581;
Best Local Similarity 71.4%; Pred. No. 1.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 SNSWPH 9
Db 1176 NNSWPT 1182
RESULT 11
POLR_OYMW STANDARD; PRT; 1776 AA.
AC P20127;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE RNA replicase polyprotein (EC 2.7.7.48).
OS Ononis yellow mosaic virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Tymovirus.
OX NCBI_TaxID=12153;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90021186; PubMed=2800337;
RA Ding S.W., Keese P., Gibbs A.;
RT "Nucleotide sequence of the ononis yellow mosaic tymovirus genome.";
RL Virology 172:555-563(1989).
CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC [RNA](N).
CC -----
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CC -----
DR EMBL; J04375; AAA46796.1; -
DR PIR; J00106; RRPVYM.
DR MEROPS; C21.001;
DR InterPro; IPR001788; RNA_dep_RNAPol2.
DR InterPro; IPR000606; Viral_helicase1.
DR Pfam; PF00978; RNA_dep_RNAPol2; 1.
DR Pfam; PF01443; Viral_helicase1; 1.
KW Transferase; RNA-directed RNA polymerase; Polyprotein; ATP-binding.
FT NP_BIND 899 906 ATP (BY SIMILARITY).
SQ SEQUENCE 1776 AA; 198127 MW; 1C2E37B9EC3A5333 CRC64;
Query Match 65.5%; Score 36; DB 1; Length 1776;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3 SNSWPH 8
Db 1191 SNKWP 1196
RESULT 12
ALR2_VIBCH STANDARD; PRT; 392 AA.
ID ALR2_VIBCH
AC Q9KSE5;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Alanine racemase 2 (EC 5.1.1.1).
GN ALR2 OR VC1312.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=El Tor N16961 / Serotype O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,

RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen *Vibrio*
RT *cholerae*.";
RL Nature 406:477-483(2000).
CC -1- FUNCTION: Provides the D-alanine required for cell wall
CC biosynthesis (By similarity).
CC -1- CATALYTIC ACTIVITY: L-alanine -> D-alanine.
CC -1- COFACTOR: Pyridoxal phosphate (By similarity).
CC -1- PATHWAY: Along with D-alanine-D-alanine ligase, it makes up the
CC D-alanine branch of the peptidoglycan biosynthetic route.
CC -1- SIMILARITY: BELONGS TO THE ALANINE RACEMASE FAMILY.
CC -----
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CC -----
CC EMBL: AE004211; AAF94470.1; ALT_INIT.
CC TIGR: VC1312;
CC InterPro: IPR000821; Ala_racemase.
CC Pfam: PF00842; Ala_racemase; 1.
CC PRINTS: PR00992; ALARACEMASE.
CC PROSITE: PS00395; ALANINE_RACEMASE; 1.
CC Isomerase; Pyridoxal phosphate; Cell wall; Peptidoglycan synthesis;
CC Complete proteome.
CC ACT_SITE 59 59 CATALYTIC BASE SPECIFIC TO D-ALANINE
CC (BY SIMILARITY).
CC FT ACT_SITE 284 284 CATALYTIC BASE SPECIFIC TO L-ALANINE
CC (BY SIMILARITY).
CC FT BINDING 59 59 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC FT SEQUENCE 392 AA; 42498 MW; C0211DC2661691FD CRC64;
CC -----
CC Query Match 63.6%; Score 35; DB 1; Length 392;
CC Best Local Similarity 100.0%; Pred. No. 47;
CC Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC -----
CC QY 1 QQNSW 6
CC | | | | |
CC Db 24 QQNSW 29
CC -----
CC RESULT 13
CC KVI_V_HUMAN STANDARD; PRT; 108 AA.
CC AC P04430;
CC DT 13-AUG-1987 (Rel. 05, Created)
CC DT 13-AUG-1987 (Rel. 05, Last sequence update)
CC DT 15-JUL-1999 (Rel. 38, Last annotation update)
CC DE Ig kappa chain V-I region BAN.
CC OS Homo sapiens (Human).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CC OX NCBI_TaxID=9606;
CC RN [1]
CC RP SEQUENCE.
CC RX MEDLINE=86174817; PubMed=3083240;
CC RA Dwulet F.E., O'Connor T.P., Benson M.D.;
CC RT "Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";
CC RL Mol. Immunol. 23:73-78(1986).
CC DR PIR; A01878; KIHUBN.
CC DR HSSP; P80362; IWTLL.
CC DR InterPro; IPR003006; Ig_MHC.
CC DR InterPro; IPR003596; Ig_V.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IgV; 1.
CC DR Immunoglobulin V region; Anyloid.
CC KW Immunoglobulin V region; FRAMEWORK-1.
CC FT DOMAIN 1 23
CC FT DOMAIN 23 34 COMPLEMENTARITY-DETERMINING-1.

FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11840 MW; CD3FD944FE96FD37 CRC64;
CC -----
CC Query Match 61.8%; Score 34; DB 1; Length 108;
CC Best Local Similarity 66.7%; Pred. No. 19;
CC Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
CC -----
CC QY 1 QQNSWPHPT 9
CC | | | | |
CC Db 89 QQNSWPHPT 97
CC -----
CC RESULT 14
CC NU4M_PELSU STANDARD; PRT; 459 AA.
CC ID NU4M_PELSU
CC AC O79677;
CC DT 15-JUL-1999 (Rel. 38, Created)
CC DT 15-JUL-1999 (Rel. 38, Last sequence update)
CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
CC DE NADH-ubiquinone oxidoreductase chain 4 (EC 1.6.5.3).
CC GN MTND4 OR ND4.
CC OS Pelomedusa subrufa (African side-necked turtle).
CC OG Mitochondrion.
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Testudines; Pleurodira; Pelomedusidae; Pelomedusa.
CC OX NCBI_TaxID=44522;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RA Zardoya R.;
CC RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
CC CC -1- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol;
CC -----
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CC -----
CC EMBL: AF039066; RAD05057.1;
CC DR InterPro; IPR003918; NADHUb_Oxred4.
CC DR InterPro; IPR001750; Oxidored_q1.
CC DR InterPro; IPR00260; Oxidored_q5_N.
CC DR Pfam; PF00361; Oxidored_q1; 1.
CC DR Pfam; PF01059; Oxidored_q5_N; 1.
CC DR PRINTS; PR01437; NUOXDRDTASE4.
CC KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
CC SQ SEQUENCE 459 AA; 51629 MW; 89BC451BD09482CC CRC64;
CC -----
CC Query Match 61.8%; Score 34; DB 1; Length 459;
CC Best Local Similarity 71.4%; Pred. No. 83;
CC Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
CC -----
CC QY 3 SNSWPHPT 9
CC | | | | |
CC Db 188 TNSWAHT 194
CC -----
CC RESULT 15
CC TYTR_TRYCR STANDARD; PRT; 492 AA.
CC ID TYTR_TRYCR
CC AC P28593;
CC DT 01-DEC-1992 (Rel. 24, Created)
CC DT 01-DEC-1992 (Rel. 24, Last sequence update)
CC DT 15-JUN-2002 (Rel. 41, Last annotation update)
CC DE Trypanothione reductase (EC 1.6.4.8) (TR) (N(1),N(8))-

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DE bis(glutathionyl)spermidine reductase).
GN TPR.
OS Trypanosoma cruzi.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5693;
[1]
RN SEQUENCE FROM N.A. PubMed=2011150;
RX MEDLINE=91187059; PubMed=2011150;
RA Sullivan F.X., Walsh C.T.;
RT "Cloning, sequencing, overproduction and purification of
RT trypanothione reductase from Trypanosoma cruzi.";
RL Mol. Biochem. Parasitol. 44:145-148(1991).
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=Silvio;
RX MEDLINE=95255281; PubMed=7737173;
RA Borges A., Cunningham M.L., Tover J., Fairlamb A.H.;
RT "Site-directed mutagenesis of the redox-active cysteines of
RT Trypanosoma cruzi trypanothione reductase.";
RL Eur. J. Biochem. 228:745-752(1995).
RN [3]
RN X-RAY CRYSTALLOGRAPHY (3.3 ANGSTROMS).
RX MEDLINE=94211757; PubMed=8159665;
RA Lantwin C.B., Schlichting I., Kabsch W., Pai E.F., Krauth-Siegel R.L.;
RT "The structure of Trypanosoma cruzi trypanothione reductase in the
RT oxidized and NADPH reduced state.";
RL Proteins 18:161-173(1994).
RN [4]
RN X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RC STRAIN=Silvio;
RX MEDLINE=96367082; PubMed=8771196;
RA Zhang Y., Bond C.S., Bailey S., Cunningham M.L., Fairlamb A.H.,
RA Hunter W.N.;
RT "The crystal structure of trypanothione reductase from the human
RT pathogen Trypanosoma cruzi at 2.3-A resolution.";
RL Protein Sci. 5:52-61(1996).
CC -!- FUNCTION: TRYPAOTHIONE IS THE PARASITE ANALOG OF GLUTATHIONE;
CC THIS ENZYME IS THE EQUIVALENT OF GLUTATHIONE REDUCTASE.
CC -!- CATALYTIC ACTIVITY: NADPH + trypanothione = NADP(+) + reduced
CC trypanothione.
CC -!- COFACTOR: FAD.
CC -!- SUBUNIT: HOMODIMER.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- MISCELLANEOUS: THE ACTIVE SITE IS A REDOX-ACTIVE DISULFIDE BOND.
CC -!- SIMILARITY: BELONGS TO THE PYRIDINE NUCLEOTIDE-DISULFIDE
CC OXIDOREDUCTASES CLASS-I.
CC -----
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CC -----
DR EMBL: M38051; AAA63547.1; -.
DR EMBL: Z13958; CAA78360.1; -.
DR PIR: S30204; S30204.
DR PDB: 1NDA; 30-SEP-94.
DR PDB: 1AOG; 17-SEP-97.
DR InterPro: IPR001327; FAD_pyr_redox.
DR InterPro: IPR001100; Pyr_redox.
DR InterPro: IPR001864; Trypnrth_redctse.
DR InterPro: IPR004099; pyr_redox_dim.
DR Pfam: PF00070; pyr_redox; 1.
DR Pfam: PF02852; pyr_redox; 1.
DR PRINTS: PR00368; FADPNR.
DR PRINTS: PR00411; PNDROTASET.
DR PRINTS: PR00470; TRYPNARDTASE.
DR ProDom: PD000139; FAD_pyr_redox; 1.
DR PROSITE: PS00076; PYRIDINE_REDOX_1; 1.
KW Redox-active center; Oxidoreductase; Flavoprotein; FAD; NADP;
KW 3D-structure.

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FT NP_BIND 7 37 FAD (ADP PART) (PROBABLE).
FT DISULFID 53 58 REDOX-ACTIVE.
FT NP_BIND 317 327 FAD (FLAVIN PART) (BY SIMILARITY).
FT ACT_SITE 461 461 BY SIMILARITY.
FT VARIANT 95 95 K -> N (IN STRAIN SILVIO).
FT VARIANT 140 140 E -> A (IN STRAIN SILVIO).
FT VARIANT 156 156 N -> H (IN STRAIN SILVIO).
FT VARIANT 353 353 N -> T (IN STRAIN SILVIO).
FT VARIANT 402 403 NI -> KV (IN STRAIN SILVIO).
FT VARIANT 441 441 V -> I (IN STRAIN SILVIO).
SQ SEQUENCE 492 AA; 53868 MW; 4AF179952A20750F CRC64;

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Query Match 61.8%; Score 34; DB 1; Length 492;
 Best Local Similarity 83.3%; Pred. No. 89;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 SNSWPH 8

DB 161 SGSWPH 166

Search completed: November 18, 2002, 17:51:36
 Job time : 5.85526 secs

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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:40:56 : Search time 20.1316 Seconds
(without alignments)
92.115 Million cell updates/sec

Title: US-09-016-061-86
Perfect score: 55
Sequence: 1 QQNSNSWPT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44	80.0	1194	5 Q9VSI2	Q9vsi2 drosophila
2	39	70.9	413	10 Q9M9E4	Q9m9e4 arabidopsis
3	39	70.9	523	15 P89903	P89903 chimpanzee
4	39	70.9	581	10 Q9C9Q9	Q9c9q9 arabidopsis
5	38	69.1	242	16 Q8ZGE9	Q8zge9 versinia pe
6	38	69.1	242	16 Q8XEM3	Q8xem3 salmonella
7	38	69.1	271	16 Q8YJH2	Q8yjh2 brucella me
8	38	69.1	278	5 Q25679	Q25679 podocoryne
9	38	69.1	497	5 O01350	O01350 drosophila
10	38	69.1	1109	5 Q9VTB9	Q9vtb9 drosophila
11	38	69.1	1109	10 Q9ZVK6	Q9zvz6 arabidopsis
12	37	67.3	169	2 Q9AEG4	Q9aeg4 enterobacte
13	37	67.3	202	16 Q8XH10	Q8xh10 clostridium
14	37	67.3	656	5 Q9VSJ8	Q9vsj8 drosophila
15	37	67.3	693	5 Q8T0E9	Q8t0e9 drosophila
16	37	67.3	850	2 Q8VM80	Q8vm80 rhodococcus

17	37	67.3	919	4 Q9NOS7	Q9nos7 homo sapien
18	36	65.5	94	2 Q9XCE0	Q9xce0 mycobacteri
19	36	65.5	96	2 Q9Z9Y5	Q9z9y5 frateuria s
20	36	65.5	109	4 Q90LH5	Q90lh5 homo sapien
21	36	65.5	118	3 Q13548	Q13548 saccharomyc
22	36	65.5	270	5 Q27824	Q27824 uca pugilat
23	36	65.5	402	3 Q8X019	Q8x019 neurospora
24	36	65.5	455	16 Q9F388	Q9f388 streptomyce
25	36	65.5	458	16 Q8ZIF3	Q8zif3 yersinia pe
26	36	65.5	467	16 Q8ZRG3	Q8zrg3 salmonella
27	36	65.5	467	16 Q8Z912	Q8z912 salmonella
28	36	65.5	534	16 Q8ZC03	Q8zc03 yersinia pe
29	36	65.5	640	5 Q9XWZ6	Q9xwz6 caenorhabdi
30	36	65.5	978	6 Q9XS93	Q9xs93 canis famil
31	36	65.5	979	6 Q8WN23	Q8wn23 canis famil
32	36	65.5	993	4 Q8WXQ5	Q8wxq5 homo sapien
33	35	63.6	145	16 P73353	P73353 synecocyst
34	35	63.6	207	15 Q90LW6	Q90lw6 human immun
35	35	63.6	211	15 Q90LW7	Q90lw7 human immun
36	35	63.6	211	15 Q90LW5	Q90lw5 human immun
37	35	63.6	310	4 Q9BSV6	Q9bsv6 homo sapien
38	35	63.6	315	4 Q9H6H5	Q9h6h5 homo sapien
39	35	63.6	316	11 Q9CYW1	Q9cyw1 mus musculu
40	35	63.6	316	11 Q9SLV6	Q9slv6 mus musculu
41	35	63.6	374	11 Q88768	Q88768 rattus norv
42	35	63.6	374	11 Q9QU19	Q9qu19 rattus norv
43	35	63.6	390	4 Q9BVT1	Q9bvt1 homo sapien
44	35	63.6	419	11 Q63629	Q63629 rattus norv
45	35	63.6	458	3 Q96TV0	Q96tv0 debaryomyce

ALIGNMENTS

RESULT 1

Q9VSI2	ID	Q9VSI2	PRELIMINARY;	PRT;	1194 AA.
AC	Q9VSI2;				
DT	01-MAY-2000 (TrEMBLrel. 13, Created)				
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)				
DT	01-JUN-2001 (TrEMBLrel. 17, Last annotation update)				
DE	CG7112 protein.				
GN	CG7112.				
OS	Drosophila melanogaster (Fruit fly).				
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;				
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;				
OC	Ephydroidea; Drosophilidae; Drosophila.				
OX	NCBI_TaxID=7227;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=BERKELEY.				
RX	MEDLINE=20196006; PubMed=107311132;				
RA	Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,				
RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,				
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,				
RA	Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,				
RA	Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,				
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,				
RA	Abriil J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,				
RA	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,				
RA	Beeson K.Y., Benos P.V., Beriman B.P., Bhandari D., Bolshakov S.,				
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,				
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,				
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,				
RA	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,				
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,				
RA	Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,				
RA	Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,				
RA	Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,				
RA	Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck C.,				
RA	Hoskin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,				
RA	Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,				
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,				

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RA "The genome sequence of *Drosophila melanogaster*.";
RL Science 287:2185-2195(2000).
DR EMBL: AE003555; AAF50437.1; -;
DR FlyBase: FBgn0035879; CG7112.
DR InterPro: IPR000050; PID_domain.
DR InterPro: IPR000195; RabGAP_TBC.
DR Pfam: PF00566; TBC; 1.
DR SMART: SM00462; PTB; 1.
DR SMART: SM00164; TBC; 1.
SQ SEQUENCE 1194 AA; 133393 MW; E0E3DB547B4924E0 CRC64;
Query Match 80.0%; Score 44; DB 5; Length 1194;
Best Local Similarity 77.8%; Pred. No. 10;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 QQSNWPH 9
Db 461 QQSSWPT 469
RESULT 2
Q9M9E4 PRELIMINARY; PRT; 413 AA.
AC Q9M9E4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE F3F9.22.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Chao Q., Brooks S., Buehler E., Johnson-Hopson C., Khan S., Kim C.,
RA Shinn P., Altafi H., Bei Q., Chin C., Chlou J., Choi E., Conn L.,
RA Conway A., Gonzales A., Hansen N., Howng B., Koo T., Lam B., Lee J.,
RA Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M.,
RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
RA Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
RA Ecker J.R.;
RT "Genomic sequence for Arabidopsis thaliana BAC F3F9 from chromosome
I.";
RT Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RL SEQUENCE FROM N.A.
RN [2]
RA Ecker J.R.;
RP SEQUENCE FROM N.A.
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
RA Khan S., Kim C., Altafi H., Bei B., Chin C., Chlou J., Choi E.,
RA Conn L., Conway A., Gonzalez A., Hansen N., Howng B., Koo T., Lam B.,
RA Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,
RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
RA Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
RA Theologis A., Ecker J.;

RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC013430; AAF71805.1; -;
DR InterPro: IPR001611; LRR.
DR InterPro: IPR003591; LRR_typ.
DR Pfam: PF00560; LRR; 5.
DR PRINTS: PR00019; LEURICHRPT.
DR SMART: SM00369; LRR_typ; 1.
SQ SEQUENCE 413 AA; 45745 MW; 2F0D48E28FAF6A43 CRC64;
Query Match 70.9%; Score 39; DB 10; Length 413;
Best Local Similarity 75.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 QQSNWPH 8
Db 76 QSSNLMPH 83
RESULT 3
P89903 PRELIMINARY; PRT; 523 AA.
AC P89903;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE GAG polyprotein [Contains: core protein(s) P24].
GN GAG.
OS Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11723;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TANTALUS-1;
RX MEDLINE=97223354; PubMed=9123848;
RA Soares M.A., Robertson D.L., Hui H., Allan J.S., Shaw G.M., Hahn B.H.;
RT "A full-length and replication-competent proviral clone of SIVAGM from
tantalus monkeys.";
RL Virology 228:394-399(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=TANTALUS-1;
RA Soares M.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO GAG GENE PROTEIN P24 (CORE NUCLEOCAPSID PROTEIN).
DR EMBL: U58991; AAC57051.1; -;
DR HSP: P03351; LEIA.
DR InterPro: IPR000721; Gag_p24.
DR InterPro: IPR000071; Retrovir_p17.
DR InterPro: IPR001878; Znf_CCHC.
DR Pfam: PF00540; Gag_p17; 1.
DR Pfam: PF00607; Gag_p24; 1.
DR Pfam: PF00098; zf-CCHC; 2.
DR PRINTS: PR00939; C2HCZNFINGER.
DR PRINTS: PR00234; HIVIMATRIX.
DR SMART: SM00343; Znf_C2HC; 2.
KW AIDS; Core protein; Polyprotein.
KW AIDS; Core protein; Polyprotein.
SQ SEQUENCE 523 AA; 57688 MW; F623CED7277681AA CRC64;
Query Match 70.9%; Score 39; DB 15; Length 523;
Best Local Similarity 66.7%; Pred. No. 36;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 QQSNWPH 9
Db 145 QQNQWHT 153
RESULT 4
Q9C9Q9 PRELIMINARY; PRT; 581 AA.
AC Q9C9Q9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical 64.8 kDa protein.
GN T111.17 OR A1G78230.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=CV. COLUMBIA;
RX MEDLINE=21016719; PubMed=11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Dunn P., Egu P., Feldblum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kvan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziani A.,
RA Militischer J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
thaliana";
RL Nature 408:816-820(2000).
[2]
RN SEQUENCE FROM N.A.
RP Yamada K., Ban J., Chang C.H., Chang E., Dale J.M., Goldsmith A.D.,
RA Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Wu H.C.,
RA Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H., Cheuk R.,
RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Kim C., Lam B., Lin J., Meyers M.C., Miranda M.,
RA Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M.,
RA Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RT "Full length cDNA of gene A1G78230 (GI:15218262).";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC012680; AAG52107.1; -
DR EMBL: AY065224; AAL38700.1; -
DR InterPro: IPR001611; LRR.
DR InterPro: IPR003592; LRR_out.
DR InterPro: IPR003591; LRR_cyp.
DR Pfam: PF00360; LRR; 5.
DR PRINTS: PR00019; LEURICHRPT.
DR SMART: SM00370; LRR; 3.
DR SMART: SM00369; LRR_TVP; 3.
KW Hypothetical protein.
SQ SEQUENCE 581 AA; 64828 MW; 5E6AC53FDD49FD4 CRC64;

Query Match 70.9%; Score 39; DB 10; Length 581;
Best Local Similarity 75.0%; Pred. No. 40;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 QQNSWPH 8
| | | | |
DB 244 QSSNLWPH 251

RESULT 5
Q8ZGE9
ID Q8ZGE9 PRELIMINARY; PRT; 242 AA.
AC Q8ZGE9;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE Arginine transport ATP-binding protein.
GN ARTP OR YP01352.

OS Yersinia pestis.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Yersinia.
OX NCBI_TaxID=632;
RN SEQUENCE FROM N.A.
RP STRAIN=CO-92 / BIOVAR ORIENTALIS;
RX MEDLINE=21470413; PubMed=11586360;
RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
RA Prentice M.B., Sebahia M., James K.D., Churcher C., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdano-Tarraga A.M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Fellwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
RA Leather S., Mouton S., Oyston P.C.F., Quail M., Rutherford K.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
RL "Genome sequence of Yersinia pestis, the causative agent of plague";
RT Nature 413:523-527(2001).
DR EMBL: AJ414147; CAC90181.1; -
DR InterPro: IPR003593; AAA_ATPase.
DR Pfam: PF00003; ABC_tran; 1.
DR ProDom: PD000006; ABC_transportr; 1.
DR SMART: SM00382; AAA; 1.
DR PROSITE: PS00211; ABC_TRANSPORTER; 1.
KW ATP-binding; Complete proteome.
SQ SEQUENCE 242 AA; 26637 MW; 05B26E270030EACF CRC64;

Query Match 69.1%; Score 38; DB 16; Length 242;
Best Local Similarity 75.0%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 QQNSWPH 8
| | | | |
DB 89 QQNLWPH 96

RESULT 6
Q8XEM3
ID Q8XEM3 PRELIMINARY; PRT; 242 AA.
AC Q8XEM3;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE ABC superfamily (ATPmemb), arginine transport system (Arginine
transport ATP-binding protein Artp).
GN ARTP OR STM0891 OR STY0924.
OS Salmonella typhimurium, and
OS Salmonella typhi.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=602, 601;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
LT2";
RL Nature 413:852-856(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=S.typhi; STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Fellwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,

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RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrell B.G.;
RA "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi C718.";
RL Nature 413:848-852(2001).
DR EMBL: AE008737; AAL19826.1; -.
DR EMBL: AL627268; CAD05330.1; -.
DR InterPro: IPR003593; AAA_ATPase.
DR InterPro: IPR003439; ABC_transportr.
DR Pfam: PF00005; ABC_tran; 1.
DR ProDom: PD000006; ABC_transportr; 1.
DR SMART: SM00382; AAA; 1.
DR PROSITE: PS00211; ABC_TRANSPORTER; 1.
DR ATP-binding; Complete proteome.
SQ SEQUENCE 242 AA; 26933 MW; F8F6065B6E677F7F CRC64;

Query Match 69.1%; Score 38; DB 16; Length 242;
Best Local Similarity 75.0%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQNSNWP 8
DB 89 QQYNLWPH 96

RESULT 7
Q8YJH2 PRELIMINARY; PRT; 271 AA.
AC Q8YJH2;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Asparagine transport ATP-binding protein.
GN BMEI011.
OS Brucella melitensis.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29459;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=16M / ATCC 23456 / BIOTYPE 1;
RX MEDLINE=20020109; PubMed=11756688;
RA DelVecchio V.G., Kapral V., Redkar R.J., Patra G., Mujar C., Los T.,
RA Ivanova N., Anderson I., Bhattacharya A., Lykidis A., Reznik G.,
RA Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltzman E.,
RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
RA Haselkorn R., Kyrpides N., Overbeek R.;
RT "The genome sequence of the facultative intracellular pathogen
RT Brucella melitensis.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
DR EMBL: AE009454; AAL51293.1; -.
DR InterPro: IPR003593; AAA_ATPase.
DR InterPro: IPR003439; ABC_transportr.
DR Pfam: PF00005; ABC_tran; 1.
DR ProDom: PD000006; ABC_transportr; 1.
DR SMART: SM00382; AAA; 1.
DR PROSITE: PS00211; ABC_TRANSPORTER; 1.
DR Complete proteome.
SQ SEQUENCE 271 AA; 29464 MW; E9F55E6C7BF5B6F9 CRC64;

Query Match 69.1%; Score 38; DB 16; Length 271;
Best Local Similarity 75.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQNSNWP 8
DB 99 QQYNLWPH 106

RESULT 8
Q25679 PRELIMINARY; PRT; 278 AA.
ID Q25679;
AC Q25679;

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DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Hox1 protein.
GN HOX1.
OS Podocoryne carnea.
OC Eukaryota; Metazoa; Chndaria; Hydrozoa; Hydroida; Anthomedusae;
OC Hydractiniidae; Podocoryne.
OX NCBI_TaxID=6096;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95301097; PubMed=7781898;
RA Aerne B., Baader C.D., Schmid V.;
RT "Life stage and tissue-specific expression of the homeobox gene cnxol-
RT pc of the Hydrozoan Podocoryne carnea.";
RL Dev. Biol. 169:547-556(1995).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL: X81455; CAA57211.1; -.
DR TRANSFAC: T03733; -.
DR InterPro: IPR001356; Homeobox.
DR Pfam: PF00046; homeobox; 1.
DR PRINTS: PR00024; HOMEBOX.
DR ProDom: PD000010; Homeobox; 1.
DR SMART: SM00389; HOX; 1.
DR PROSITE: PS00027; HOMEBOX_1; 1.
DR PROSITE: PS00071; HOMEBOX_2; 1.
DR DNA-binding; Homeobox; Nuclear protein.
KW SEQUENCE 278 AA; 32680 MW; 259BD1156B271BA8 CRC64;

Query Match 69.1%; Score 38; DB 5; Length 278;
Best Local Similarity 85.7%; Pred. No. 29;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SNSWPT 9
DB 256 SNSWPT 262

RESULT 9
O01350 PRELIMINARY; PRT; 497 AA.
AC O01350;
DT 01-JUL-1997 (TReMBLrel. 04, Created)
DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE GAG protein.
GN BURDOCK\GAG OR GAG.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90136512; PubMed=2559313;
RA Tchurikov N.A., Gerasimova T.I., Johnson T.K., Barbakar N.I.,
RA Kenzior A.L., Georgiev G.P.;
RT "Mobile elements and transposition events in the cut locus of
RT Drosophila melanogaster.";
RL Mol. Gen. Genet. 219:241-248(1989).
RN [2]
RP SEQUENCE FROM N.A.
RA Tchurikov N.A., Ponomarenko N.A., Krasnov A.N.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: U89994; AAB50147.1; -.
DR FlyBase: FBgn0043782; Burdock\gag.
SQ SEQUENCE 497 AA; 56804 MW; 6498A941089BCD4A CRC64;

Query Match 69.1%; Score 38; DB 5; Length 497;
Best Local Similarity 85.7%; Pred. No. 52;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 QQSNSWP 7
DB 381 QQNSWP 387

RESULT 10
Q9VTB9 PRELIMINARY; PRT; 1109 AA.
AC Q9VTB9
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE CG7958 protein.
GN CG7958
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY.
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.E.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abrial J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrieria S., Fleischmann W.,
RA Foslter C., Gabriellian A.C., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harrits N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Wellenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL; AE003547; AAF50133.1;
DR FlyBase; FBgn0036103; CG7958.
DR InterPro; IPR004181; znf_MIZ.
DR Pfam; PF02891; znf-MIZ; 1.
SQ SEQUENCE 1109 AA; 116491 MW; 4FD726183EE642AC CRC64;

Query Match 69.1%; Score 38; DB 5; Length 1109;
Best Local Similarity 55.6%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQSNSWP 9
DB 1 : : : : :

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DB 591 QMNTNWPHT 599

RESULT 11
Q9ZVX6 PRELIMINARY; PRT; 1109 AA.
AC Q9ZVX6
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative disease resistance protein.
GN AT2G16870.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ranning C.M., Koo H., Moffat K.S.,
RA Cronin L.A., Shen M., VanAken S.E., Unayam L., Tallon L.J., Gill J.E.,
RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
RA Salzberg S.L., Fraser C.M., Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
thaliana."
RL Nature 402:761-768(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Lin X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC005167; AAC64218.1;
DR InterPro; IPR000767; Disease_resist.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR002182; NB-ARC.
DR InterPro; IPR000157; TIR_domain.
DR Pfam; PF00560; LRR; 4.
DR Pfam; PF00931; NB-ARC; 1.
DR Pfam; PF01582; TIR; 1.
DR PRINTS; PR00364; DISEASERSIST.
DR SMART; SM00255; TIR; 1.
SQ SEQUENCE 1109 AA; 125680 MW; 865678FBC55DE694 CRC64;

Query Match 69.1%; Score 38; DB 10; Length 1109;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQSNSWPHT 9
DB 900 QQOHSWEHT 908

RESULT 12
Q9AEG4 PRELIMINARY; PRT; 169 AA.
AC Q9AEG4
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Putative AefA protein (Fragment).
GN AEFa.
OS Enterobacter aerogenes (Aerobacter aerogenes).
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Enterobacter.
OX NCBI_TaxID=548;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BW16627;

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RA Pradel E., Pages J.M.;
RT "rhe AcrA/AcrB/TolC efflux pump participates in multidrug resistance
RT in Enterobacter aerogenes.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ306389; CAC35722.1; -.
FT NON_TER 169
SQ SEQUENCE 169 AA; 19014 MW; 33BEC250079FD0E5 CRC64;

Query Match
Best Local Similarity 67.3%; Score 37; DB 2; Length 169;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQSNSWPH 8
Db I:|||||
2 QHTNRWPH 9

RESULT 13
O8XH10 PRELIMINARY; PRT; 202 AA.
AC QXKH10;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Hypothetical protein CPE2504.
GN CPE2504.
OS Clostridium perfringens.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC Clostridiales; Clostridiaceae; Clostridium.
OX NCBI_TaxID=1502;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=13 / TYPE A;
RX PubMed=11792842;
RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
RT "Complete genome sequence of Clostridium perfringens, an anaerobic
RT flesh-eater.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
DR EMBL: AP003194; BAB82210.1; -.
DR InterPro: IPR002819; HD.
DR Pfam: PF01966; HD; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 202 AA; 23318 MW; 85673772D327E774 CRC64;

Query Match
Best Local Similarity 67.3%; Score 37; DB 16; Length 202;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QSNPWPH 9
Db |||||
52 QSNPWTH 59

RESULT 14
Q9VSJ8 PRELIMINARY; PRT; 656 AA.
AC QVSJ8;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE ANON-D52 protein.
GN EXO70 OR ANON-D52 OR CG7127.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

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RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballou R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burks K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrier S., Fleischmann W.,
RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalili M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL: AF003553; AAF50421.1; -.
DR FlyBase: FBgn010431; exo70.
DR InterPro: IPR004140; Exo70.
DR Pfam: PF03081; Exo70; 1.
SQ SEQUENCE 656 AA; 75789 MW; DB4311709EDEF52 CRC64;

Query Match
Best Local Similarity 67.3%; Score 37; DB 5; Length 656;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSNSWPH 8
Db I:|||||
195 QKSNSWGH 202

RESULT 15
Q8TOE9 PRELIMINARY; PRT; 693 AA.
AC Q8TOE9;
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE LD07014p.
GN EXO70.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nunco J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,

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RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY069366; AAL39511.1; -.
SQ SEQUENCE 693 AA; 80060 MW; E3BA3BC08B03359C CRC64;

Query Match 67.3%; Score 37; DB 5; Length 693;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSNSWPH 8
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Db 232 QKSNSNGH 239

Search completed: November 18, 2002, 17:54:33
Job time : 21.1316 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:31:45 ; Search time 26.4079 Seconds
(without alignments)
45.413 Million cell updates/sec

Title: US-09-016-061-86

Perfect score: 55

Sequence: 1 QQSNSWPHT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query		Length	DB	ID	Description
	Score	Match				
1	55	100.0	9	19	AAW76033	LM609 grafted anti
2	55	100.0	9	20	AAW06372	Murine monoclonal
3	55	100.0	9	22	AAB61391	Mutant VL CDR3 pep
4	55	100.0	107	13	AAW25729	Humanised VL regio
5	55	100.0	107	22	AAB69677	Murine CMV5 antibo
6	55	100.0	107	22	AAB69678	Humanised CMV5 ant
7	55	100.0	107	22	AAB69690	Human woi antibody
8	55	100.0	109	20	AAW06388	Humanised LM609 an
9	55	100.0	109	20	AAW06380	Murine monoclonal
10	55	100.0	109	20	AAW06382	Humanised LM609 an

11	55	100.0	127	15	AA854093	Sequence of mouse
12	55	100.0	127	22	AA854093	Murine CMV5 antibody
13	50	90.9	259	21	AA859687	TMV 30K movement p
14	49	89.1	9	19	AA830975	LM609 grafted anti
15	49	89.1	9	19	AAW76034	LM609 grafted anti
16	49	89.1	9	22	AAW76013	LM609 VL CDR3 pept
17	49	89.1	9	22	AA861371	Mutant VL CDR3 pep
18	49	89.1	107	14	AA861392	HYH light chain.
19	49	89.1	107	14	AA838601	LM609 grafted anti
20	49	89.1	107	19	AAW76006	Vitaxin antibody 1
21	49	89.1	107	19	AAW76002	LM609 antibody lig
22	49	89.1	107	19	AAW76004	Murine HYH antibody
23	49	89.1	107	22	AAW58482	A light chain vari
24	49	89.1	107	22	AA863588	A light chain vari
25	49	89.1	107	22	AA863590	Vitaxin light chai
26	49	89.1	107	22	AA861360	Antibody LM609 lig
27	49	89.1	107	22	AA861362	Light chain variab
28	49	89.1	108	12	AA861364	Light chain variab
29	49	89.1	109	15	AA815438	Light chain variab
30	49	89.1	109	15	AA852203	Light chain variab
31	49	89.1	143	18	AAW19580	Mouse anti-Idiotyp
32	46	83.6	240	12	AA815443	Single chain Fv fr
33	46	83.6	105	20	AAW87456	JK gene product.
34	46	83.6	105	20	AAW87458	Humanised anti- α p
35	46	83.6	107	20	AAW84098	Humanised anti- α p
36	46	83.6	108	20	AAW84094	Murine vitronectin
37	46	83.6	112	20	AAW84100	Vitronectin alpha-
38	42	80.0	1194	22	AB8623985	Drosophila melanog
39	42	76.4	101	20	AAW89161	Anti-p53 monoclon
40	42	76.4	20	20	AAW89169	Anti-p53 monoclon
41	42	76.4	82	23	ABP34862	Human ORF3835 prot
42	42	76.4	107	14	AA832129	Anti-IL2R beta ant
43	42	76.4	109	20	AAW89176	Anti-p53 monoclon
44	42	76.4	114	22	AAW898665	Murine protein #2.
45	42	76.4	240	14	AA834510	Fv(TU27). Homo sa
46	41	74.5	9	19	AAW76036	LM609 grafted anti

ALIGNMENTS

RESULT. T 1

RESULTS 1
AAW76033
ID AAW76033 standard: Protein: 9 AA:

AA AAW76033:

XX
DT 02-NOV-1998 (first entry)

DE LM609 grafted antibody V-L region CDR3 protein fragment #2.

Vitaxin; antibody; variable region; heavy chain; light chain; integrin; LM609; inhibitor; integrin-mediated signal transduction; treatment; diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy; neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine; macular degeneration; osteoporosis; primer; V-L region; CDR; complementarity determining region.

AA
OS
Mus. Sp.

XX PN WO9833919-A2

XX
PD
06-AUG-1998

XX
PF 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

XX PA (IXSY-) IXSYS INC.

AA	Glaser SM,	Huse WD:
PI		

AA
DR WPI; 1998-437472/37.

DR N-PSDB: AAV49870.

XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
PS Claim 62; Page 41; 129pp; English.
XX
CC AA76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphaVbeta3 and can be used to
CC inhibit binding of alphaVbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphaVbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
CC antibodies contain non-murine framework regions so are suitable for use
CC in humans. Enhanced types of LM609 have affinity more than 90 times
CC greater than that of parent the parent antibody.
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 55; DB 19; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQSNSWPHT 9
| | | | | | | |
Db 1 QQSNSWPHT 9

RESULT 2
AAY06372
ID AAY06372 standard; Peptide; 9 AA.
XX
AC AAY06372;
XX
DT 06-SEP-1999 (first entry)
XX
DE Murine monoclonal antibody LM609 VL CDR3.
XX
KW Humanised antibody; antibody humanisation; antibody engineering;
KW LM609; monoclonal antibody; complementarity determining region;
KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
KW cancer; therapy; diagnosis.
XX
OS Mus musculus.
XX
PN WO9929888-A1.
XX
PD 17-JUN-1999.
XX
PF 04-DEC-1998; 98WO-US25828.
XX
PR 05-DEC-1997; 97US-0986016.
XX
XX (SCRI) SCRIPPS RES INST.
XX
PA Barbas CF, Rader C;
XX
PI WPI; 1999-394979/33.
XX
DR Production of humanized mouse monoclonal antibodies
XX
PT Disclosure; Page 45; 55pp; English.
XX
XX This sequence represents complementarity determining region 3
CC (CDR3) of the light chain of murine monoclonal antibody LM609.
CC LM629 is directed to integrin alpha-v beta-3. It selectively
CC promotes apoptosis of vascular cells stimulated to undergo
CC angiogenesis, making it a tool for cancer diagnosis and therapy.
CC The invention provides humanised antibodies, especially humanised

CC LM609. In such humanized antibodies, a light chain CDR from a
CC mouse antibody such as LM609 is grafted onto a human light chain.
CC and a heavy chain CDR from a mouse antibody is grafted onto a human
CC antibody heavy chain to produce libraries from which a humanised
CC murine antibody having the desired specificity is selected. By
CC preserving the original CDR sequences such as the HCDR3 and LCDR3
CC sequences of LM609, the humanisation strategy ensures epitope
CC conservation.
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 55; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQSNSWPHT 9
| | | | | | | |
Db 1 QQSNSWPHT 9

RESULT 3
AAB61391
ID AAB61391 standard; peptide; 9 AA.
XX
AC AAB61391;
XX
DT 03-APR-2001 (first entry)
XX
DE Mutant VL CDR3 peptide #1.
XX
KW LM609; grafted antibody; alphaVbeta_3 integrin; angiogenesis;
KW inflammatory; cancer; retina; restenosis; osteoporosis.
XX
OS Unidentified.
XX
PN WO200078815-A1.
XX
PD 28-DEC-2000.
XX
PF 23-JUN-2000; 2000WO-US17454.
XX
PR 24-JUN-1999; 99US-0339922.
XX
XX (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX
PI Huse WD, Wu H;
XX
DR WPI; 2001-050110/06.
XX
PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity
PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
PT osteoporosis -
XX
PS Disclosure; Page 41; 132pp; English.
XX
XX The present invention relates to enhanced LM609 grafted antibodies
CC exhibiting selective binding affinity to alphaVbeta_3 integrin or
CC their functional fragments. The antibodies or their functional
CC fragments can be used in the diagnosis and treatment of
CC alphaVbeta_3-mediated diseases such as angiogenesis, inflammatory
CC diseases (such as psoriasis and chronic articular rheumatism),
CC disorders associated with inappropriate or inopportune invasion of
CC vessels (such as diabetic retinopathy, neovascular glaucoma and
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
CC diseases (such as macular degeneration), restenosis and
CC osteoporosis.
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 55; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSNSWPHT 9
 Db 1 QOSNSWPHT 9

RESULT 4
 AAR25729
 ID AAR25729 standard; Protein; 107 AA.

XX AC AAR25729;
 XX AC AAR25729;
 DT 13-JAN-1993 (first entry)
 XX Humanised VL region of the mouse CMV5 antibody.
 DE Murine; immunoglobulin; CDR; non immunogenic; cytomegalovirus;
 KW GH; light chain; variable region; framework; human; Wol.
 XX Mus musculus.

XX Key Location/Qualifiers
 FH Region 24..34
 FT /note= "CDR"
 FT Region 50..56
 FT /note= "CDR"
 FT Region 89..97
 FT /note= "CDR"
 FT Misc-difference 49
 FT /note= "mutated residue"

XX WO9211018-A.
 PN 09-JUL-1992.
 XX 19-DEC-1991; 91WO-US09711.
 XX 19-DEC-1990; 90US-0634278.
 PR (PROT-) PROTEIN DESIGN LABS INC.

XX Co MS, Coelling KL, Landolfi NF, Queen CL, Schneider WP;
 XX WPI; 1992-249842/30.
 XX New immunoglobulin(s) having murine CDRs in human framework
 PT regions - have lower antigenicity; useful for treating e.g. HSV,
 PT CMV, T-cell disorders, myeloid disorders and auto-immune
 PT conditions

XX Claim 40; Fig 27A; 141pp; English.
 XX The sequence shows the humanised mature light chain variable
 CC region of the mouse CMV5 antibody. Murine CDRs were used
 CC in a human Wol framework to produce a pure humanised immunoglobulin
 CC (Ig) which is capable of binding to the gH glycoprotein of
 CC cytomegalovirus. The Ig is non immunogenic, due to the human
 CC framework, and has a strong affinity for its predetermined
 CC antigen. They can be produced in large quantities via recombinant
 CC DNA and monoclonal antibody technology. The humanised Igs may be
 CC used alone or in combination with chemotherapeutic agents such as
 CC non-steroidal anti-inflammatory drugs or immunosuppressants.
 CC See also AAR25721-32.

XX Sequence 107 AA;
 CC Query Match 100.0%; Score 55; DB 13; Length 107;
 CC Best Local Similarity 100.0%; Pred. No. 0.026;
 CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSNSWPHT 9
 Db 89 QOSNSWPHT 97

RESULT 5
 AAB69677
 ID AAB69677 standard; Protein; 107 AA.

XX AC AAB69677;
 XX AC AAB69677;
 DT 30-APR-2001 (first entry)
 XX Murine CMV5 antibody light chain SEQ ID NO: 62.

XX Humanised immunoglobulin; mouse; human; antibody; heavy chain; diabetes;
 KW light chain; graft versus host disease; transplant; autoimmune disease;
 KW multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus;
 KW myasthenia gravis; herpes infection; myeloid leukaemia; CMV infection.

XX Mus sp.
 PN US6180370-B1.

XX 30-JAN-2001.
 XX 07-JUN-1995; 95US-0484537.
 XX 28-DEC-1988; 88US-0290975.
 PR 13-FEB-1989; 89US-0310252.
 PR 28-SEP-1990; 90US-0590274.
 PR 19-DEC-1990; 90US-0634278.

XX (PROT-) PROTEIN DESIGN LABS INC.
 PA Queen CL, Sellick HE;
 XX WPI; 2001-190856/19.

XX Producing humanized immunoglobulin, involves producing a cell
 PT containing DNA segments encoding humanized heavy and light chain
 PT variable regions, and expressing the DNA segments in the cell -
 XX Disclosure; Fig 6; 145pp; English.

XX The present invention describes a method of producing humanised
 CC immunoglobulins involving expressing in a cell a nucleic acid encoding a
 CC humanised version of an immunoglobulin. This is obtained by comparing a
 CC donor and human immunoglobulin and producing a combined antibody which
 CC contains part of each. These are useful in the treatment of
 CC graft-versus-host disease, transplant rejection, autoimmune diseases such
 CC as diabetes, rheumatoid arthritis, myasthenia gravis, multiple sclerosis
 CC and systemic lupus erythematosus, herpes infections, CMV virus infections
 CC and myeloid leukaemia. The present sequence is an antibody used to
 CC demonstrate the method of the invention.

XX Sequence 107 AA;
 CC Query Match 100.0%; Score 55; DB 22; Length 107;
 CC Best Local Similarity 100.0%; Pred. No. 0.026;
 CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSNSWPHT 9
 Db 89 QOSNSWPHT 97

RESULT 6
 AAB69678
 ID AAB69678 standard; Protein; 107 AA.

XX AC AAB69678;
 XX AC AAB69678;
 DT 30-APR-2001 (first entry)
 XX Humanised CMV5 antibody light chain SEQ ID NO: 63.

XX	Humanised immunoglobulin; mouse; human; antibody; heavy chain; diabetes; light chain; graft versus host disease; transplant; autoimmune disease; multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus; myasthenia gravis; herpes infection; myeloid leukaemia; CMV infection.
OS	Mus sp.
OS	Homo sapiens.
XX	
XX	US6180370-B1.
XX	
XX	30-JAN-2001.
XX	
XX	07-JUN-1995; 95US-0484537.
XX	
XX	28-DEC-1988; 88US-0290975.
PR	13-FEB-1989; 89US-0310252.
PR	28-SEP-1990; 90US-0590274.
PR	19-DEC-1990; 90US-0634278.
XX	
XX	(PROT-) PROTEIN DESIGN LABS INC.
XX	
PI	Queen CL, Selick HE;
XX	
XX	WPI; 2001-190856/19.
XX	
XX	Producing humanized immunoglobulin, involves producing a cell containing DNA segments encoding humanized heavy and light chain variable regions, and expressing the DNA segments in the cell - disclosure; Fig 6; 145pp; English.
XX	
XX	The present invention describes a method of producing humanised immunoglobulins involving expressing in a cell a nucleic acid encoding a humanised version of an immunoglobulin. This is obtained by comparing a donor and human immunoglobulin and producing a combined antibody which contains part of each. These are useful in the treatment of
CC	CC graft-versus-host disease, transplant rejection, autoimmune diseases such as diabetes, rheumatoid arthritis, myasthenia gravis, multiple sclerosis and systemic lupus erythematosus; herpes infections, CMV virus infections and myeloid leukaemia. The present sequence is an antibody used to demonstrate the method of the invention.
XX	
XX	Sequence 107 AA;
XX	
Query Match	100.0%; Score 55; DB 22; Length 107;
Best Local Similarity	100.0%; Pred. No. 0.026;
Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY	1 QQNSWPHT 9
Db	89 QQNSWPHT 97
RESULT 7	
AAB69690	
ID	AAB69690 standard; Protein; 107 AA.
AC	AAB69690;
XX	
XX	
DT	30-APR-2001 (first entry)
XX	
DE	Human Wol antibody light chain SEQ ID NO: 87.
XX	
XX	Humanised immunoglobulin; mouse; human; antibody; heavy chain; diabetes; light chain; graft versus host disease; transplant; autoimmune disease; multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus; myasthenia gravis; herpes infection; myeloid leukaemia; CMV infection.
OS	Homo sapiens.
XX	
XX	US6180370-B1.
XX	

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PD 17-JUN-1999.
XX
XX 04-DEC-1998; 98WO-US25828.
XX
XX 05-DEC-1997; 97US-0986016.
XX
XX (SCRI ) SCRIPPS RES INST.
XX
XX Barbas CF, Rader C;
XX
XX WPI; 1999-394979/33.
XX
XX Production of humanized mouse monoclonal antibodies
XX
XX Disclosure; Page 52; 55pp; English.
XX
XX This sequence represents the light chain variable region of a
XX humanised LM609 antibody. LM609 is directed to human integrin
XX alpha-v beta-3. It selectively promotes apoptosis of vascular
XX cells that have been stimulated to undergo angiogenesis, making it
XX a tool for cancer diagnosis and therapy. The invention provides
XX humanised antibodies, especially humanised LM609. In such humanized
XX antibodies, a light chain CDR from a mouse antibody such as LM609 is
XX grafted onto a human light chain, and a heavy chain CDR from a mouse
XX antibody is grafted onto a human antibody heavy chain to produce
XX libraries from which a humanised murine antibody having the desired
XX specificity is selected. By preserving the original CDR sequences
XX such as the HCDR3 and LCDR3 sequences of LM609 (see AAY06371-72), the
XX humanisation strategy ensures epitope conservation.
XX
XX Sequence 109 AA;
XX
XX Query Match 100.0%; Score 55; DB 20; Length 109;
XX Best Local Similarity 100.0%; Pred. No. 0.027;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 QOSNSWPHT 9
DB 89 QOSNSWPHT 97
XX
RESULT 9
AAY06380
ID AAY06380 standard; Protein; 109 AA.
XX
XX AAY06380;
XX
XX 06-SEP-1999 (first entry)
XX
XX Murine monoclonal antibody LM609 V lambda.
XX
XX Humanised antibody; antibody humanisation; antibody engineering;
XX LM609; monoclonal antibody; complementarity determining region;
XX CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
XX cancer; therapy; diagnosis.
XX
XX Mus musculus.
XX
XX Key Location/Qualifiers
XX Peptide 1..2
XX Region /note= "vector-encoded residues"
XX Region 24..34
XX Region /note= "CDR1"
XX Region 50..56
XX Region /note= "CDR2"
XX Region 89..97
XX Region /note= "CDR3"
XX
XX WO9929888-A1.
XX
XX 17-JUN-1999.
XX
XX 04-DEC-1998; 98WO-US25828.
XX
XX 05-DEC-1997; 97US-0986016.
XX
XX (SCRI ) SCRIPPS RES INST.
XX
XX Barbas CF, Rader C;
XX
XX WPI; 1999-394979/33.
XX
XX Production of humanized mouse monoclonal antibodies
XX
XX Disclosure; Page 52; 55pp; English.
XX
XX This sequence represents the light chain variable region of a
XX humanised LM609 antibody. LM609 is directed to human integrin
XX alpha-v beta-3. It selectively promotes apoptosis of vascular
XX cells that have been stimulated to undergo angiogenesis, making it
XX a tool for cancer diagnosis and therapy. The invention provides
XX humanised antibodies, especially humanised LM609. In such humanized
XX antibodies, a light chain CDR from a mouse antibody such as LM609 is
XX grafted onto a human light chain, and a heavy chain CDR from a mouse
XX antibody is grafted onto a human antibody heavy chain to produce
XX libraries from which a humanised murine antibody having the desired
XX specificity is selected. By preserving the original CDR sequences
XX such as the HCDR3 and LCDR3 sequences of LM609 (see AAY06371-72), the
XX humanisation strategy ensures epitope conservation.
XX
XX Sequence 109 AA;
XX
XX Query Match 100.0%; Score 55; DB 20; Length 109;
XX Best Local Similarity 100.0%; Pred. No. 0.027;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 QOSNSWPHT 9
DB 89 QOSNSWPHT 97
XX
RESULT 9
AAY06380
ID AAY06380 standard; Protein; 109 AA.
XX
XX AAY06380;
XX
XX 06-SEP-1999 (first entry)
XX
XX Murine monoclonal antibody LM609 V lambda.
XX
XX Humanised antibody; antibody humanisation; antibody engineering;
XX LM609; monoclonal antibody; complementarity determining region;
XX CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
XX cancer; therapy; diagnosis.
XX
XX Mus musculus.
XX
XX Key Location/Qualifiers
XX Peptide 1..2
XX Region /note= "vector-encoded residues"
XX Region 24..34
XX Region /note= "CDR1"
XX Region 50..56
XX Region /note= "CDR2"
XX Region 89..97
XX Region /note= "CDR3"
XX
XX WO9929888-A1.
XX
XX 17-JUN-1999.
XX
XX 04-DEC-1998; 98WO-US25828.
XX
XX 05-DEC-1997; 97US-0986016.
XX
XX (SCRI ) SCRIPPS RES INST.
XX
XX Barbas CF, Rader C;
XX
XX WPI; 1999-394979/33.
XX
XX Production of humanized mouse monoclonal antibodies
XX
XX Disclosure; Page 49-50; 55pp; English.
XX
XX This sequence represents the light chain V lambda region of
XX murine monoclonal antibody LM609. LM609 is directed to integrin
XX alpha-v beta-3. It selectively promotes apoptosis of vascular
XX cells that have been stimulated to undergo angiogenesis, making it
XX a tool for cancer diagnosis and therapy. The invention provides
XX humanised antibodies, especially humanised LM609. In such humanized
XX antibodies, a light chain CDR from a mouse antibody such as LM609 is
XX grafted onto a human light chain, and a heavy chain CDR from a mouse
XX antibody is grafted onto a human antibody heavy chain to produce
XX libraries from which a humanised murine antibody having the desired
XX specificity is selected. By preserving the original CDR sequences
XX such as the HCDR3 and LCDR3 sequences of LM609 (see AAY06371-72), the
XX humanisation strategy ensures epitope conservation.
XX
XX Sequence 109 AA;
XX
XX Query Match 100.0%; Score 55; DB 20; Length 109;
XX Best Local Similarity 100.0%; Pred. No. 0.027;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 QOSNSWPHT 9
DB 89 QOSNSWPHT 97
XX
RESULT 10
AAY06382
ID AAY06382 standard; Protein; 109 AA.
XX
XX AAY06382;
XX
XX 06-SEP-1999 (first entry)
XX
XX Humanised LM609 antibody VL domain.
XX
XX Humanised antibody; antibody humanisation; antibody engineering;
XX LM609; monoclonal antibody; complementarity determining region;
XX CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
XX cancer; therapy; diagnosis.
XX
XX Homo sapiens.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Peptide 1..2
XX Region /note= "vector-encoded residues"
XX Region 24..34
XX Region /note= "CDR1"
XX Region 50..56
XX Region /note= "CDR2"
XX Region 89..97
XX Region /note= "CDR3"
XX
XX WO9929888-A1.
XX
XX 17-JUN-1999.
XX
XX 04-DEC-1998; 98WO-US25828.
XX
XX 05-DEC-1997; 97US-0986016.
```


XX (SCRI) SCRIPPS RES INST.
 PA Barbas CF, Rader C;
 XX WPI; 1999-394979/33.
 DR Production of humanized mouse monoclonal antibodies
 XX Disclosure; Page 50; 55pp; English.
 XX This sequence represents the light chain variable region of a
 CC humanised LM609 antibody. LM609 is directed to human integrin
 CC alpha-v beta-3. It selectively promotes apoptosis of vascular
 CC cells that have been stimulated to undergo angiogenesis, making it
 CC a tool for cancer diagnosis and therapy. The invention provides
 CC humanised antibodies, especially humanised LM609. In such humanized
 CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
 CC grafted onto a human light chain, and a heavy chain CDR from a mouse
 CC antibody is grafted onto a human antibody heavy chain to produce
 CC libraries from which a humanised murine antibody having the desired
 CC specificity is selected. By preserving the original CDR sequences
 CC such as the HCDR3 and LCDR3 sequences of LM609 (see AAY06371-72), the
 CC humanisation strategy ensures epitope conservation.
 XX SQ Sequence 109 AA;
 Query Match 100.0%; Score 55; DB 20; Length 109;
 Best Local Similarity 100.0%; Pred. No. 0.027;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QQSNSWPHT 9
 Db 89 QQSNSWPHT 97
 RESULT 11
 AAR54093
 ID AAR54093 standard; Protein; 127 AA.
 AC AAR54093;
 XX 29-DEC-1994 (first entry)
 DT
 DE Sequence of mouse V-kappa showing the sequences of recombinant
 DE anti-FHV-1 antibody CDRs 1, 2 and 3.
 XX Feline herpes virus; FHV-1; monoclonal antibody; CDR;
 KW complementarity determining region.
 XX Mus musculus.
 OS
 XX Key Location/Qualifiers
 FH Peptide 1..20
 FT /label= leader
 FT Region 21..43
 FT /label= FR1
 FT Region 44..54
 FT /label= CDR1
 FT Region 55..70
 FT /label= FR2
 FT Region 71..76
 FT /label= CDR2
 FT Region 77..108
 FT /label= FR3
 FT Region 109..117
 FT /label= CDR3
 FT Region 118..127
 FT /label= FR4
 XX WO9412661-A.
 PN 09-JUN-1994.

XX 25-NOV-1993; 93WO-JP01724.
 XX 28-NOV-1992; 92JP-0341255.
 XX (KAGA) CHEMA SERO THERAPEUTIC RES INST.
 XX Kimachi K, Maeda H, Nishiyama K, Tokiyoshi S;
 XX WPI; 1994-200288/24.
 XX N-PSDB; AAQ64167.
 XX Feline monoclonal antibody and recombinant antibodies specific
 PT for FHV-1 - for detection, treatment and prevention of FHV-1
 PT infection.
 XX Disclosure; Page 18-19; 53pp; Japanese.
 XX The inventors claim a monoclonal antibody against feline herpes
 CC virus (FHV-1). They also claim a recombinant antibody against FHV-1
 CC and fragments of VH and VL CDR1, CDR2 and CDR3. The antibodies are
 CC used in the detection, treatment and prevention of FHV-1. The
 CC sequences of the CDRs in the VH of the recombinant anti-FHV-1
 CC antibody are given in AAR54092. The sequences of the CDRs in the VL of
 CC the recombinant anti-FHV-1 antibody are given in AAR54093. These CDR
 CC sequences are claimed.
 XX SQ Sequence 127 AA;
 Query Match 100.0%; Score 55; DB 15; Length 127;
 Best Local Similarity 100.0%; Pred. No. 0.032;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QQSNSWPHT 9
 Db 109 QQSNSWPHT 117
 RESULT 12
 AAB69687
 ID AAB69687 standard; Protein; 127 AA.
 AC AAB69687;
 XX 30-APR-2001 (first entry)
 DT
 DE Murine CMV5 antibody light chain SEQ ID NO: 83.
 XX Humanised immunoglobulin; mouse; human; antibody; heavy chain; diabetes;
 KW light chain; graft versus host disease; transplant; autoimmune disease;
 KW multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus;
 KW myasthenia gravis; herpes infection; myeloid leukaemia; CMV infection.
 OS Mus sp.
 XX US6180370-B1.
 XX 30-JAN-2001.
 XX 07-JUN-1995; 95US-0484537.
 XX 28-DEC-1988; 88US-0290975.
 PR 13-FEB-1989; 89US-0310252.
 PR 28-SEP-1990; 90US-0590274.
 PR 19-DEC-1990; 90US-0634278.
 XX (PROT-) PROTEIN DESIGN LABS INC.
 XX Queen CL, Selick HE;
 XX WPI; 2001-190856/19.
 XX N-PSDB; AAF58747.

PT Producing humanized immunoglobulin, involves producing a cell
 PT containing DNA segments encoding humanized heavy and light chain
 PT variable regions, and expressing the DNA segments in the cell -
 XX
 XX Example 8; Fig 39; 145pp; English.

CC The present invention describes a method of producing humanised
 CC immunoglobulins involving expressing in a cell a nucleic acid encoding a
 CC humanised version of an immunoglobulin. This is obtained by comparing a
 CC donor and human immunoglobulin and producing a combined antibody which
 CC contains part of each. These are useful in the treatment of
 CC graft-versus-host disease, transplant rejection, autoimmune diseases such
 CC as diabetes, rheumatoid arthritis, myasthenia gravis, multiple sclerosis
 CC and systemic lupus erythematosus, herpes infections, CMV virus infections
 CC and myeloid leukaemia. The present sequence is an antibody used to
 CC demonstrate the method of the invention.

XX SQ Sequence 127 AA;

Query Match 100.0%; Score 55; DB 22; Length 127;
 Best Local Similarity 100.0%; Pred. No. 0.032;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQSNSWPH 9
 | | | | | | | |
 DB 109 QQSNSWPH 117

RESULT 13

AA09775
 ID AAB09775 standard; Protein; 259 AA.

XX AAB09775;

XX DT 06-SEP-2000 (first entry)

XX DE TWV 30K movement protein and scFv fusion protein scFv 30-1 SEQ ID NO:29.

XX KW Molecular pathogenicity; plant disease; resistance; antibody; scFv;
 KW gene construct; pathogen; toxin; fusion protein; antimicrobial;
 KW deoxyribonuclease; RNase; ribosome inactivator; immunomodulator.

XX OS Tobacco mosaic virus.

XX PN WO200023593-A2.

XX PD 27-APR-2000.

XX PF 15-OCT-1999; 99WO-EP07844.

XX PR 16-OCT-1998; 98EP-0119630.

XX PR 16-OCT-1998; 98IN-0000666.

XX PA (FRAU) FRAUNHOFER GES FOERDERUNG ANGEWANDTEN.

XX PI Fischer R, Schillberg S, Nahrang J, Sack M, Monecke M, Liao Y;
 PI Spiegel H, Zimmerman S, Emans N, Holzem A;

XX DR WPI; 2000-339692/29.

XX PT New fusion proteins and gene constructs for expressing agents
 PT (antibodies, enzymes, vectors or molecular pathogenicity), useful for
 PT protecting plants against pathogens and increasing resistance to
 PT disease -

XX PS Example 5; Page 149-150; 193pp; English.

XX CC The present invention describes a fusion protein (I) comprising at least
 CC one binding domain specifically recognising an epitope of a plant
 CC pathogen and at least one further domain comprising a protein or peptide
 CC sequence which is toxic to the pathogen or detrimental to its
 CC replication, transmission or life cycle. Also described is a
 CC pathogenicity (II) comprising (I) and a cellular targeting sequence

CC and/or membrane localisation sequence and/or motif that leads to
 CC membrane anchoring; or at least one binding domain that specifically
 CC recognises a viral movement and/or replicase protein. The fusion
 CC protein, pathogenicity, polynucleotide, vectors, and compositions from
 CC the present invention are useful for the protection of a plant against
 CC the action of a pathogen. The kit from the present invention is useful
 CC for carrying out the methods and may be employed in different
 CC applications, for example in the diagnostic field or as research tools.
 CC The kit or its components, such as the fusion protein, pathogenicity,
 CC polynucleotides, vectors or compositions are useful in plant cell and
 CC plant tissue culture, in agriculture. They are extremely useful for
 CC breeding new varieties of plants that display improved properties such as
 CC resistance to pathogens. AAB56587 to AAB56702 and AAB09774 to B097820
 CC represent sequences used in the exemplification of the present
 CC invention.

XX SQ Sequence 259 AA;

Query Match 90.9%; Score 50; DB 21; Length 259;
 Best Local Similarity 100.0%; Pred. No. 0.51;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQSNSWPH 8
 | | | | | | | |
 DB 220 QQSNSWPH 227

RESULT 14

AAW76034
 ID AAW76034 standard; Protein; 9 AA.

XX AC AAW76034;

XX DT 02-NOV-1998 (first entry)

XX DE LM609 grafted antibody V-L region CDR3 protein fragment #3.

XX KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-L region; CDR;
 KW complementarity determining region.

XX OS Mus sp.

XX PN WO9833919-A2.

XX PD 06-AUG-1998.

XX PF 30-JAN-1998; 98WO-US01826.

XX PR 30-JAN-1997; 97US-0791391.

XX PA (IXSY-) IXSYS INC.

XX PI Glaser SM, Huse WD;

XX DR WPI; 1998-437472/37.

XX DR N-PSDB; AAV49871.

XX PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

XX PS Claim 62; Page 41; 129pp; English.

XX CC AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,

CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
 CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
 CC antibodies contain non-murine framework regions so are suitable for use
 CC in humans. Enhanced types of LM609 have affinity more than 90 times
 CC greater than that of parent the parent antibody.

XX
 SQ Sequence 9 AA;
 Query Match 89.1%; Score 49; DB 19; Length 9;
 Best Local Similarity 88.9%; Pred. No. 7.8e+05;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 QQSNSWPHT 9
 ||| |||||
 Db 1 QQSTSWPHT 9

RESULT 15
 AAW76013
 ID AAW76013 standard; Protein; 9 AA.
 XX AC
 XX AAW76013;
 XX DT
 XX 02-NOV-1998 (first entry)
 XX LM609 grafted antibody V-L region CDR3 protein fragment #1.
 XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-L region; CDR;
 KW complementarity determining region.

XX Mus sp.
 XX WO9833919-A2.
 XX 06-AUG-1998.
 XX 30-JAN-1998; 98WO-US01826.
 XX 30-JAN-1997; 97US-0791391.
 XX (IXSY-) IXSYS INC.
 XX Glaser SM, Huse WD;
 PI WPI; 1998-437472/37.
 XX N-PSDB; AAV49850.
 XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX Disclosure; Page 40; 129pp; English.

CC AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
 CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
 CC antibodies contain non-murine framework regions so are suitable for use
 CC in humans. Enhanced types of LM609 have affinity more than 90 times
 CC greater than that of parent the parent antibody.

SQ Sequence 9 AA;
 Query Match 89.1%; Score 49; DB 19; Length 9;
 Best Local Similarity 88.9%; Pred. No. 7.8e+05;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 QQSNSWPHT 9
 ||| |||||
 Db 1 QQSGSWPHT 9

Search completed: November 18, 2002, 17:50:48
 Job time : 27.4079 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 18:45:22 ; Search time 4.14474 Seconds
(without alignments)
32.704 Million cell updates/sec

Title: US-09-016-061-86

Perfect score: 55

Sequence: 1 QQSNSWPH 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 97044 seqs, 15060890 residues

Total number of hits satisfying chosen parameters: 97044

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB pep.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	49	89.1	33	9	US-09-956-206A-12
2	49	89.1	107	8	US-08-790-540A-4
3	49	89.1	107	8	US-08-790-540A-8
4	49	89.1	107	8	US-08-791-391A-4
5	49	89.1	107	8	US-08-791-391A-8
6	49	89.1	107	8	US-08-791-391A-32
7	44	80.0	128	12	US-10-006-773-6
8	41	74.5	107	10	US-09-756-301A-3
9	41	74.5	107	10	US-09-927-703-3
10	41	74.5	107	10	US-09-766-535A-3
11	41	74.5	107	10	US-09-756-161A-3
12	41	74.5	107	12	US-10-010-229-3
13	41	74.5	107	12	US-10-043-450-3
14	41	74.5	107	12	US-10-044-534-3
15	37	67.3	76	10	US-09-864-761-38506
16	37	67.3	244	10	US-09-940-391-1
17	36	65.5	134	10	US-09-864-761-47478
18	35	63.6	20	10	US-09-205-658-281
19	34	61.8	9	9	US-09-968-561A-72

20	34	61.8	9	9	US-09-968-561A-240	Sequence 240, Appl
21	34	61.8	9	10	US-09-192-85A-48	Sequence 48, Appl
22	34	61.8	100	10	US-09-899-896-2	Sequence 2, Appl
23	34	61.8	102	10	US-09-864-761-48570	Sequence 48570, A
24	34	61.8	494	10	US-09-764-864-1235	Sequence 1235, Ap
25	34	61.8	774	9	US-09-974-298-122	Sequence 122, App
26	34	61.8	774	10	US-09-782-980-16	Sequence 16, Appl
27	34	61.8	774	10	US-09-909-743-7	Sequence 7, Appl
28	33	60.0	33	8	US-08-424-550B-411	Sequence 411, App
29	33	60.0	72	10	US-09-764-869-744	Sequence 744, App
30	33	60.0	100	10	US-09-899-896-4	Sequence 4, Appl
31	33	60.0	154	10	US-09-759-143-383	Sequence 383, App
32	33	60.0	154	10	US-09-780-659-383	Sequence 383, App
33	33	60.0	154	10	US-09-822-827-383	Sequence 383, App
34	33	60.0	154	10	US-09-764-864-814	Sequence 814, App
35	33	60.0	155	10	US-09-764-864-825	Sequence 825, App
36	33	60.0	161	10	US-09-759-143-846	Sequence 846, App
37	33	60.0	161	10	US-09-780-659-846	Sequence 846, App
38	33	60.0	161	10	US-09-822-827-846	Sequence 846, App
39	33	60.0	235	12	US-10-020-139-3	Sequence 3, Appl
40	33	60.0	307	10	US-09-886-055-229	Sequence 229, App
41	33	60.0	535	10	US-09-988-200-4	Sequence 4, Appl
42	33	60.0	822	10	US-09-981-900B-9	Sequence 9, Appl
43	32	58.2	30	10	US-09-864-761-48623	Sequence 48623, A
44	32	58.2	66	10	US-09-764-869-719	Sequence 719, App
45	32	58.2	101	10	US-09-864-761-45932	Sequence 45932, A

ALIGNMENTS

RESULT 1

US-09-956-206A-12

; Sequence 12, Application US/09956206A

; Patent No. US20020164339A1

; GENERAL INFORMATION:

; APPLICANT: DO COUTO, FERNANDO J.R.

; PETERSON, JERRY A.

; CERIANI, ROBERTO L.

; TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE

; MC3 ANTI-BMA6 ANTIBODY, METHODS OF USE THEREOF, AND

; METHODS OF HUMANIZING ANTIBODY PEPTIDES

; NUMBER OF SEQUENCES: 81

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MORRISON & FOERSTER

; STREET: 755 Page Mill Road

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304-1018

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/956,206A

; FILING DATE: 19-Apr-2002

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/525,539

; FILING DATE: 14-SEP-1995

; APPLICATION NUMBER: PCT/US95/11683

; FILING DATE: 14-SEP-1995

; APPLICATION NUMBER: 08/487,598

; FILING DATE: 7-JUNE-1995

; APPLICATION NUMBER: 08/307,868

; FILING DATE: 16-SEPT-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: WITT, ERIC

; REGISTRATION NUMBER: 44,408

; REFERENCE/DOCKET NUMBER: 276332000101

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-956-206A-12

Query Match 89.1%; Score 49; DB 9; Length 33;
Best Local Similarity 88.9%; Pred. No. 0.031; Indels 0;
Matches 8; Conservative 1; Mismatches 0; Gaps 0;

QY 1 QQSNWPHT 9
| | | | | | | | | |
DB 21 QQSNWPHT 29

RESULT 2

US-08-790-540A-4
; Sequence 4, Application US/08790540A
; Patent No. US20010011125A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,540A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405

; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-790-540A-4

Query Match 89.1%; Score 49; DB 8; Length 107;
Best Local Similarity 88.9%; Pred. No. 0.092; Indels 1;
Matches 8; Conservative 0; Mismatches 1; Gaps 0;

QY 1 QQSNWPHT 9
| | | | | | | | | |
DB 89 QQSNWPHT 97

RESULT 3

US-08-790-540A-8
; Sequence 8, Application US/08790540A

; Patent No. US20010011125A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,540A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-790-540A-8

Query Match 89.1%; Score 49; DB 8; Length 107;
Best Local Similarity 88.9%; Pred. No. 0.092; Indels 1;
Matches 8; Conservative 0; Mismatches 1; Gaps 0;

QY 1 QQSNWPHT 9
| | | | | | | | | |
DB 89 QQSGSWPHT 97

RESULT 4

US-08-791-391A-4
; Sequence 4, Application US/08791391A
; Patent No. US20010016645A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,391A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX 1482
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-791-391A-4

Query Match 89.1%; Score 49; DB 8; Length 107;
Best Local Similarity 88.9%; Pred. No. 0.092;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSNSWPHT 9
Db 89 QOSGSWPHT 97

RESULT 5

US-08-791-391A-8
Sequence 8, Application US/08791391A
Patent No. US20010016645A1
GENERAL INFORMATION:
APPLICANT: Huse, William D.
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/791,391A
FILING DATE: 30-JAN-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX 1482
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-791-391A-8

Query Match 89.1%; Score 49; DB 8; Length 107;
Best Local Similarity 88.9%; Pred. No. 0.092;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSNSWPHT 9
Db 89 QOSGSWPHT 97

RESULT 6

US-08-791-391A-32
Sequence 32, Application US/08791391A
Patent No. US20010016645A1
GENERAL INFORMATION:
APPLICANT: Huse, William D.
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/791,391A
FILING DATE: 30-JAN-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX 1482
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-791-391A-32

Query Match 89.1%; Score 49; DB 8; Length 107;
Best Local Similarity 88.9%; Pred. No. 0.092;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSNSWPHT 9
Db 89 QOSGSWPHT 97

RESULT 7

US-10-006-773-6
Sequence 6, Application US/10006773
Patent No. US20020132983A1
GENERAL INFORMATION:
APPLICANT: Junghans, Richard P.
TITLE OF INVENTION: Antibodies as Chimeric Effector Cell Receptors Against Tumor A
FILE REFERENCE: 003
CURRENT APPLICATION NUMBER: US/10/006,773
CURRENT FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: 60/250,089
PRIOR FILING DATE: 2000-11-30
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 128
TYPE: PRT
ORGANISM: Mus sp.
US-10-006-773-6

Query Match 80.0%; Score 44; DB 12; Length 128;
Best Local Similarity 88.9%; Pred. No. 0.71;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOSNSWPHT 9
| | | | | | | |
Db 109 QOSNSWPLT 117

RESULT 8

US-09-756-301A-3

; Sequence 3, Application US/09756301A
; Patent No. US20010027249A1
; GENERAL INFORMATION:
; APPLICANT: Le, Junming
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Grayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
; Human Tumor Necrosis Factor
; FILE REFERENCE: 0975.1005-008
; CURRENT APPLICATION NUMBER: US/09756.301A
; CURRENT FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: U.S. 09/133,119
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1994-10-18
; PRIOR APPLICATION NUMBER: U.S. 08/192,102
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,861
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/010,406
; PRIOR FILING DATE: 1993-01-29
; PRIOR APPLICATION NUMBER: U.S. 08/013,413
; PRIOR FILING DATE: 1993-02-02
; PRIOR APPLICATION NUMBER: U.S. 07/943,852
; PRIOR FILING DATE: 1992-09-11
; PRIOR APPLICATION NUMBER: U.S. 07/853,606
; PRIOR FILING DATE: 1992-03-18
; PRIOR APPLICATION NUMBER: U.S. 07/670,827
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus Balb/c
US-09-756-301A-3

Query Match 74.5%; Score 41; DB 10; Length 107;
Best Local Similarity 77.8%; Pred. No. 1.9;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOSNSWPHT 9
| | | | | | | |
Db 89 QOSHSWPFT 97

RESULT 9

US-09-927-703-3

; Sequence 3, Application US/09927703
; Patent No. US20020022720A1
; GENERAL INFORMATION:
; APPLICANT: Le, Junming
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Grayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of

; TITLE OF INVENTION: Human Tumor Necrosis Factor
; FILE REFERENCE: 0975.1005-013
; CURRENT APPLICATION NUMBER: US/09/927,703
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: U.S. 09/756,398
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: U.S. 09/133,119
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1994-10-18
; PRIOR APPLICATION NUMBER: U.S. 08/192,102
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,861
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,093
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/010,406
; PRIOR FILING DATE: 1993-01-29
; PRIOR APPLICATION NUMBER: U.S. 08/013,413
; PRIOR FILING DATE: 1993-02-02
; PRIOR APPLICATION NUMBER: U.S. 07/943,852
; PRIOR FILING DATE: 1992-09-11
; PRIOR APPLICATION NUMBER: U.S. 07/853,606
; PRIOR FILING DATE: 1992-03-18
; PRIOR APPLICATION NUMBER: U.S. 07/670,827
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus Balb/c
US-09-927-703-3

Query Match 74.5%; Score 41; DB 10; Length 107;
Best Local Similarity 77.8%; Pred. No. 1.9;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOSNSWPHT 9
| | | | | | | |
Db 89 QOSHSWPFT 97

RESULT 10

US-09-766-535A-3

; Sequence 3, Application US/09766535A
; Patent No. US20020106372A1
; GENERAL INFORMATION:
; APPLICANT: Le, Junming
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Grayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
; Human Tumor Necrosis Factor
; FILE REFERENCE: 0975.1005-010
; CURRENT APPLICATION NUMBER: US/09/766,535A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: U.S. 09/133,119
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1994-10-18
; PRIOR APPLICATION NUMBER: U.S. 08/192,102
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,861
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,093
; PRIOR FILING DATE: 1994-02-04

; PRIOR APPLICATION NUMBER: U.S. 08/010,406
; PRIOR FILING DATE: 1993-01-29
; PRIOR APPLICATION NUMBER: U.S. 08/013,413
; PRIOR FILING DATE: 1993-02-02
; PRIOR APPLICATION NUMBER: U.S. 07/943,852
; PRIOR FILING DATE: 1992-09-11
; PRIOR APPLICATION NUMBER: U.S. 07/853,606
; PRIOR FILING DATE: 1992-03-18
; PRIOR APPLICATION NUMBER: U.S. 07/670,827
; PRIOR FILING DATE: 1991-03-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus Balb/c
US-09-756-161A-3

Query Match 74.5%; Score 41; DB 10; Length 107;
Best Local Similarity 77.8%; Pred. No. 1.9;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSNWPFT 9
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Db 89 QQSHSWPFT 97

RESULT 11
US-09-756-161A-3

; Sequence 3, Application US/09756161A
; Patent No. US20020132307A1
; GENERAL INFORMATION:
; APPLICANT: Le, Junming
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Ghayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
; FILE REFERENCE: Human Tumor Necrosis Factor
; FILE REFERENCE: 0975.1005-007
; CURRENT APPLICATION NUMBER: US/09/756,161A
; CURRENT FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: U.S. 09/133,119
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1994-10-18
; PRIOR APPLICATION NUMBER: U.S. 08/192,102
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,861
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,093
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/010,406
; PRIOR FILING DATE: 1993-01-29
; PRIOR APPLICATION NUMBER: U.S. 08/013,413
; PRIOR FILING DATE: 1993-02-02
; PRIOR APPLICATION NUMBER: U.S. 07/943,852
; PRIOR FILING DATE: 1992-09-11
; PRIOR APPLICATION NUMBER: U.S. 07/853,606
; PRIOR FILING DATE: 1992-03-18
; PRIOR APPLICATION NUMBER: U.S. 07/670,827
; PRIOR FILING DATE: 1991-03-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus Balb/c
US-09-756-161A-3

Query Match 74.5%; Score 41; DB 10; Length 107;
Best Local Similarity 77.8%; Pred. No. 1.9;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSNWPFT 9
| | | : | | | |
Db 89 QQSHSWPFT 97

RESULT 12
US-10-010-229-3

; Sequence 3, Application US/10010229
; Patent No. US20020114805A1
; GENERAL INFORMATION:
; APPLICANT: Le, Junming
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Ghayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
; FILE REFERENCE: Human Tumor Necrosis Factor
; FILE REFERENCE: 0975.1005-013
; CURRENT APPLICATION NUMBER: US/10/010,229
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US/09/927,703
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus Balb/c
US-10-010-229-3

Query Match 74.5%; Score 41; DB 12; Length 107;
Best Local Similarity 77.8%; Pred. No. 1.9;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSNWPFT 9
| | | : | | | |
Db 89 QQSHSWPFT 97

RESULT 13
US-10-043-450-3

; Sequence 3, Application US/10043450
; Patent No. US20020141996A1
; GENERAL INFORMATION:
; APPLICANT: Le, Junming
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Ghayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
; FILE REFERENCE: Human Tumor Necrosis Factor
; FILE REFERENCE: 0975.1005-013
; CURRENT APPLICATION NUMBER: US/10/043,450
; CURRENT FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: 09/927,703
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: U.S. 09/756,398
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: U.S. 09/133,119
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1994-10-18
; PRIOR APPLICATION NUMBER: U.S. 08/192,102
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,861


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; PRIOR FILING DATE: 1994-02-04      08/192,093
; PRIOR APPLICATION NUMBER: U.S.
; PRIOR FILING DATE: 1994-02-04      08/010,406
; PRIOR APPLICATION NUMBER: U.S.
; PRIOR FILING DATE: 1993-01-29      08/013,413
; PRIOR APPLICATION NUMBER: U.S.
; PRIOR FILING DATE: 1993-02-02      07/943,852
; PRIOR APPLICATION NUMBER: U.S.
; PRIOR FILING DATE: 1992-09-11      07/853,606
; PRIOR APPLICATION NUMBER: U.S.
; PRIOR FILING DATE: 1992-03-18      07/670,827
; PRIOR APPLICATION NUMBER: U.S.
; PRIOR FILING DATE: 1991-03-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus Balb/c
US-10-043-450-3
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Query Match      74.5%; Score 41; DB 12; Length 107;
Best Local Similarity 77.8%; Pred. No. 1.9;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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QY      1 QQSNSWPHT 9
      |||:|||||
Db      89 QQSHSWPFT 97
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RESULT 14
US-10-044-534-3
; Sequence 3, Application US/10044534
; Patent No. US20020146419A1
; GENERAL INFORMATION:
; APPLICANT: Le, Junming
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Grayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
; FILE REFERENCE: 0975.1003-013
; CURRENT APPLICATION NUMBER: US/10/044,534
; CURRENT FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: 09/927,703
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: U.S. 09/756,398
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: U.S. 09/133,119
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1994-10-18
; PRIOR APPLICATION NUMBER: U.S. 08/192,102
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,861
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,093
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/010,406
; PRIOR FILING DATE: 1993-01-29
; PRIOR APPLICATION NUMBER: U.S. 08/013,413
; PRIOR FILING DATE: 1993-02-02
; PRIOR APPLICATION NUMBER: U.S. 07/943,852
; PRIOR FILING DATE: 1992-09-11
; PRIOR APPLICATION NUMBER: U.S. 07/853,606
; PRIOR FILING DATE: 1992-03-18
; PRIOR APPLICATION NUMBER: U.S. 07/670,827
; PRIOR FILING DATE: 1991-03-18
; NUMBER OF SEQ ID NOS: 19
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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus Balb/c
US-10-044-534-3
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Query Match      74.5%; Score 41; DB 12; Length 107;
Best Local Similarity 77.8%; Pred. No. 1.9;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY      1 QQSNSWPHT 9
      |||:|||||
Db      89 QQSHSWPFT 97
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RESULT 15
US-09-864-761-38506
; Sequence 38506, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; FILE REFERENCE: Aeomica-x-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 38506
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
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; OTHER INFORMATION: MAP TO AC004161.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.8
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.1
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.8
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.3
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.1
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.5
; OTHER INFORMATION: SWISSPROT HIT: O00501, EVALUE 1.40e+00
US-09-864-761-38506

Query Match 67.3%; Score 37; DB 10; Length 76;
Best Local Similarity 55.6%; Pred. No. 6.2;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQNSNSWPH 9
: | | | | | :
Db 37 KQNSWPYS 45

Search completed: November 18, 2002, 19:04:21
Job time : 4.14474 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 18, 2002, 17:43:42 : Search time 8.52632 Seconds
(without alignments)
31.056 Million cell updates/sec

Title: US-09-016-061-86

Perfect score: 55

Sequence: 1 QQSNWPHT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	55	100.0	100	1	US-08-436-463-19
2	55	100.0	107	1	US-07-634-278-62
3	55	100.0	107	1	US-07-634-278-62
4	55	100.0	107	1	US-07-634-278-62
5	55	100.0	107	1	US-08-477-728-62
6	55	100.0	107	1	US-08-477-728-62
7	55	100.0	107	1	US-08-477-728-62
8	55	100.0	107	1	US-08-474-040-62
9	55	100.0	107	1	US-08-474-040-63
10	55	100.0	107	1	US-08-474-040-87
11	55	100.0	107	1	US-08-487-200-62
12	55	100.0	107	1	US-08-487-200-63
13	55	100.0	107	1	US-08-487-200-87
14	55	100.0	107	4	US-08-484-537-62
15	55	100.0	107	4	US-08-484-537-63
16	55	100.0	107	4	US-08-484-537-87
17	55	100.0	127	1	US-07-634-278-83
18	55	100.0	127	1	US-08-477-728-83
19	55	100.0	127	1	US-08-474-040-83
20	55	100.0	127	1	US-08-487-200-83
21	55	100.0	127	1	US-08-436-463-4
22	55	100.0	127	4	US-08-484-537-83
23	49	89.1	33	4	US-08-525-539A-12
24	49	89.1	107	1	US-08-436-463-20
25	49	89.1	107	1	US-08-107-669D-1
26	49	89.1	107	1	US-08-472-788A-1
27	49	89.1	107	2	US-08-477-531B-1

28 49 89.1 107 2 US-08-082-842A-1 Sequence 1, Appli
29 49 89.1 109 1 US-07-942-245-4 Sequence 4, Appli
30 49 89.1 143 2 US-08-653-402B-8 Sequence 8, Appli
31 44 80.0 103 1 US-08-436-463-21 Sequence 21, Appli
32 44 80.0 127 1 US-08-436-463-18 Sequence 18, Appli
33 42 76.4 240 2 US-07-956-399-2 Sequence 2, Appli
34 41 74.5 13 1 US-08-221-580-7 Sequence 7, Appli
35 41 74.5 13 5 PCT-US95-04018-69 Sequence 69, Appli
36 41 74.5 107 1 US-08-192-102-3 Sequence 3, Appli
37 41 74.5 107 1 US-08-324-799-3 Sequence 3, Appli
38 41 74.5 107 2 US-08-192-861A-3 Sequence 3, Appli
39 41 74.5 107 4 US-09-133-119-3 Sequence 3, Appli
40 41 74.5 107 4 US-08-192-093A-3 Sequence 3, Appli
41 40 72.7 9 2 US-08-476-176B-55 Sequence 55, Appli
42 40 72.7 9 3 US-08-127-721A-55 Sequence 55, Appli
43 40 72.7 9 3 US-08-485-246A-55 Sequence 55, Appli
44 40 72.7 106 2 US-08-800-198-4 Sequence 4, Appli
45 40 72.7 106 3 US-09-296-595-4 Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-08-436-463-19
: Sequence 19, Application US/08436463
: Patent No. 5760185
: GENERAL INFORMATION:
: APPLICANT: KIMACHI, Kazuhiko
: APPLICANT: MAEDA, Hiroaki
: APPLICANT: NISHIYAMA, Kiyoto
: APPLICANT: TOKIYOSHI, Sachio
: TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT
: TITLE OF INVENTION: ANTIBODY AND GENE FRAGMENT CODING FOR SAID ANTIBODY
: NUMBER OF SEQUENCES: 21
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: BROWDY AND NEWMARK, P.L.L.C.
: STREET: 419 Seventh Street, N.W., Suite 400
: CITY: Washington
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20004
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/436,463
: FILING DATE: 26-JUN-1995
: CLASSIFICATION: 536
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 341255/1992
: FILING DATE: 28-NOV-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: YUN, Allen C.
: REGISTRATION NUMBER: 37,971
: REFERENCE/DOCKET NUMBER: KIMACHI-1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-628-5197
: TELEFAX: 202-628-5197
: INFORMATION FOR SEQ ID NO: 19:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 100 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-08-436-463-19

Query Match 100.0%; Score 55; DB 1; Length 100;
Best Local Similarity 100.0%; Pred. No. 0.0091;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSNSWPHT 9
| | | | | | | | | |
Db 89 QOSNSWPHT 97

RESULT 2
US-07-634-278-62
; Sequence 62, Application US/07634278
; Patent No. 5530101
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/634,278
; FILING DATE: 19-DEC-1990
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELEPHONE: (415) 326-2400
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-634-278-62

Query Match 100.0%; Score 55; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.0098;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSNSWPHT 9
| | | | | | | | | |
Db 89 QOSNSWPHT 97

RESULT 3
US-07-634-278-63
; Sequence 63, Application US/07634278
; Patent No. 5530101

; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/634,278
; FILING DATE: 19-DEC-1990
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-634-278-63

Query Match 100.0%; Score 55; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.0098;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSNSWPHT 9
| | | | | | | | | |
Db 89 QOSNSWPHT 97

RESULT 4
US-07-634-278-87
; Sequence 87, Application US/07634278
; Patent No. 5530101
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/634,278
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 87:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-634-278-87

Query Match 100.0%; Score 55; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.0098;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQSNSWPHT 9
|||||||
Db 89 QQSNSWPHT 97

RESULT 5
US-08-477-728-62
Sequence 62, Application US/08477728
Patent No. 5585089
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/477,728

FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-477-728-62

Query Match 100.0%; Score 55; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.0098;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQSNSWPHT 9
|||||||
Db 89 QQSNSWPHT 97

RESULT 6
US-08-477-728-63
Sequence 63, Application US/08477728
Patent No. 5585089
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/477,728
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252

; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-477-728-63

Query Match 100.0%; Score 55; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.0098;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQSNSWPHT 9
Db 89 QQSNSWPHT 97

RESULT 7

US-08-477-728-87
; Sequence 87, Application US/08477728
; Patent No. 5585089
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,728
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400

; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 87:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-477-728-87

Query Match 100.0%; Score 55; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.0098;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQSNSWPHT 9
Db 89 QQSNSWPHT 97

RESULT 8

US-08-474-040-62
; Sequence 62, Application US/08474040
; Patent No. 5693761
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,040
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-474-040-62

Query Match 100.0%; Score 55; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.0098;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQSNSWPHT 9
|||||

Db 89 QQSNSWPHT 97

RESULT 9

US-08-474-040-63

; Sequence 63, Application US/08474040
; Patent No. 5693761
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,040
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-474-040-63

Query Match 100.0%; Score 55; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.0098;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQSNSWPHT 9
|||||

Db 89 QQSNSWPHT 97

RESULT 10

US-08-474-040-87
; Sequence 87, Application US/08474040
; Patent No. 5693761
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,040
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 87:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

Query Match 100.0%; Score 55; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.0098;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQSNSWPHT 9
|||||

Db 89 QQSNSWPHT 97

RESULT 11

US-08-487-200-62
; Sequence 82, Application US/08487200
; Patent No. 5693762
; GENERAL INFORMATION:

APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,200
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-487-200-62

Query Match 100.0%; Score 55; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.0098;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSNSWPHT 9
Db 89 QOSNSWPHT 97

RESULT 12
US-08-487-200-63
Sequence 63, Application US/08487200
Patent No. 5693762
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS

NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,200
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-487-200-63

Query Match 100.0%; Score 55; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.0098;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSNSWPHT 9
Db 89 QOSNSWPHT 97

RESULT 13
US-08-487-200-87
Sequence 87, Application US/08487200
Patent No. 5693762

GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US

ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,200
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002610
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 87:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-487-200-87

Query Match 100.0%; Score 55; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.0098;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQSNSWPHT 9
Db 89 QQSNSWPHT 97

RESULT 14
US-08-484-537-62
Sequence 62, Application US/08484537
Patent No. 6180370
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/484,537
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-484-537-62

Query Match 100.0%; Score 55; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.0098;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQSNSWPHT 9
Db 89 QQSNSWPHT 97

RESULT 15
US-08-484-537-63
Sequence 63, Application US/08484537
Patent No. 6180370
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,537
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-484-537-63

Query Match 100.0%; Score 55; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.0098;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQSNSWPHT 9
Db 89 QQSNSWPHT 97
```

Search completed: November 18, 2002, 17:55:51
Job time : 9.52632 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:47:14 : Search time 9.5921 Seconds
(without alignments)
90.200 Million cell updates/sec

Title: US-09-016-061-88

Perfect score: 54

Sequence: 1 QQSTSWPHT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_73.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	90.7	107	2 A45722	anti-glycoprotein
2	49	90.7	123	2 S35479	Ig kappa chain pre
3	46	85.2	107	2 B45722	anti-glycoprotein
4	43	79.6	106	2 P0267	Ig kappa chain v r
5	41	75.9	67	2 P1081	Ig light chain v r
6	41	75.9	69	2 P1080	Ig light chain v r
7	40	74.1	102	2 S26346	Ig kappa chain v r
8	38	70.4	104	2 B43413	Ig kappa chain v r
9	38	70.4	108	2 C30502	Ig kappa chain v r
10	38	70.4	138	2 A26471	Ig kappa chain pre
11	38	70.4	235	1 SQMS	parotid secretory
12	37	68.5	433	2 B2965	hypothetical prote
13	37	68.5	551	2 E84106	hypothetical prote
14	37	68.5	739	2 S47772	biotin sulfoxide r
15	37	68.5	739	2 D91183	biotin sulfoxide r
16	37	68.5	739	2 H86029	biotin sulfoxide r
17	37	68.5	777	2 AD0982	biotin sulfoxide r
18	37	68.5	922	2 AG1827	maltooligosyltreha
19	36	66.7	87	2 P1082	Ig light chain v r
20	36	66.7	100	2 S9860	hypothetical prote
21	36	66.7	115	1 KWSL7	Ig kappa chain pre
22	36	66.7	128	2 PND445	Ig kappa chain pre
23	36	66.7	323	2 T46671	probable aromatase
24	36	66.7	419	2 B85035	hypothetical prote
25	36	66.7	534	2 F90031	PTS system, abutit
26	36	66.7	653	2 E84386	oligopeptide bindi
27	36	66.7	654	2 AG3522	iron-regulated ont
28	35	64.8	170	2 C82480	hypothetical prote
29	35	64.8	235	2 B42337	parotid secretory

30	35	64.8	400	1 JC1428	ketol-acid reducto
31	35	64.8	484	2 F82165	glycogen synthase
32	35	64.8	731	2 A83536	conserved hypothet
33	35	64.8	735	2 F98228	1,4-alpha-glucan b
34	35	64.8	735	2 AH3057	glycogen branching
35	35	64.8	770	2 S76095	hypothetical prote
36	35	64.8	774	1 JQ0550	1,4-alpha-glucan b
37	35	64.8	1109	2 C84545	probable disease r
38	35	64.8	4845	2 T31067	BIR repeat contain
39	34	63.0	96	2 JC5945	regulatory protein
40	34	63.0	97	2 D82789	hypothetical prote
41	34	63.0	118	2 S40374	Ig kappa chain - h
42	34	63.0	122	2 S40338	Ig kappa chain - h
43	34	63.0	128	2 S40343	Ig kappa chain v-j
44	34	63.0	133	2 S23230	Ig kappa chain pre
45	34	63.0	254	2 S30957	gene 12 protein -

ALIGNMENTS

RESULT 1

A45722
anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 5) - mouse (C;Species: Mus musculus (house mouse))
C;Date: 03-Mar-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C;Accession: A45722
R;Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Va J. Virol. 67, 489-496, 1993
A;Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on A;Reference number: A45722; MUID:93100833; PMID:7677958
A;Accession: A45722
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-107 <SIM>
A;Note: sequence extracted from NCBI backbone (NCBIP:120589)
C;Superfamily: Immunoglobulin V region; immunoglobulin homology
C;Keywords: glycoprotein
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 90.7%; Score 49; DB 2; Length 107;

Best Local Similarity 88.9%; Pred. No. 0.088;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSTSWPHT 9

DB 89 QQSNSWPHT 97

RESULT 2

S35479
Ig kappa chain precursor V region - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 19-Mar-1997 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000

C;Accession: S35479

R;Takeda, Y.; Wise, K.S.; Hoffman, R.W.

Nucleic Acids Res. 20, 4099, 1992

A;Title: Nucleotide sequences of immunoglobulin heavy and light chain V-regions from A;Reference number: S35479; MUID:92375706; PMID:1387203

A;Accession: S35479

A;Status: nucleic acid sequence not shown

A;Molecule type: DNA

A;Residues: 1-123 <TAK>

A;Cross-references: EMBL:M93959; NID:g197572; PIDN:AAA39079.1; PID:g554148

C;Genetics:

A;Map position: 6

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotrimer; immunoglobulin

F;1-12/Domain: signal sequence (fragment) #status predicted <SIG>

F;13-123/Product: Ig kappa chain V region (fragment) #status predicted <MAT>

F;28-102/Domain: immunoglobulin homology <IMM>

Query Match 90.7%; Score 49; DB 2; Length 123;

```

Best Local Similarity 88.9%; Pred. No. 0.1;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOQTSWPHT 9
    ||| |||||
Db 101 QOQNSWPHT 109

RESULT 3
B45722
anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 33) - mouse (fr
C:Species: Mus musculus (house mouse)
C:Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: B45722
R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Vasqu
J. Virol. 67, 489-496, 1993
A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on hu
A:Reference number: A45722; MUID:93100833; PMID:7677958
A:Accession: B45722
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-107 <SIM>
A:Note: sequence extracted from NCBI backbone (NCBIP:120590)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: glycoprotein
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 85.2%; Score 46; DB 2; Length 107;
Best Local Similarity 77.8%; Pred. No. 0.3;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOQTSWPHT 9
    ||| |||||
Db 89 QOQNSWPHT 97

RESULT 4
PL0267
Ig kappa chain V region (anti-DNA, DP12VK) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C:Accession: PL0267
R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A
J. Exp. Med. 171, 265-297, 1990
A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
A:Reference number: PL0231; MUID:90111618; PMID:2104919
A:Accession: PL0267
A:Molecule type: mRNA
A:Residues: 1-106 <SHL>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-23/Region: framework 1
F:16-90/Domain: immunoglobulin homology <IMM>
F:24-34/Region: complementarity-determining 1
F:33-49/Region: framework 2
F:50-56/Region: complementarity-determining 2
F:57-88/Region: framework 3
F:89-97/Region: complementarity-determining 3
F:98-106/Region: framework 4

Query Match 79.6%; Score 43; DB 2; Length 106;
Best Local Similarity 77.8%; Pred. No. 0.98;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOQTSWPHT 9
    ||| |||||
Db 89 QOQNSWPHT 97

RESULT 5
PH1081
Ig light chain V region (clone 165.6) - mouse (fragment)
C:Species: Mus musculus (house mouse)

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```

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 15-Jun-1996
C:Accession: PH1081
R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marlon, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective
A:Reference number: PH0971; MUID:92381444; PMID:1512540
A:Accession: PH1081
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-67 <TIL>
A:Experimental source: B cell, strain [NZB x NZW]F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin

Query Match 75.9%; Score 41; DB 2; Length 67;
Best Local Similarity 77.8%; Pred. No. 1.4;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QOQTSWPHT 9
    ||| |||||
Db 58 QOQNSWPHT 66

RESULT 6
PH1080
Ig light chain V region (clone 165.60) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 15-Jun-1996
C:Accession: PH1080
R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marlon, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective
A:Reference number: PH0971; MUID:92381444; PMID:1512540
A:Accession: PH1080
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-69 <TIL>
A:Experimental source: B cell, strain [NZB x NZW]F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin

Query Match 75.9%; Score 41; DB 2; Length 69;
Best Local Similarity 77.8%; Pred. No. 1.4;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QOQTSWPHT 9
    ||| |||||
Db 60 QOQNSWPHT 68

RESULT 7
S26346
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C:Accession: S26346
R:Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A:Title: Antibodies that are specific for a single amino acid interchange in a protei
A:Reference number: S26309; MUID:91341421; PMID:1908510
A:Accession: S26346
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-102 <STA>
A:Cross-references: EMBL:X59211; NID:g52338; PIDN:CAA41921.1; PID:g1334075
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:14-88/Domain: immunoglobulin homology <IMM>

Query Match 74.1%; Score 40; DB 2; Length 102;
Best Local Similarity 66.7%; Pred. No. 3.2;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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QY 1 QOQSTSWPHT 9
 ||| :|||
 Db 87 QOQSTWPT 95

RESULT 8

B43413
 Ig kappa chain V region - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
 C:Accession: B43413
 R:Tomiyama, Y.; Brojer, E.; Ruggeri, Z.M.; Shattil, S.J.; Smiltneck, J.; Gorski, J.; Kum
 J. Biol. Chem. 267, 18085-18092, 1992
 A:Title: A molecular model of RGD ligands. Antibody D gene segments that direct specific
 A:Reference number: A43413; MUID:92388177; PMID:1517241

A:Accession: B43413
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: nucleic acid
 A:Residues: 1-104 <TOM>
 A:Note: sequence extracted from NCBI backbone (NCBIP:112818)
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:13-87/Domain: immunoglobulin homology <IMM>

Query Match 70.4%; Score 38; DB 2; Length 104;
 Best Local Similarity 77.8%; Pred. No. 7.2;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOQSTSWPHT 9
 ||| ||||
 Db 86 QOQSNWPLT 94

RESULT 9

C30502
 Ig kappa chain V region (D444) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 03-Nov-1988 #sequence_revision 03-Nov-1988 #text_change 21-Jan-2000
 C:Accession: C30502
 R:Eilat, D.; Webster, D.M.; Rees, A.R.
 J. Immunol. 141, 1745-1753, 1988
 A:Title: V region sequences of anti-DNA and anti-RNA autoantibodies from NZB/NZW F-1 m
 A:Reference number: A30502; MUID:88315787; PMID:2457627

A:Accession: C30502
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-108 <EIL>
 A:Cross-references: GB:M21907; NID:g197071; PIDN:AAA38907.1; PID:g197072
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 70.4%; Score 38; DB 2; Length 108;
 Best Local Similarity 66.7%; Pred. No. 7.5;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOQSTSWPHT 9
 ||: ||||
 Db 89 QOQSNWPT 97

RESULT 10

A26471
 Ig kappa chain precursor V region (MAK33) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 23-Jul-1999
 C:Accession: A26471
 R:Buckel, P.; Hubner-Parajsz, C.; Mattes, R.; Lenz, H.; Haug, H.; Beaucamp, K.
 Gene 51, 13-19, 1987
 A:Title: Cloning and nucleotide sequence of heavy- and light-chain cDNAs from a creatine
 A:Reference number: A91572; MUID:87248058; PMID:3110009
 A:Accession: A26471
 A:Molecule type: mRNA

A:Residues: 1-138 <BUO>
 A:Cross-references: GB:M16162; NID:g196893; PIDN:AAA38823.1; PID:g196894
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-20/Domain: signal sequence #status predicted <SIG>
 F:21-138/Product: Ig kappa chain V region #status predicted <MAT>

Query Match 70.4%; Score 38; DB 2; Length 138;
 Best Local Similarity 77.8%; Pred. No. 9.8;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOQSTSWPHT 9
 ||| ||||
 Db 109 QOQSNWPLT 117

RESULT 11

SQMS
 parotid secretory protein precursor - mouse
 N:Alternate names: PSP
 C:Species: Mus musculus (house mouse)
 C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 22-Jun-1999
 C:Accession: A23031; I53236
 R:Madsen, H.O.; Hjorth, J.P.
 Nucleic Acids Res. 13, 1-13, 1985
 A:Title: Molecular cloning of mouse PSP mRNA.
 A:Reference number: A23031; MUID:85215456; PMID:2582349
 A:Accession: A23031
 A:Molecule type: mRNA

A:Residues: 1-235 <MAD>
 A:Cross-references: GB:X01697; NID:g53810; PIDN:CAA25846.1; PID:g758163
 R:Poulsen, K.; Jakobsen, B.K.; Mikkelsen, B.M.; Harmark, K.; Nielsen, J.T.; Hjorth, J
 EMBO J. 5, 1891-1896, 1986
 A:Title: Coordination of murine parotid secretory protein and salivary amylase expres
 A:Reference number: I53236; MUID:87004556; PMID:2428613

A:Accession: I53236
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-87 <RES>

A:Cross-references: GB:M26807; NID:g200556; PIDN:AAA40009.1; PID:g554264
 C:Comment: PSP is the most abundant protein in the parotid gland. Its function is not
 C:Genetics:

A:Gene: Psp
 A:Map position: 2
 A:Introns: 41/1
 A:Note: list of introns may be incomplete
 C:Superfamily: parotid secretory protein
 C:Keywords: parotid gland; saliva
 F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-235/Product: parotid secretory protein #status predicted <MAT>

Query Match 70.4%; Score 38; DB 1; Length 235;
 Best Local Similarity 85.7%; Pred. No. 17;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOQSTSWP 7
 ||: ||||
 Db 54 QOQATSWP 60

RESULT 12

B82965
 hypothetical protein PA5456 [imported] - Pseudomonas aeruginosa (strain PAO1)
 C:Species: Pseudomonas aeruginosa
 C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
 C:Accession: B82965
 R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.;
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L
 ; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A:Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pa
 A:Reference number: B82950; MUID:20437337; PMID:10984043
 A:Accession: B82965

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-433 <STO>
A:Cross-references: GB:AE004958; GB:AE004091; NID:g9951776; PIDN:AAG08841.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA5456

Query Match 68.5%; Score 37; DB 2; Length 433;
Best Local Similarity 50.0%; Pred. No. 49;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSTSWPH 8
:::|||||
Db 346 BEATAWPH 353

RESULT 13

E84106
hypothetical protein BH3653 [Imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C:Accession: E84106
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: E84106
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-551 <STO>
A:Cross-references: GB:AP001519; GB:BA000004; NID:g10176109; PIDN:BA807372.1; GSPDB:GN00
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH3653

Query Match 68.5%; Score 37; DB 2; Length 551;
Best Local Similarity 56.7%; Pred. No. 62;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSTSWPHT 9
:|||||:
Db 524 EQSTSWKYT 532

RESULT 14

S47772
biotin sulfoxide reductase (EC 1.-.-.-) 1 - Escherichia coli (strain K-12)
C:Species: Escherichia coli
C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 01-Mar-2002
C:Accession: S47772; JY0071; A65154
R:Plunkett, G.
submitted to the EMBL Data Library, March 1994
A:Reference number: S47666
A:Accession: S47772
A:Molecule type: DNA
A:Residues: 1-739 <PLU>
A:Cross-references: EMBL:U00039; NID:g466582; PIDN:AAB18528.1; PID:g4666689
R:Pierston, D.E.; Campbell, A.
J. Bacteriol. 172, 2194-2198, 1990
A:Title: Cloning and nucleotide sequence of bisc, the structural gene for biotin sulfoxi
A:Reference number: JY0071; MUID:90202748; PMID:2180922
A:Accession: JY0071
A:Molecule type: DNA
A:Residues: 1-544, 'ATLPSAGD', 554-557, 'QR', 561-708, 'MAVYRVRHWGKNTTVRN' <PIE>
A:Cross-references: GB:M34827; NID:g145435; PIDN:AAA3522.1; PID:g145436
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: A65154
A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA
A:Residues: 1-739 <BLAT>

A:Cross-references: GB:AE000432; GB:U000096; NID:g2367241; PIDN:AAC76575.1; PID:g17899
A:Experimental source: strain K-12, substrain MG1655
C:Comment: This enzyme may serve as a scavenger, allowing the cell to utilize biotin
C:Genetics:
A:Gene: bisc
A:Map position: 79 min
C:Superfamily: trimethylamine-N-oxide reductase
C:Keywords: ATP; molybdenum; nucleotide binding; oxidoreductase; P-loop
F:486-493/Region: nucleotide-binding motif A (P-loop)

Query Match 68.5%; Score 37; DB 2; Length 739;
Best Local Similarity 85.7%; Pred. No. 85;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSTSWP 7
|||
Db 129 QOOTSWP 135

RESULT 15

D91183
biotin sulfoxide reductase [Imported] - Escherichia coli (strain O157:H7, substrain R
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C:Accession: D91183
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and g
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: D91183
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-739 <HAY>
A:Cross-references: GB:BA000007; PIDN:BA837859.1; PID:g13363910; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain RIMD 0509952
C:Genetics:
A:Gene: ECS4436
C:Superfamily: trimethylamine-N-oxide reductase

Query Match 68.5%; Score 37; DB 2; Length 739;
Best Local Similarity 85.7%; Pred. No. 85;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSTSWP 7
|||
Db 129 QOOTSWP 135

Search completed: November 18, 2002, 17:57:20
Job time : 10.5921 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:33:36 ; Search time 4.85526 Seconds
(without alignments)
76.883 Million cell updates/sec

Title: US-09-016-061-88
Perfect score: 54
Sequence: 1 QOSTSWPHT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	38	70.4	235	1 PSP_MOUSE	P07743 mus musculu
2	37	68.5	777	1 BISC_ECOLI	P20099 escherichia
3	36	66.7	115	1 KVS1_MOUSE	P01642 mus musculu
4	35	64.8	400	1 ILV5_NEUCR	P38674 neurospora
5	35	64.8	484	1 GLGA_VIBCH	Q9krb6 vibrio chol
6	35	64.8	734	1 GLGB_AGRTU	P52979 agrobacteri
7	35	64.8	770	1 GLGB_SYNY3	P52981 synechocyst
8	35	64.8	773	1 GLGB_SYNP7	P16954 synechococc
9	35	64.8	4829	1 BIR6_HUMAN	Q9nr09 homo sapien
10	34	63.0	96	1 CTCL_ACTLW	Q33947 acinetobact
11	34	63.0	178	1 ATPQ_DROME	Q24251 drosophila
12	34	63.0	254	1 VG12_BPML5	Q05328 mycobacteri
13	34	63.0	452	1 IE63_VZVD	P09269 varicella-z
14	34	63.0	608	1 PRL_MOUSE	Q08501 mus musculu
15	34	63.0	809	1 TOR2_ECO57	P58362 escherichia
16	34	63.0	809	1 TOR2_ECOLI	P46923 escherichia
17	34	63.0	817	1 PWT1_YEAST	P33775 saccharomyc
18	34	63.0	848	1 TOR2_ECO57	P38360 escherichia
19	34	63.0	848	1 TOR2_ECOLI	P33225 escherichia
20	34	63.0	1189	1 PTNE_MOUSE	Q62130 mus musculu
21	34	63.0	1926	1 LPH_RABIT	P09849 oryctolagus
22	33	61.1	591	1 LAC1_CRYPA	Q03966 cryptonectr
23	33	61.1	605	1 VP40_VZVD	P09286 varicella-z
24	33	61.1	668	1 MTMW_METWO	Q59647 methanobact
25	33	61.1	765	1 YF63_MYCTU	Q10768 mycobacteri
26	33	61.1	780	1 NH48_CAEEL	Q94407 caenorhabdi
27	33	61.1	810	1 IL4R_MOUSE	P16382 mus musculu
28	33	61.1	862	1 PGCV_MACNE	Q28858 macaca neme
29	33	61.1	1417	1 BLM_HUMAN	P54132 homo sapien
30	33	61.1	1517	1 YD22_SCHPO	Q10250 schizosacch
31	33	61.1	3396	1 PGCV_HUMAN	P13611 homo sapien
32	32	59.3	105	1 RNF2_GIBBA	P16411 gibberella
33	32	59.3	105	1 RNF2_GIBBA	P16412 gibberella

ALIGNMENTS

RESULT 1

ID	PSP_MOUSE	STANDARD;	PRT;	235 AA.
AC	P07743;			
DT	01-AUG-1988 (Rel. 08, Created)			
DT	01-AUG-1988 (Rel. 08, Last sequence update)			
DT	01-NOV-1997 (Rel. 35, Last annotation update)			
DE	Parotid secretory protein precursor (PSP).			
GN	PSP.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Parotid gland;			
RX	MEDLINE=85215456; PubMed=2582349;			
RA	Madsen H.O., Hjorth J.P.;			
RT	"Molecular cloning of mouse PSP mRNA.";			
RL	Nucleic Acids Res. 13:1-13(1985).			
RN	[2]			
RP	SEQUENCE OF 1-87 FROM N.A.			
RC	STRAIN=C3H; TISSUE=Spleen;			
RX	MEDLINE=87004556; PubMed=2428613;			
RA	Poulsen K., Jakobsen B.K., Mikkelsen B.M., Harmark K.,			
RT	Nielsen J.T., Hjorth J.P.;			
RL	"Coordination of murine parotid secretory protein and salivary amylase expression.";			
CC	EMBO J. 5:1891-1896(1986).			
CC	FUNCTION: PSP IS THE MOST ABUNDANT PROTEIN IN THE PAROTID GLAND.			
CC	WITH THAT OF SALIVARY AMYLASE.			
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CC	EMBL; X01697; CAA25846.1; .			
DR	EMBL; M26807; AAA40009.1; .			
DR	EMBL; M26806; AAA40009.1; JOINED.			
DR	PIR; A23031; SQMS.			
DR	MGD; MGI:97787; Psp.			
KW	Parotid gland; Signal.			
FT	SIGNAL 1 20			POTENTIAL.
FT	CHAIN 21 235			PAROTID SECRETORY PROTEIN.
SQ	SEQUENCE 235 AA; 24753 MW; 23311BAE1E62EF3 CRC64;			
Query Match	70.4%;	Score 38;	DB 1;	Length 235;
Best Local Similarity	85.7%;	Pred. No. 6.3;		
Matches	6;	Conservative 1;	Mismatches 0;	Indels 0; Gaps 0;
QY	1 QOSTSWP 7			

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Db 54 QOATSWP 60
|||||
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 2
BISC_ECOLI
ID BISC_ECOLI STANDARD; PRT; 777 AA.
AC P20099;
DT 01-FEB-1991 (Rel. 17, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Biotin sulfoxide reductase (EC 1.-.-.-) (BDS reductase) (BSO
reductase);
GN BISC OR B3551.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=90202748; PubMed=2180922;
RX Pierson D.E., Campbell A.;
RA "Cloning and nucleotide sequence of bisc, the structural gene for
RT biotin sulfoxide reductase in Escherichia coli.";
RL J. Bacteriol. 172:2194-2198(1990).
RN [2]
SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=94316500; PubMed=8041620;
RA Sofia H.J., Burland V., Daniels D.L., Plunkett G. III, Blattner F.R.;
RT "Analysis of the Escherichia coli genome. V. DNA sequence of the
RT region from 76.0 to 81.5 minutes.";
RL Nucleic Acids Res. 22:2576-2586(1994).
CC -!- FUNCTION: THIS ENZYME MAY SERVE AS A SCAVENGER, ALLOWING THE CELL
CC TO UTILIZE BIOTIN SULFOXIDE AS A BIOTIN SOURCE. IT REDUCES A
CC SPONTANEOUS OXIDATION PRODUCT OF BIOTIN, D-BIOTIN D-SULFOXIDE (BSO
CC OR BBS), BACK TO BIOTIN.
CC -!- COFACTOR: MOLYBDENUM (MOLYBDOPTERIN).
CC -!- MISCELLANEOUS: REQUIRES A SMALL THIOREDOXIN-LIKE PROTEIN FOR
CC ACTIVITY.
CC -!- SIMILARITY: BELONGS TO THE PROKARYOTIC MOLYBDOPTERIN-CONTAINING
CC OXIDOREDUCTASE FAMILY.
CC -----
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CC -----
DR EMBL; M34827; AAA23522.1; ALT_FRAME.
DR EMBL; U00039; AAB18528.1; ALT_INIT.
DR EMBL; AE000432; AAC76575.1; ALT_INIT.
DR PIR; JY0071; JY0071.
DR HSP; Q57366; IEU1.
DR EcoGene; EG10124; bisc.
DR InterPro; IPR001467; Prok_Mboxed.
DR Pfam; PF00384; molybdopterin_1.
DR Pfam; PF01568; molybdop_binding; 1.
DR TIGRfams; TIGR00509; bisc_fam; 1.
DR PROSITE; PS00551; MOLYBDOPTERIN_PROK_1; FALSE_NEG.
DR PROSITE; PS00490; MOLYBDOPTERIN_PROK_2; 1.
DR PROSITE; PS00932; MOLYBDOPTERIN_PROK_3; 1.
KW Oxidoreductase; Molybdenum; Complete proteome.
FT CONFLICT 583 591 DFCRDLPAH -> AFLPRAGD (IN REF. 1).
FT CONFLICT 596 598 ASG -> QR (IN REF. 1).
FT CONFLICT 747 777 NGCAGNTALAWLERKINGPELTLTAFEPASS ->
FT MAVRVIRRWGWKNTIVRN (IN REF. 1).
FT SEQUENCE 777 AA; 85850 MW; 51087D957E4FB38B CRC64;

Query Match 68.5%; Score 37; DB 1; Length 777;
Best Local Similarity 85.7%; Pred. No. 31;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOATSWP 7
||| |||
Db 167 QOATSWP 173

RESULT 3
KV51_MOUSE
ID KV51_MOUSE STANDARD; PRT; 115 AA.
AC P01642;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-V region L7 precursor (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=81220975; PubMed=6264318;
RA Pech M., Hochl J., Schnell H., Zachau H.G.;
RT "Differences between germ-line and rearranged immunoglobulin V kappa
RT coding sequences suggest a localized mutation mechanism.";
RL Nature 291:668-670(1981).
CC -!- MISCELLANEOUS: THERE APPEAR TO BE TWO POSSIBLE SPLICING JUNCTIONS AT
CC THE 3' END OF THE INTRON. THE ALTERNATE WOULD CODE FOR A PROTEIN
CC LACKING RESIDUES 17-19.
DR PIR; A01925; KVM5L7.
DR HSP; P80362; IWTLL.
DR InterPro; IPR003006; Ig_MHC.
DR PIR; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 >115 IG KAPPA CHAIN V-V REGION L7.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 69 FRAMEWORK-2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 77 108 FRAMEWORK-3.
FT DOMAIN 109 >115 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12615 MW; C17BEC758C577E00 CRC64;

Query Match 66.7%; Score 36; DB 1; Length 115;
Best Local Similarity 85.7%; Pred. No. 6.9;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOATSWP 7
||| |||
Db 109 QOATSWP 115

RESULT 4
ILV5_NEUCR
ID ILV5_NEUCR STANDARD; PRT; 400 AA.
AC P38674;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ketol-acid reductoisomerase, mitochondrial precursor (EC 1.1.1.86)
DE (Acetol-hydroxy-acid reductoisomerase) (Alpha-keto-beta-hydroxyacil
DE reductoisomerase).
GN ILV-2.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
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RP SEQUENCE FROM N.A.
RX MEDLINE=93013010; PubMed=1398116;
RA Sista H., Bowman B.;
RT "Characterization of the ilv-2 gene from Neurospora crassa encoding
RL Gene 120:115-118(1992).
CC -1- CATALYTIC ACTIVITY: (R)-2,3-dihydroxy-3-methylbutanoate + NADP(+)
CC - (S)-2-hydroxy-2-methyl-3-oxobutanoate + NADPH.
CC -1- COFACTOR: REQUIRES MAGNESIUM.
CC -1- PATHWAY: Valine and isoleucine biosynthesis; second step.
CC -1- SUBCELLULAR LOCATION: Mitochondrial.
CC -1- SIMILARITY: BELONGS TO THE KETOL-ACID REDUCTOISOMERASE FAMILY.
CC -----
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CC -----
DR EMBL; M84189; AAB00797.1; -.
DR PIR; JC1428; JC1428.
DR HSP; O01292; IQMG
DR InterPro; IPR00506; ACh_isomrctse.
DR TIGR; PF01450; ilvc; 1.
DR TIGR; TIGR00465; ilvc; 1.
KW NADP: Mitochondrion; Branched-chain amino acid biosynthesis; Magnesium;
KW NADP: Mitochondrion; Transit peptide.
FT TRANSIT 1 26 MITOCHONDRION (POTENTIAL).
FT CHAIN 27 400 KETOL-ACID REDUCTOISOMERASE.
FT NP_BIND 90 99 NADPH (POTENTIAL).
FT ACT_SITE 177 177 POTENTIAL.
FT ACT_SITE 177 177 POTENTIAL.
SQ SEQUENCE 400 AA; 44508 MW; D8AA4COA3F4BD7CB CRC64;

Query Match 64.8%; Score 35; DB 1; Length 400;
Best Local Similarity 71.4%; Pred. No. 36;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QSTSWPH 8
DB 156 QSETWPH 162
II :|||

RESULT 5
GLGA_VIBCH STANDARD; PRT; 484 AA.
AC Q9KR66;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Glycogen synthase (EC 2.4.1.21) (Starch [bacterial glycogen]
DE synthase).
GN GLGA OR VC1726.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=El Tor N16961 / Serotype O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RA McDonald L., Uitterlinden T., Fleischmann R.D., Nierman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae".
RL Nature 406:477-483(2000).
CC -1- FUNCTION: Synthesizes alpha-1,4-glucan chains using ADP-glucose.
CC -1- CATALYTIC ACTIVITY: ADP-glucose + {(1,4)-alpha-D-glucosyl}(N) =

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CC ADP + {(1,4)-alpha-D-glucosyl}(N+1).
CC -1- PATHWAY: Glycogen biosynthesis; second step.
CC -1- SIMILARITY: BELONGS TO THE BACTERIAL/PLANT GLYCOGEN SYNTHASE
CC FAMILY.
CC -----
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CC -----
DR EMBL; AE004250; AAF94876.1; -.
DR TIGR; VC1726; -.
DR InterPro; IPR001296; Glycos_transf_1.
DR Pfam; PF00534; Glycos_transf_1.
KW Glycogen biosynthesis; Transferase; Glycosyltransferase;
KW Complete proteome.
FT BINDING 18 18 ADP-GLUCOSE (BY SIMILARITY).
SQ SEQUENCE 484 AA; 55066 MW; 776D1D3E6BCC0920 CRC64;

Query Match 64.8%; Score 35; DB 1; Length 484;
Best Local Similarity 83.3%; Pred. No. 44;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TSWPHT 9
DB 65 THWPHT 70
II :|||

RESULT 6
GLGB_AGRTU STANDARD; PRT; 734 AA.
ID GLGB_AGRTU
AC P52979;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 1,4-alpha-glucan branching enzyme (EC 2.4.1.18) (Glycogen branching
DE enzyme).
GN GLGB.
OS Agrobacterium tumefaciens.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=358;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A348;
RX MEDLINE=99069330; PubMed=9851999;
RA Ugaldé J.E., Lepek V., Uttaro A.D., Estrella J., Iglesias A.,
RA Ugaldé R.A.;
RT "Gene organization and transcription analysis of the Agrobacterium
RT tumefaciens glycogen (glg) operon: two transcripts for the single
RT phosphoglucotransferase gene."
RL J. Bacteriol. 180:6557-6564(1998).
CC -1- CATALYTIC ACTIVITY: Formation of 1,6-glucosidic linkages of
CC glycogen.
CC -1- PATHWAY: Glycogen biosynthesis; third step.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
CC KNOWN AS THE ALPHA-AMYLASE FAMILY.
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CC -----
DR EMBL; AF033856; AAD03472.1; -.
DR InterPro; IPR000461; Alpha_amylase.
DR InterPro; IPR004193; Isoamylase_N.

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DR Pfam: PF00128; alpha-amylase; 1.
KW Glycogen biosynthesis; Transferase; Glycosyltransferase.
FT ACT_SITE 417 417 BY SIMILARITY.
FT ACT_SITE 470 470 BY SIMILARITY.
FT ACT_SITE 538 538 BY SIMILARITY.
SQ SEQUENCE 734 AA; 83623 MW; 70A3CD35A77F31E6 CRC64;

Query Match 64.8%; Score 35; DB 1; Length 734;
Best Local Similarity 71.4%; Pred. No. 67;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSTSWP 7
Db 470 EESTSWP 476

RESULT 7
GLGB_SYNP3 STANDARD; PRT; 770 AA.
AC P52981;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 1,4-alpha-glucan branching enzyme (EC 2.4.1.18) (Glycogen branching
enzyme).
GN GLGB OR SLL0158.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96127529; PubMed=8590279;
RA Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
RA Sugita M., Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
region from map positions 64% to 92% of the genome.";
RL DNA Res. 2:153-166(1995).
CC -!- CATALYTIC ACTIVITY: Formation of 1,6-glucosidic linkages of
glycogen.
CC -!- PATHWAY: Glycogen biosynthesis; third step.
CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
KNOWN AS THE ALPHA-AMYLASE FAMILY.
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-----
EMBL: D63999; BAA10073.1; -.
DR InterPro: IPR000461; Alpha_amylase.
DR InterPro: IPR004193; Isoamylase_N.
DR Pfam: PF00128; alpha-amylase; 1.
DR Pfam: PF02922; isoamylase_N; 2.
KW Glycogen biosynthesis; Transferase; Glycosyltransferase;
Complete proteome.
FT ACT_SITE 433 433 BY SIMILARITY.
FT ACT_SITE 486 486 BY SIMILARITY.
FT ACT_SITE 554 554 BY SIMILARITY.
SQ SEQUENCE 770 AA; 89527 MW; A435AFCAT7703FA8A CRC64;

Query Match 64.8%; Score 35; DB 1; Length 770;
Best Local Similarity 71.4%; Pred. No. 70;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSTSWP 7
Db 486 EESTSWP 492

us-09-016-061-88.rsp

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RESULT 8
GLGB_SYNP7 STANDARD; PRT; 773 AA.
AC P16954;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 1,4-alpha-glucan branching enzyme (EC 2.4.1.18) (Glycogen branching
enzyme).
GN GLGB.
OS Synechococcus sp. (strain PCC 7942) (Anacystis nidulans R2).
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX NCBI_TaxID=1140;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90323609; PubMed=2142668;
RA Kiel J.A.K.W., Boels J.M., Beldman G., Venema G.;
RT "Nucleotide sequence of the Synechococcus sp. PCC7942 branching
enzyme gene (glgB): expression in Bacillus subtilis.";
RL Gene 89:77-84(1990).
CC -!- CATALYTIC ACTIVITY: Formation of 1,6-glucosidic linkages of
glycogen.
CC -!- PATHWAY: Glycogen biosynthesis; third step.
CC -!- SUBUNIT: MONOMER.
CC -!- MISCELLANEOUS: THE TEMPERATURE FOR OPTIMAL ACTIVITY IS
APPROXIMATELY 35 DEGREES CELSIUS.
CC -!- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
KNOWN AS THE ALPHA-AMYLASE FAMILY.
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-----
EMBL: M31544; AAB39038.1; -.
DR PIR: JQ0550; JQ0550.
DR InterPro: IPR000461; Alpha_amylase.
DR InterPro: IPR004193; Isoamylase_N.
DR Pfam: PF00128; alpha-amylase; 1.
DR Pfam: PF02922; isoamylase_N; 2.
KW Glycogen biosynthesis; Transferase; Glycosyltransferase.
FT INIT_MET 0 0
FT ACT_SITE 439 439 BY SIMILARITY.
FT ACT_SITE 492 492 BY SIMILARITY.
FT ACT_SITE 560 560 BY SIMILARITY.
SQ SEQUENCE 773 AA; 89063 MW; 52BAA17CA337BF57 CRC64;

Query Match 64.8%; Score 35; DB 1; Length 773;
Best Local Similarity 71.4%; Pred. No. 70;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSTSWP 7
Db 492 EESTSWP 498

us-09-016-061-88.rsp

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RESULT 9
BIR6_HUMAN STANDARD; PRT; 4829 AA.
AC Q9NR09; Q9ULDI;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 6 (Ubiquitin-conjugating
BIR-domain enzyme apollon).
GN BIRC6 OR KIAA1289.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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DT	15-JUL-1999 (Rel. 38, Last annotation update)
DE	Muconolactone delta-isomerase 1 (EC 5.3.3.4) (Miaase 1).
GN	CATC1.
OS	Acinetobacter lwoffii.
OC	Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;
OC	Acinetobacter.
OX	NCBI_TaxID=28090;
RN	[1]
RN	SEQUENCE FROM N.A.
RC	STRAIN=K24;
RC	MEDLINE=97405925; PubMed=9260969;
RX	Kim S.-I., Leem S.-H., Choi J.-S., Chung Y.H., Kim S., Park Y.-M.,
RA	Park Y.K., Lee Y.N., Ha K.-S.;
RA	"Cloning and characterization of two catA genes in Acinetobacter
RT	lwoffii K24.";
RT	J. Bacteriol. 179:5226-5231(1997).
RL	[2]
RN	SEQUENCE FROM N.A.
RP	STRAIN=K24;
RC	MEDLINE=98139907; PubMed=9473520;
RX	Kim S.-I., Leem S.-H., Choi J.-S., Ha K.-S.;
RA	"Organization and transcriptional characterization of the catI gene
RT	cluster in Acinetobacter lwoffii K24.";
RL	Biochem. Biophys. Res. Commun. 243:289-294(1998).
CC	-1- CATALYTIC ACTIVITY: 2,5-dihydro-5-oxofuran-2-acetate = 3,4-
CC	dihydro-5-oxofuran-2-acetate.
CC	PATHWAY: THIRD STEP IN THE METABOLISM OF CATECHOL TO SUCCINATE-
CC	AND ACETYL-COA IN THE BETA-KETOADIPATE PATHWAY.
CC	-1- SUBUNIT: HOMODECAMER (BY SIMILARITY).
CC	-----
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CC	or send an email to licensee@isb-sib.ch).
CC	-----
DR	EMBL: U77658; AAC46227.1; -.
DR	InterPro: IPR003464; Miase.
DR	Pfam: PF02426; Miaase; 1.
KW	Aromatic hydrocarbons catabolism; Isomerase.
SQ	SEQUENCE 96 AA; 11048 MW; 6955AC14A5DDDEFA CRC64;
Query Match 63.0%; Score 34; DB 1; Length 96;	
Best Local Similarity 62.5%; Pred.No. 13;	
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;	
Qy	1 QOQTSPHP 8
:	
Dd	35 QKSQKWPH 42
RESULT 11	
ID	ATPO_DROME STANDARD; PRT; 178 AA.
AC	Q24251; Q9VE03;
DT	01-NOV-1997 (Rel. 35, Created)
DT	16-OCT-2001 (Rel. 40, Last sequence update)
DT	15-JUN-2002 (Rel. 41, Last annotation update)
DE	ATP synthase D chain, mitochondrial (EC 3.6.3.14).
GN	APTSYN-D OR CG6030.
OS	Drosophila melanogaster (Fruit fly).
OC	Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC	Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC	Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX	NCBI_TaxID=7227;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Ovary;
RX	MEDLINE=99168769; PubMed=10071211;
RA	Caggese C., Ragone G., Perrini B., Moschetti R., De Pinto V.,
RA	Caizzi R., Barsanti P.;

RT "Identification of nuclear genes encoding mitochondrial proteins:
 RT isolation of a collection of D. melanogaster cDNAs homologous to
 RT sequences in the Human Gene Index database.";
 RL Mol. Gen. Genet. 261:64-70(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Helt G., Miklos G.L.G.,
 RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.V., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrier S., Fleischmann W.,
 RA Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klamis I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stepleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhou W., Zhou X., Zhu S., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 CC -I- FUNCTION: THIS IS ONE OF THE CHAINS OF THE NONENZYMATIC
 CC COMPONENT (CF(0) SUBUNIT) OF THE MITOCHONDRIAL ATPASE COMPLEX.
 CC IT HAS NO APPARENT BACTERIAL HOMOLOG AND ITS EXACT FUNCTION IS
 CC UNKNOWN.
 CC -I- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate +
 CC H(+)(Out).
 CC -I- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC
 CC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(0) SEEMS TO
 CC HAVE NINE SUBUNITS: A, B, C, D, E, F, G, F6 AND 8 (OR A6L).
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 CC -----
 CC EMBL; X99667; CAA67981.1;
 DR EMBL; AE003725; AAF55633.1;
 DR FlyBase; FBgn0016120; ATPsyn-d.
 DR Hydrogen ion transport; CF(0); Mitochondrion.
 FT CONFLICT 99 99 S -> N (IN REF.1).
 SQ SEQUENCE 178 AA; 20201 MW; 3671667150B502A3 CRC64;
 Query Match 63.0%; Score 34; DB 1; Length 178;
 Best Local Similarity 83.3%; Pred. No. 24;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 4 TSWPHT 9
 | | | |
 DB 152 TSWPHT 157

 RESULT 12
 VG12_BPML5
 ID VG12_BPML5 STANDARD; PRT; 254 AA.
 AC Q05328;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DE 01-FEB-1994 (Rel. 28, Last annotation update)
 DE Gene 12 protein (gp12).
 GN 12.
 OS Mycobacteriophage L5.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
 OC L5-like viruses.
 OC NCBI_TaxID=31757;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93211282; PubMed=8459766;
 RA Hatfull G.F., Sarkis G.J.;
 RT "DNA sequence, structure and gene expression of mycobacteriophage L5:
 RT a phage system for mycobacterial genetics.";
 RL Mol. Microbiol. 7:395-405(1993).
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 CC -----
 CC EMBL; Z18946; CAA79388.1;
 DR PIR; S30957; S30957.
 DR InterPro; IPR003650; Orange.
 DR SMART; SM00511; ORANGE; 1.
 SQ SEQUENCE 254 AA; 28847 MW; 8627B76D26E42360 CRC64;
 Query Match 63.0%; Score 34; DB 1; Length 254;
 Best Local Similarity 71.4%; Pred. No. 35;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 QSTSWPH 8
 | | | |
 DB 234 QGFSWPH 240

 RESULT 13
 IE63_VZVD
 ID IE63_VZVD STANDARD; PRT; 452 AA.
 AC P09269;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 01-APR-1993 (Rel. 25, Last annotation update)
 DE Transcriptional regulator IE63 homolog.
 GN 4.
 OS Varicella-zoster virus (strain Dumas) (VZV).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Alphaherpesvirinae; Varicellovirus.
 OC NCBI_TaxID=10338;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86306657; PubMed=3018124;
 RA Davison A.J., Scott J.E.;
 RT "The complete DNA sequence of varicella-zoster virus.";
 RL J. Gen. Virol. 67:1759-1816(1986).
 CC -I- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL54,
 CC HSV-2 UL54, EBV-1 5, VZV 4, EBV BMLF1, HCMV UL69, AND HVS-1 57.
 CC -----

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DR EMBL; X04370; CAA27887.1; -
 DR PIR; D27212; WZBE4.

KW Transcription regulation.

SQ SEQUENCE 452 AA; 51543 MW; 42926B4A71E380B4 CRC64;

Query Match 63.0%; Score 34; DB 1; Length 452;
 Best Local Similarity 71.4%; Pred. No. 62;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSTSWP 7

:|:||||

Db 242 KONTSWP 248

RESULT 14

PRLR_MOUSE STANDARD; PRT; 608 AA.
 AC Q08501; Q82099; P15213; P15212;

DT 01-APR-1990 (Rel. 14, Created)

DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Prolactin receptor precursor (PRL-R).

GN PRLR.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RA Moore R.C., Oka T.;

RA "Cloning and sequencing of the cDNA encoding the murine mammary gland

long-form prolactin receptor.";

RA Gene 134:263-265(1993).

[2]

RA SEQUENCE FROM N.A. (FORM PRL-R3).

RA STRAIN=C3H; TISSUE=Mammary gland;

RA MEDLINE=94085788; PubMed=8262385;

RA Clarke D.L., Linzer D.I.H.;

RA "Changes in prolactin receptor expression during pregnancy in the

mouse ovary.";

RA Endocrinology 133:224-232(1993).

[3]

RA SEQUENCE FROM N.A. (FORM PRL-R3).

RA Submitted (JUL-1992) to the EMBL/GenBank/DBJ databases.

[4]

RA SEQUENCE FROM N.A. (FORM PRL-R3).

RA STRAIN=BALB/c; TISSUE=Mammary gland;

RA Edery M., Pezet A., Nandi S., Kelly P.A.;

RA Submitted (JUN-1993) to the EMBL/GenBank/DBJ databases.

[5]

RA SEQUENCE FROM N.A. (FORMS PRL-R2 AND PRL-R1).

RA STRAIN=Swiss Webster; TISSUE=Liver;

RA MEDLINE=89261824; PubMed=2725531;

RA Davis J.A., Linzer D.I.H.;

RA "Expression of multiple forms of the prolactin receptor in mouse

liver.";

RA Mol. Endocrinol. 3:674-680(1989).

CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE

PROLACTIN, AS WELL AS PLACENTAL LACTOGEN I AND II.

CC -1- SUBCELLULAR LOCATION: Type I membrane protein.

CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS; PRL-R1, PRL-R2 AND PRL-R3 (SHOWN

HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.

CC

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CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC
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DR EMBL; LJ3593; AAC37641.1; -
 DR EMBL; LJ4811; AAA02686.1; -
 DR EMBL; D10214; BAA01066.1; -
 DR EMBL; X73372; CAA51789.1; -
 DR EMBL; M22959; AAA39977.1; -
 DR EMBL; M22958; AAA39976.1; -
 DR PIR; JT0671; JT0671.
 DR HSSP; P16471; IBP3.
 DR MGD; MGI:97763; Prlr.

DR InterPro; IPR002996; PRLR.

DR InterPro; IPR003961; FN_III.

DR InterPro; IPR003528; Hemtopoptn_L_Fl.

DR Pfam; PF00041; fn3; 2.

DR SMART; SM00060; FN3; 1.

DR PROSITE; PS01352; HEMATOPO_REC_L_Fl; 1.

KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat;

KW Alternative splicing.

FT SIGNAL 1 19

FT CHAIN 20 608

FT DOMAIN 20 229

FT TRANSMEM 230 253

FT DOMAIN 254 608

FT DOMAIN 20 117

FT DOMAIN 119 222

FT DISULFID 31 41

FT DISULFID 70 81

FT CARBOHYD 54 54

FT CARBOHYD 99 99

FT CARBOHYD 127 127

FT VARSPLIC 281 292

FT VARSPLIC 293 608

FT VARSPLIC 281 303

FT VARSPLIC 304 608

FT CONFLICT 558 558

FT CONFLICT 558 558

SQ SEQUENCE 608 AA; 68240 MW; B8CE20B2EFC9FC6 CRC64;

Query Match 63.0%; Score 34; DB 1; Length 608;

Best Local Similarity 71.4%; Pred. No. 83;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSTSWP 7

:|:||||

Db 474 KONTSWP 480

RESULT 15

TORZ_ECO57 STANDARD; PRT; 809 AA.

ID TORZ_ECO57

AC P58362;

DT 15-JUN-2002 (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Trimethylamine-N-oxide reductase 2 precursor (EC 1.6.6.9) (TMAO

reductase 2) (Trimethylamine oxidase 2).

DE TORZ OR BISZ OR Z2925 OR ECS2582.

OS Escherichia coli O157:H7.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Escherichia.

OX NCBI_TaxID=83334;

RN [1]

```

RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Apodaca E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kunara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
CC -1- FUNCTION: Reduces trimethylamine-N-oxide (TMAO) into
CC trimethylamine; an anaerobic reaction coupled to energy-yielding
CC reactions. Can also reduce other N- and S-oxide compounds such as
CC 4-methylmorpholine-N-oxide and biotin sulfoxide (BSO), but with a
CC lower catalytic efficiency (By similarity).
CC -1- CATALYTIC ACTIVITY: NADH + trimethylamine-N-oxide = NAD(+) +
CC trimethylamine + H(2)O.
CC -1- COFACTOR: Molybdenum (Molybdopterin) (By similarity).
CC -1- SUBCELLULAR LOCATION: Periplasmic (By similarity).
CC -1- MISCELLANEOUS: Expression of torYz allows E.coli to grow
CC anaerobically on a wider range of substrates than does expression
CC of torCAD (By similarity).
CC -1- SIMILARITY: BELONGS TO THE PROKARYOTIC MOLYBDOPTERIN-CONTAINING
CC OXIDOREDUCTASE FAMILY.
CC -----
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CC -----
DR EMBL; AE005409; AAG56862.1; ALT_INIT.
DR EMBL; AP002559; BAB36005.1; ALT_INIT.
DR InterPro; IPR001467; Prok_Mboxred.
DR Pfam; PF00384; molybdopterin; 1.
DR TIGRFAMs; TIGR00509; bIsC_fam; 1.
DR PROSITE; PS00551; MOLYBDOPTERIN_PROK_1; FALSE_NEG.
DR PROSITE; PS00490; MOLYBDOPTERIN_PROK_2; 1.
DR PROSITE; PS00932; MOLYBDOPTERIN_PROK_3; 1.
DR OXIDOREDUCTASE; NAD; Molybdenum; Periplasmic; Signal;
KW Complete proteome.
FT SIGNAL 1 31 BY SIMILARITY.
FT CHAIN 32 809 TRIMETHYLAMINE-N-OXIDE REDUCTASE 2.
SQ SEQUENCE 809 AA; 88979 MW; 261F38E9A34798E9 CRC64;

Query Match 63.0%; Score 34; DB 1; Length 809;
Best Local Similarity 71.4%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSTSWP 7
Db 195 EQOTSWP 201

```

Search completed: November 18, 2002, 17:51:38
 Job time : 6.85526 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:40:56 ; Search time 20.1316 Seconds
(without alignments)
92.115 Million cell updates/sec

Title: US-09-016-061-88

Perfect score: 54

Sequence: 1 QQSTSWPHT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archepa:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	44	81.5	1194	5 Q9VSI2	Q9vsi2 drosophila
2	43	79.6	1109	5 Q9VTB9	Q9vtb9 drosophila
3	41	75.9	993	4 Q8WQ05	Q8wxq5 homo sapien
4	39	72.2	237	5 Q8S2M4	Q8szn4 drosophila
5	38	70.4	235	11 Q9D734	Q9d734 mus musculus
6	37	68.5	433	16 Q9HTB4	Q9htb4 pseudomonas
7	37	68.5	551	16 Q9K6S3	Q9k6s3 bacillus ha
8	37	68.5	608	11 Q99J21	Q99j21 mus musculus
9	37	68.5	739	16 Q8XDP3	Q8xdp3 escherichia
10	37	68.5	777	16 Q8ZLA2	Q8zla2 salmonella
11	37	68.5	777	16 Q8Z2A7	Q8z2a7 salmonella
12	37	68.5	850	2 Q8VM80	Q8vm80 rhodococcus
13	37	68.5	922	16 Q8Z0D1	Q8z0d1 anabaena sp
14	37	68.5	2556	5 Q9VX7	Q9vxp7 drosophila
15	36	66.7	296	13 Q93312	Q93312 brachydanio
16	36	66.7	297	13 Q73779	Q73779 brachydanio

17	36	66.7	323	2 Q54490	Q54490 streptomyce
18	36	66.7	330	10 Q9FMV9	Q9fmv9 arabidopsis
19	36	66.7	419	10 Q8SY03	Q8sy03 arabidopsis
20	36	66.7	534	16 Q99RV0	Q99rv0 staphylococ
21	36	66.7	653	17 Q9HWW4	Q9hww4 halobacteri
22	36	66.7	654	16 Q8YDS0	Q8yds0 brucella me
23	36	66.7	674	16 Q8XPA2	Q8xpa2 clostridium
24	35	64.8	170	16 Q9KMR2	Q9kmr2 vibrio chol
25	35	64.8	201	5 Q95W40	Q95w40 brachiosteo
26	35	64.8	234	10 Q94HC4	Q94hc4 oryza sativ
27	35	64.8	235	11 Q63471	Q63471 rattus norv
28	35	64.8	284	13 Q9DDU0	Q9ddu0 brachydanio
29	35	64.8	311	16 Q98BE5	Q98be5 rhizobium l
30	35	64.8	315	13 Q9YGU0	Q9ygu0 brachydanio
31	35	64.8	327	13 Q9YH10	Q9yh10 cyprinus ca
32	35	64.8	402	3 Q8X019	Q8x019 neurospora
33	35	64.8	731	16 Q9I570	Q9i570 pseudomonas
34	35	64.8	735	16 Q8U8L4	Q8u8l4 agrobacteri
35	35	64.8	736	16 Q92M14	Q92m14 rhizobium m
36	35	64.8	737	16 Q985P4	Q985p4 rhizobium l
37	35	64.8	1109	10 Q9ZVX6	Q9zvx6 arabidopsis
38	35	64.8	1313	5 Q9NE28	Q9ne28 leishmania
39	35	64.8	4845	11 Q88738	Q88738 mus musculu
40	34	63.0	94	2 Q9XCE0	Q9xce0 mycobacteri
41	34	63.0	96	2 Q9Z9Y5	Q9z9y5 frateuria s
42	34	63.0	97	16 Q9FFS1	Q9ffs1 xyella fas
43	34	63.0	110	11 Q9CVX9	Q9cvx9 mus musculu
44	34	63.0	310	4 Q9BSV6	Q9bsv6 homo sapien
45	34	63.0	315	4 Q9H6H5	Q9h6h5 homo sapien

ALIGNMENTS

RESULT 1

Q9VSI2	PRELIMINARY;	PRT;	1194 AA.
ID	Q9VSI2		
AC	Q9VSI2;		
DT	01-MAY-2000 (TrEMBLrel. 13, Created)		
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)		
DT	01-JUN-2001 (TrEMBLrel. 17, Last annotation update)		
DE	CG7112 protein.		
GN	CG7112.		
OS	Drosophila melanogaster (Fruit fly).		
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;		
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;		
OC	Ephydroidea; Drosophilidae; Drosophila.		
OX	NCBI_TaxID=7227;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=BERKELEY;		
RX	MEDLINE=20196006; PubMed=10731132;		
RA	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,		
RA	Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Calle R.F.,		
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,		
RA	Sutton G.G., Wortman J.R., Vandell M.D., Zhang Q., Chen L.X.,		
RA	Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,		
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,		
RA	Abriel J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,		
RA	Balieu R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,		
RA	Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,		
RA	Borkova D., Botchan M.A., Bouck J., Brokstein P., Brothier P.,		
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,		
RA	Cherry J.M., Cawley S., Dahike C., Davenport L.B., Davies P.,		
RA	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,		
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,		
RA	Durbin K.J., Evangelista C.C., Ferraz C., Ferrier S., Fleischmann W.,		
RA	Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,		
RA	Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,		
RA	Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,		
RA	Hostin D., Houston K.A., Howland T.J., Wei M.-H., Thegwan C.,		
RA	Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,		
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,		

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RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Morbarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL: AE003555; AAF50437.1; -.
DR FlyBase: FBgn0035879; CG7112.
DR InterPro: IPR000050; PID.Domain.
DR Pfam: PF00566; TBC; 1.
DR SMART: SM00462; PTB; 1.
DR SMART: SM00164; TBC; 1.
SQ SEQUENCE 1194 AA; 133393 MW; E0E3DB547B4924E0 CRC64;

Query Match 81.5%; Score 44; DB 5; Length 1194;
Best Local Similarity 77.8%; Pred. No. 11;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSTSWPHT 9
|:|:|:|:|
DB 461 QOSSSWPYT 469

RESULT 2
Q9VTB9
ID Q9VTB9 PRELIMINARY; PRT; 1109 AA.
AC Q9VTB9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE CG7958 protein.
GN CG7958.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY.
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gokey J.D.,
RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers J.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris S.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
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RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Morbarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL: AE003547; AAF50133.1; -.
DR FlyBase: FBgn0036103; CG7958.
DR InterPro: IPR004181; Znf.Miz.
DR Pfam: PF02891; zf-MIZ; 1.
SQ SEQUENCE 1109 AA; 116491 MW; 4FD726183E5642AC CRC64;

Query Match 79.6%; Score 43; DB 5; Length 1109;
Best Local Similarity 66.7%; Pred. No. 15;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSTSWPHT 9
|:|:|:|:|
DB 591 QMNTNMPHT 599

RESULT 3
Q8WXQ5
ID Q8WXQ5 PRELIMINARY; PRT; 993 AA.
AC Q8WXQ5;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Serine/threonine protein kinase kkalre-like 1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hu W.-X., Tang L.-J., Shi Y.-W.;
RT "The cloning of 2nd splicing version of human serine/threonine-protein
kinase kkalre (cyclin-dependent kinase like-1).";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF390028; AAL58838.1; -.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00069; pkinase; 2.
DR ProDom: PD000001; Euk_pkinase; 3.
DR SMART: SM00220; S_TKc; 1.
DR SMART: SM00219; TyrKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE: PS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.
KW Kinase.
SQ SEQUENCE 993 AA; 108961 MW; 1D06F298145B5C67 CRC64;

Query Match 75.9%; Score 41; DB 4; Length 993;
Best Local Similarity 85.7%; Pred. No. 31;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QOSTSWPH 8
|:|:|:|:|
DB 948 QATSWPH 954
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RESULT 4
Q8SZN4
ID Q8SZN4 PRELIMINARY: PRT: 237 AA.
AC Q8SZN4;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE RH01588P.
GN Cg18467.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227; [1]
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RA Stapleton M., Brokstein P., Hong L., Agbavani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF070634; AAL48105.1; -.
SQ SEQUENCE 237 AA; 28077 MW; FC3DFF60D57833D2 CRC64;

Query Match 72.2%; Score 39; DB 5; Length 237;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 STSWP 8
DB 7 STSWP 12

RESULT 5
Q9D734
ID Q9D734 PRELIMINARY: PRT: 235 AA.
AC Q9D734;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Parotid secretory protein.
GN PSP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090; [1]
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=TONGUE;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawal J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa K., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kontsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
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RL Nature 409:685-690(2001).
DR EMBL: AK009654; BAB26418.1; -.
DR MGD: MGI:97787; Psp.
SQ SEQUENCE 235 AA; 24737 MW; A29D0160268DA0CF CRC64;

Query Match 70.4%; Score 38; DB 11; Length 235;
Best Local Similarity 85.7%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSTSWP 7
DB 54 QOATSWP 60

RESULT 6
Q9HTB4
ID Q9HTB4 PRELIMINARY: PRT: 433 AA.
AC Q9HTB4;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)
DE Hypothetical protein PA5456.
GN PA5456.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287; [1]
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen."
RL Nature 406:959-964(2000).
DR EMBL: AE004958; AAG08841.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 433 AA; 49370 MW; C8D3C55219B97E18 CRC64;

Query Match 68.5%; Score 37; DB 16; Length 433;
Best Local Similarity 50.0%; Pred. No. 70;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSTSWP 8
DB 346 BEATSWP 353

RESULT 7
Q9K6S3
ID Q9K6S3 PRELIMINARY: PRT: 551 AA.
AC Q9K6S3;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE BH3653 protein (L-glutamate-dependent ATP hydrolase).
GN BH3653 OR PLG2.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=86665; [1]
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
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RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RL halodurans and genomic sequence comparison with Bacillus subtilis."
RL Nucleic Acids Res. 28:4317-4331(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Ashiuchi M., Yamamoto T., Kamei T., Komatsu K., Nakamura H.;
RT "Characterization of poly-gamma-L-glutamate synthetic system of
RL Bacillus halodurans C-125.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AP001519; BAB07372.1; -.
DR EMBL: AB071407; BAB64938.1; -.
DR InterPro: IPR001792; Acylphosphatase.
DR Pfam: PF00708; Acylphosphatase; 1.
DR ProDom: PD001884; Acylphosphatase; 1.
DR HydroLase: Complete proteome.
SQ SEQUENCE 551 AA; 62089 MW; A43731188B9C1F60 CRC64;

Query Match 68.5%; Score 37; DB 16; Length 551;
Best Local Similarity 66.7%; Pred. No. 90;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSTSWPHT 9
Db 524 EQSTSWKYT 532
:|||||:

RESULT 8
Q99JZ1 PRELIMINARY; PRT; 608 AA.
AC Q99JZ1
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Prolactin receptor.
GN PRLR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.; to the EMBL/GenBank/DBJ databases.
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC005555; AAH05555.1; -.
DR EMBL: BC006652; AAH06652.1; -.
DR HSSP: PL6471; 1bp3.
DR MGD: MGI:97763; Prlr.
DR InterPro: IPR002996; CRLA.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003528; Hemtopoptn_L_F1.
DR Pfam: PF00041; fn3; 2.
DR SMART: SM00060; FN3; 2.
DR PROSITE: PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.
DR Receptor.
KW Receptor.
SQ SEQUENCE 608 AA; 69223 MW; 2710DAEC2B1A8F63 CRC64;

Query Match 68.5%; Score 37; DB 11; Length 608;
Best Local Similarity 85.7%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQSTSWP 7
Db 474 QQSTSWP 480
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RESULT 9
Q8XDP3 PRELIMINARY; PRT; 739 AA.
AC Q8XDP3
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Biotin sulfoxide reductase.

GN BISC OR Z4976 OR ECS4436.
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Postfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.F., Potamoudis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7";
RL Nature 409:529-533(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tohe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
DR EMBL: AE005582; AAG58700.1; -.
DR EMBL: AP002565; BAB37859.1; -.
DR InterPro: IPR001467; Prok_Mboxred.
DR Pfam: PF00384; molybdopterin; 1.
DR Pfam: PF01568; Molydop_binding; 1.
DR TIGRFAMS: TIGR00509; biscfam; 1.
DR PROSITE: PS00490; MOLYBDOPTERIN_PROK_2; 1.
DR PROSITE: PS00932; MOLYBDOPTERIN_PROK_3; 1.
DR Complete proteome.
KW Complete proteome.
SQ SEQUENCE 739 AA; 81981 MW; 23675207DD4FE6C3 CRC64;

Query Match 68.5%; Score 37; DB 16; Length 739;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSTSWP 7
Db 129 QQSTSWP 135
:|||||:

RESULT 10
Q8ZLA2 PRELIMINARY; PRT; 777 AA.
ID Q8ZLA2
AC Q8ZLA2
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Biotin sulfoxide reductase (EC 1.-.-.-).
GN BISC OR STM3644.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
LT2.";
RL Nature 413:852-856(2001).

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DR EMBL: AE008869; AAL22504.1; -.
DR InterPro: IPR001467; Prok_Mboxred.
DR Pfam: PF00384; molybdopterin; 1.
DR Pfam: PF01568; molybdop_binding; 1.
DR TIGRFAMs: TIGR00509; bisc_fam; 1.
DR PROSITE: PS00490; MOLYBDOPTERIN_PROK_2; 1.
DR PROSITE: PS00932; MOLYBDOPTERIN_PROK_3; 1.
DR Oxidoreductase; Complete proteome.
KW OXIDOREDUCTASE; Complete proteome.
SQ SEQUENCE 777 AA; 85723 MW; 027ECC7D948A78E CRC64;

Query Match 68.5%; Score 37; DB 16; Length 777;
Best Local Similarity 85.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOQTSWP 7
II IIII
DB 167 QOQTSWP 173

RESULT 11
Q822A7 PRELIMINARY; PRT; 777 AA.
AC Q822A7;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Biotin sulfoxide reductase (EC 1.-.-.-).
GN BISC OR STY4158.
OS Salmonella typhi.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=601;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Felwell T., Hamlin N., Haque A., Hien T.T., Holtroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Bartell B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RL Nature 413:848-852(2001).
DR EMBL: AL627281; CAD07984.1; -.
DR InterPro: IPR001467; Prok_Mboxred.
DR Pfam: PF00384; molybdopterin; 1.
DR Pfam: PF01568; molybdop_binding; 1.
DR TIGRFAMs: TIGR00509; bisc_fam; 1.
DR PROSITE: PS00490; MOLYBDOPTERIN_PROK_2; 1.
DR PROSITE: PS00932; MOLYBDOPTERIN_PROK_3; 1.
DR Oxidoreductase; Complete proteome.
KW OXIDOREDUCTASE; Complete proteome.
SQ SEQUENCE 777 AA; 85705 MW; 8BC74B06716489DB CRC64;

Query Match 68.5%; Score 37; DB 16; Length 777;
Best Local Similarity 85.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOQTSWP 7
II IIII
DB 167 QOQTSWP 173

RESULT 12
Q8VM80 PRELIMINARY; PRT; 850 AA.
AC Q8VM80;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

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DE Putative steroid monooxygenase / esterase fusion protein.
OS Rhodococcus rhodochrous.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Nocardiaceae; Rhodococcus.
OX NCBI_TaxID=1829;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 11097;
RA van Beilen J.B., Fritsche U., Seeger M., Smits T.H.M., Witholt B.;
RT "Cloning of Baeyer-Villiger monooxygenases from Comamonas,
RT Xanthobacter and Rhodococcus via PCR with highly degenerate primers.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ418062; CAD10803.1; -.
DR InterPro: IPR002018; Carboxesterase8.
DR InterPro: IPR000960; Flav_cont_mnoxgn.
DR InterPro: IPR00379; Ser_estrs_site.
DR Pfam: PF00135; Coesterase; 1.
DR Pfam: PF00743; FMO-like; 1.
KW Monooxygenase.
SQ SEQUENCE 850 AA; 93517 MW; 8BC47C21437B13C8 CRC64;

Query Match 68.5%; Score 37; DB 2; Length 850;
Best Local Similarity 71.4%; Pred. No. 1.4e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QOSTSWPH 8
II IIII
DB 162 QOSTSWPH 168

RESULT 13
Q8Z0D1 PRELIMINARY; PRT; 922 AA.
AC Q8Z0D1;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Maltotoligosyltrehalose synthase.
GN ALL0167.
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain PCC 7120.";
RL DNA Res. 8:203-213(2001).
DR EMBL: AP003581; BAB77691.1; -.
DR InterPro: IPR00461; Alpha_acylase.
DR Pfam: PF00128; alpha-acylase; 1.
KW Complete proteome.
SQ SEQUENCE 922 AA; 105857 MW; 6A91E58BF13DB7C7 CRC64;

Query Match 68.5%; Score 37; DB 16; Length 922;
Best Local Similarity 55.6%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 QOSTSWPHT 9
II IIII
DB 584 QHQAHPHT 592

RESULT 14
Q9VXP7 PRELIMINARY; PRT; 2556 AA.
AC Q9VXP7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)

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DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE CG8473 protein.
GN CG8473.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
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RN SEQUENCE FROM N.A.
RP STRAIN=BERKELEY;
RC MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celiker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA April J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,
RA Beeson K.V., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Folsler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*."
RL Science 287:2185-2195(2000).
CC -1- SIMILARITY: CONTAINS 3 WD REPEATS (TRP-ASP DOMAINS).
DR ENBL: AE003500; AAF48511.1;
DR FlyBase; FBgn0030689; CG8473.
DR InterPro; IPR003439; ABC_transportr.
DR InterPro; IPR002557; Chitin_bind_perA.
DR InterPro; IPR011680; WD40.
DR Pfam; PF000005; ABC_tran; 2.
DR Pfam; PF01607; CBM_14; 2.
DR Pfam; PF00400; WD40; 2.
DR SMART; SM00494; ChEBD2; 2.
DR SMART; SM00320; WD40; 2.
DR PROSITE; PS00678; WD_REPEATS_1; 1.
DR PROSITE; PS00678; WD_REPEATS_2; 1.
DR PROSITE; PS00678; WD_REPEATS_2; 1.
DR PROSITE; PS00678; WD_REPEATS_2; 1.
KW Repeat; WD repeat.
SQ SEQUENCE 2556 AA; 290937 MW; 82612D442484D8CD CRC64;

Query Match 68.5%; Score 37; DB 5; Length 2556;
Best Local Similarity 71.4%; Pred. No. 4.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 STSWPHT 9

Db 1652 NTKWPH 1658

RESULT 15

O93312 PRELIMINARY; PRT; 296 AA.

AC O93312;

DT 01-NOV-1998 (TREMBlrel. 08, Created)

DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)

DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)

DE Forkhead-5.

GN FOXB1.1 OR FKH5

OS Brachydanio rerio (zebrafish) (zebra danio).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

OC Cyprinidae; Danio.

OX NCBI_TaxID=7955;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=98453400; PubMed=9778500;

RA Grinblat Y., Gamse J., Patel M., Sive H.;

RT "Determination of the zebrafish forebrain: induction and patterning.";

RL Development 125:4403-4416(1998).

DR EMBL; AF052651; AAC25103.1; -.

DR HSSP; Q63245; 2HFH.

DR ZFIN; ZDB-GENE-990415-77; foxb1.1.

DR InterPro; IPR001766; TF_Fork_head.

DR Pfam; PF00250; Fork_head; 1.

DR PRINTS; PR00053; FORKHEAD.

DR ProDom; PD000425; TF_Fork_head; 1.

DR SMART; SM00339; FH; 1.

DR PROSITE; PS00657; FORK_HEAD_1; 1.

DR PROSITE; PS00658; FORK_HEAD_2; UNKNOWN_1.

DR PROSITE; PS00039; FORK_HEAD_3; 1.

SQ SEQUENCE 296 AA; 33066 MW; 5909FB9552C3F61C CRC64;

Query Match

Best Local Similarity 66.7%; Score 36; DB 13; Length 296;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSTSWPH 8

DB 196 QLTWAPH 203

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Job time : 22.1316 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:31:45 ; Search time 26.4079 Seconds
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23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	54	100.0	9	AAW76034	LM609 grafted anti
2	54	100.0	9	AAW76034	Mutant VL CDR3 pep
3	49	90.7	9	AAW76033	LM609 grafted anti
4	49	90.7	9	AAW76033	Murine monoclonal
5	49	90.7	9	AAW76033	Mutant VL CDR3 pep
6	49	90.7	9	AAW76033	Humanised VL regio
7	49	90.7	107	AAW76033	Murine CMV5 antio
8	49	90.7	107	AAW76033	Humanised CMV5 ant
9	49	90.7	107	AAW76033	Human WOI antibody
10	49	90.7	109	AAW76033	Humanised LM609 an

11	49	90.7	109	20	AAW760380	Murine monoclonal
12	49	90.7	109	20	AAW760382	Humanised LM609 an
13	49	90.7	127	15	AAW760393	Sequence of mouse
14	49	90.7	127	22	AAW760393	Murine CMV5 antio
15	47	87.0	9	19	AAW76013	LM609 grafted anti
16	47	87.0	9	22	AAW76013	LM609 VL CDR3 pep
17	47	87.0	9	22	AAW76013	LM609 grafted anti
18	47	87.0	107	19	AAW76006	Vitaxin antibody 1
19	47	87.0	107	19	AAW76006	LM609 antibody lig
20	47	87.0	107	22	AAW76006	A light chain vari
21	47	87.0	107	22	AAW76006	A light chain vari
22	47	87.0	107	22	AAW76006	Vitaxin light chai
23	47	87.0	107	22	AAW76006	Antibody LM609 lig
24	47	87.0	107	22	AAW76006	Light chain variab
25	44	81.5	82	23	ABP34862	Human ORF3835 prot
26	44	81.5	259	21	AAW76006	TMV 30K movement p
27	44	81.5	1194	22	ABW62985	Drosophila melanog
28	43	79.6	107	14	AAW76001	HYH light chain.
29	43	79.6	107	19	AAW58482	Murine HYH antibod
30	43	79.6	108	12	AAW15438	Light chain variab
31	43	79.6	109	15	AAW52033	Light chain variab
32	43	79.6	143	18	AAW19580	Mouse anti-idiotyp
33	43	79.6	240	12	AAW15443	Single chain Fv fr
34	43	79.6	1109	22	ABW66902	Drosophila melanog
35	41	75.9	366	22	ABW68125	Novel human diagno
36	40	74.1	78	23	ABP05178	JK gene product.
37	40	74.1	105	20	AAW7456	Humanised anti-alp
38	40	74.1	105	20	AAW84098	Humanised anti-alp
39	40	74.1	107	20	AAW84098	Murine vitronectin
40	40	74.1	108	20	AAW84094	Vitronectin alpha-
41	40	74.1	112	20	AAW84100	hIL2R Ab L chain v
42	39	72.2	9	14	AAW37604	LM609 grafted anti
43	39	72.2	9	19	AAW76036	Mutant VL CDR3 pep
44	39	72.2	9	22	AAW76036	Human secreted pro
45	39	72.2	63	21	AAW51734	

ALIGNMENTS

RESULT 1
AAW76034
ID AAW76034 standard; Protein; 9 AA.
XX
AC AAW76034;
XX
DT 02-NOV-1998 (first entry)
XX
DE LM609 grafted antibody V-L region CDR3 protein fragment #3.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-L region; CDR;
KW complementarity determining region.
XX
OS Mus sp.
XX
PN WO9833919-A2.
XX
PD 06-AUG-1998.
XX
PF 30-JAN-1998; 98WO-US01826.
XX
PR 30-JAN-1997; 97US-0791391.
PA (IXSY-) IXSYS INC.
XX
PI Glaser SM, Huse WD;
XX
DR WPI; 1998-437472/37.
DR N-PSDB; AAW49871.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
XX
PS Claim 62; Page 41; 129pp; English.
XX
CC AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
CC antibodies contain non-murine framework regions so are suitable for use
CC in humans. Enhanced types of LM609 have affinity more than 90 times
CC greater than that of parent the parent antibody.
XX
XX Sequence 9 AA;
SQ

Query Match 100.0%; Score 54; DB 19; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQSTSWPHT 9
| | | | | | | |
Db 1 QQSTSWPHT 9

RESULT 2
AAB61392
ID AAB61392 standard; peptide; 9 AA.
XX
AC AAB61392;
XX
XX 03-APR-2001 (first entry)
DT
XX
DE Mutant VL CDR3 peptide #2.
XX
XX LM609; grafted antibody; alphaVbeta3 integrin; angiogenesis;
KW inflammatory; cancer; retina; restenosis; osteoporosis.
KW
XX Unidentified.
OS
XX WO200078815-A1.
PN
XX 28-DEC-2000.
PD
XX 23-JUN-2000; 2000WO-US17454.
PF
XX 24-JUN-1999; 99US-0339922.
PR
XX (MOLE-) APPLIED MOLECULAR EVOLUTION.
PA
XX Huse WD, Wu H;
PI
XX WPI; 2001-050110/06.
DR
XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
XX to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
PT osteoporosis -
XX
XX Disclosure; Page 41; 132pp; English.
XX
CC The present invention relates to enhanced LM609 grafted antibodies
CC exhibiting selective binding affinity to alphavbeta3 integrin or
CC their functional fragments. The antibodies or their functional
CC fragments can be used in the diagnosis and treatment of
CC alphavbeta3-mediated diseases such as angiogenesis, inflammatory

CC diseases (such as psoriasis and chronic articular rheumatism),
CC disorders associated with inappropriate or inopportune invasion of
CC vessels (such as diabetic retinopathy, neovascular glaucoma and
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
CC diseases (such as macular degeneration), restenosis and
CC osteoporosis.
XX
XX Sequence 9 AA;
SQ

Query Match 100.0%; Score 54; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQSTSWPHT 9
| | | | | | | |
Db 1 QQSTSWPHT 9

RESULT 3
AAW76033
ID AAW76033 standard; Protein; 9 AA.
XX
AC AAW76033;
XX
XX 02-NOV-1998 (first entry)
DT
XX
DE LM609 grafted antibody V-L region CDR3 protein fragment #2.
XX
XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-L region; CDR;
KW complementarity determining region.
XX
XX Mus sp.
OS
XX WO9833919-A2.
PN
XX 06-AUG-1998.
PD
XX 30-JAN-1998; 98WO-US01826.
PF
XX 30-JAN-1997; 97US-0791391.
PR
XX (IXSY-) IXSYS INC.
PA
XX Glaser SM, Huse WD;
PI
XX WPI; 1998-437472/37.
DR
XX N-PSDB; AAV49870.
DR
XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
XX Claim 62; Page 41; 129pp; English.
PS
XX
XX AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
CC antibodies contain non-murine framework regions so are suitable for use
CC in humans. Enhanced types of LM609 have affinity more than 90 times
CC greater than that of parent the parent antibody.
XX
XX Sequence 9 AA;
SQ

Query Match 90.7%; Score 49; DB 19; Length 9;
 Best Local Similarity 88.9%; Pred. No. 7.8e+05;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSTSWPHT 9
 ||| |||||
 Db 1 QQSNSWPHT 9

RESULT 4

AAV06372
 ID AAY06372 standard; Peptide; 9 AA.

XX
 AC AAY06372;

XX
 DT 06-SEP-1999 (first entry)

XX
 DE Murine monoclonal antibody LM609 VL CDR3.

XX Humanised antibody; antibody humanisation; antibody engineering;
 KW LM609; monoclonal antibody; complementarity determining region;
 KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
 KW cancer; therapy; diagnosis.

XX
 OS Mus musculus.

XX
 PN WO9929888-A1.

XX
 PD 17-JUN-1999.

XX
 PF 04-DEC-1998; 98WO-US25828.

XX
 PR 05-DEC-1997; 97US-0986016.

XX
 PA (SCRI) SCRIPPS RES INST.

XX
 PI Barbas CF, Rader C;

XX
 DR WPI; 1999-394979/33.

XX
 PT Production of humanized mouse monoclonal antibodies

XX
 PS Disclosure; Page 45; 55pp; English.

XX This sequence represents complementarity determining region 3
 CC (LCDR3) of the light chain of murine monoclonal antibody LM609.
 CC LM609 is directed to integrin alpha-v beta-3. It selectively
 CC promotes apoptosis of vascular cells stimulated to undergo
 CC angiogenesis, making it a tool for cancer diagnosis and therapy.
 CC The invention provides humanised antibodies, especially humanised
 CC LM609. In such humanized antibodies, a light chain CDR from a
 CC mouse antibody such as LM609 is grafted onto a human light chain,
 CC and a heavy chain CDR from a mouse antibody is grafted onto a human
 CC antibody heavy chain to produce libraries from which a humanised
 CC murine antibody having the desired specificity is selected. By
 CC preserving the original CDR sequences such as the HCDR3 and LCDR3
 CC sequences of LM609, the humanisation strategy ensures epitope
 CC conservation.

XX
 SQ Sequence 9 AA;

Query Match 90.7%; Score 49; DB 20; Length 9;
 Best Local Similarity 88.9%; Pred. No. 7.8e+05;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSTSWPHT 9
 ||| |||||
 Db 1 QQSNSWPHT 9

RESULT 5

AAB61391

ID AAB61391 standard; peptide; 9 AA.

XX
 AC AAB61391;

XX
 DT 03-APR-2001 (first entry)

XX
 DE Mutant VL CDR3 peptide #1.

XX
 KW LM609; grafted antibody; alphaVbeta_3 integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis.

XX
 OS Unidentified.

XX
 PN WO200078815-A1.

XX
 PD 28-DEC-2000.

XX
 PF 23-JUN-2000; 2000WO-US17454.

XX
 PR 24-JUN-1999; 99US-0339922.

XX
 PA (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX
 PI Huse WD, Wu H;

XX
 DR WPI; 2001-050110/06.

XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 CC to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 CC angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 CC osteoporosis

XX
 PS Disclosure; Page 41; 132pp; English.

XX The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphaVbeta_3 integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphaVbeta_3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.

XX
 SQ Sequence 9 AA;

Query Match 90.7%; Score 49; DB 22; Length 9;
 Best Local Similarity 88.9%; Pred. No. 7.8e+05;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSTSWPHT 9
 ||| |||||
 Db 1 QQSNSWPHT 9

RESULT 6

AAR25729

ID AAR25729 standard; Protein; 107 AA.

XX
 AC AAR25729;

XX
 DT 13-JAN-1993 (first entry)

XX
 DE Humanised VL region of the mouse CMV5 antibody.

XX Murine; immunoglobulin; CDR; non immunogenic; cytomegalovirus;
 KW gH; light chain; variable region; framework; human; Wol.

XX
 OS Mus musculus.

XX
 FH Key

Location/Qualifiers

FT Region 24..34
 FT /note= "CDR"
 FT Region 50..56
 FT /note= "CDR"
 FT Region 89..97
 FT /note= "CDR"
 FT Misc-difference 49
 FT /note= "mutated residue"

XX WO9211018-A.
 XX
 XX
 XX 09-JUL-1992.
 XX
 XX 19-DEC-1991; 91WO-US09711.
 XX
 XX 19-DEC-1990; 90US-0634278.
 XX
 XX (PROT-) PROTEIN DESIGN LABS INC.
 XX
 XX Co MS, Coelingh KL, Landolfi NF, Queen CL, Schneider WP;
 XX
 XX WPI; 1992-249842/30.
 XX
 XX New immunoglobulin(s) having murine CDRs in human framework
 PT regions - have lower antigenicity; useful for treating e.g. HSV,
 PT CMV, T-cell disorders, myeloid disorders and auto-immune
 PT conditions
 XX
 XX Claim 40; Fig 27A; 141pp; English.
 XX
 XX The sequence shows the humanised mature light chain variable
 CC region of the mouse CMV5 antibody. Murine CDRs were used
 CC in a human WOI framework to produce a pure humanised immunoglobulin
 CC (Ig) which is capable of binding to the gH glycoprotein of
 CC cytomegalovirus. The Ig is non immunogenic, due to the human
 CC framework, and has a strong affinity for its predetermined
 CC antigen. They can be produced in large quantities via recombinant
 CC DNA and monoclonal antibody technology. The humanised Igs may be
 CC used alone or in combination with chemotherapeutic agents such as
 CC non-steroidal anti-inflammatory drugs or immunosuppressants.
 CC See also AAR25721-32.
 XX
 XX SQ Sequence 107 AA;

Query Match 90.7%; Score 49; DB 13; Length 107;
 Best Local Similarity 88.9%; Pred. No. 0.23;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSTSWPHT 9
 ||| |||||
 DB 89 QQNSWPHT 97

RESULT 7
 AAB69677
 ID AAB69677 standard; Protein; 107 AA.

XX AAB69677;
 AC
 XX 30-APR-2001 (first entry)
 DE
 XX Murine CMV5 antibody light chain SEQ ID NO: 62.

XX Humanised immunoglobulin; mouse; human; antibody; heavy chain; diabetes;
 KW light chain; graft versus host disease; transplant; autoimmune disease;
 KW multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus;
 KW myasthenia gravis; herpes infection; myeloid leukaemia; CMV infection.

XX Mus sp.
 XX OS
 XX US6180370-B1.
 PN
 XX 30-JAN-2001.
 PD

XX 07-JUN-1995; 95US-0484537.
 XX
 XX 28-DEC-1988; 88US-0290975.
 PR 13-FEB-1989; 89US-0310252.
 PR 28-SEP-1990; 90US-0590274.
 PR 19-DEC-1990; 90US-0634278.
 XX
 XX (PROT-) PROTEIN DESIGN LABS INC.
 XX
 XX Queen CL, Sellick HE;
 PI
 XX WPI; 2001-190856/19.
 DR
 XX
 XX Producing humanized immunoglobulin, involves producing a cell
 PT containing DNA segments encoding humanized heavy and light chain
 PT variable regions, and expressing the DNA segments in the cell -
 XX
 XX Disclosure; Fig 6; 145pp; English.
 PS
 XX The present invention describes a method of producing humanised
 CC immunoglobulins involving expressing in a cell a nucleic acid encoding a
 CC humanised version of an immunoglobulin. This is obtained by comparing a
 CC donor and human immunoglobulin and producing a combined antibody which
 CC contains part of each. These are useful in the treatment of
 CC graft-versus-host disease, transplant rejection, autoimmune diseases such
 CC as diabetes, rheumatoid arthritis, myasthenia gravis, multiple sclerosis
 CC and systemic lupus erythematosus, herpes infections, CMV virus infections
 CC and myeloid leukaemia. The present sequence is an antibody used to
 CC demonstrate the method of the invention.
 XX
 XX SQ Sequence 107 AA;

Query Match 90.7%; Score 49; DB 22; Length 107;
 Best Local Similarity 88.9%; Pred. No. 0.23;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSTSWPHT 9
 ||| |||||
 DB 89 QQNSWPHT 97

RESULT 8
 AAB69678
 ID AAB69678 standard; Protein; 107 AA.

XX AAB69678;
 AC
 XX 30-APR-2001 (first entry)
 DT
 XX Humanised CMV5 antibody light chain SEQ ID NO: 63.

XX Humanised immunoglobulin; mouse; human; antibody; heavy chain; diabetes;
 KW light chain; graft versus host disease; transplant; autoimmune disease;
 KW multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus;
 KW myasthenia gravis; herpes infection; myeloid leukaemia; CMV infection.

XX Mus sp.
 OS Homo sapiens.
 XX
 XX US6180370-B1.
 PN
 XX 30-JAN-2001.
 PD

XX 07-JUN-1995; 95US-0484537.
 XX
 XX 28-DEC-1988; 88US-0290975.
 PR 13-FEB-1989; 89US-0310252.
 PR 28-SEP-1990; 90US-0590274.
 PR 19-DEC-1990; 90US-0634278.

XX (PROT-) PROTEIN DESIGN LABS INC.
 XX
 XX

PI Queen CL, Sellick HE;
 XX WPI; 2001-190856/19.
 XX
 PT Producing humanized immunoglobulin, involves producing a cell
 PT containing DNA segments encoding humanized heavy and light chain
 PT variable regions, and expressing the DNA segments in the cell -
 XX
 PS Disclosure; Fig 6; 145pp; English.
 XX
 CC The present invention describes a method of producing humanised
 CC immunoglobulins involving expressing in a cell a nucleic acid encoding a
 CC humanised version of an immunoglobulin. This is obtained by comparing a
 CC donor and human immunoglobulin and producing a combined antibody which
 CC contains part of each. These are useful in the treatment of
 CC graft-versus-host disease, transplant rejection, autoimmune diseases such
 CC as diabetes, rheumatoid arthritis, myasthenia gravis, multiple sclerosis
 CC and systemic lupus erythematosus, herpes infections, CMV virus infections
 CC and myeloid leukaemia. The present sequence is an antibody used to
 CC demonstrate the method of the invention.
 XX
 SQ Sequence 107 AA;
 Query Match 90.7%; Score 49; DB 22; Length 107;
 Best Local Similarity 88.9%; Pred. No. 0.23;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QQSTSWPHT 9
 DB 89 QQSNSWPHT 97
 III IIIII
 RESULT 9
 AAB69690
 ID AAB69690 standard; Protein; 107 AA.
 XX
 AC AAB69690;
 XX
 DT 30-APR-2001 (first entry)
 XX
 DE Human wol antibody light chain SEQ ID NO: 87.
 XX
 KW Humanised immunoglobulin; mouse; human; antibody; heavy chain; diabetes;
 KW light chain; graft versus host disease; transplant; autoimmune disease;
 KW multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus;
 KW myasthenia gravis; herpes infection; myeloid leukaemia; CMV infection.
 XX
 OS Homo sapiens.
 XX
 PN US6180370-B1.
 XX
 PD 30-JAN-2001.
 XX
 PF 07-JUN-1995; 95US-0484537.
 XX
 PR 28-DEC-1988; 88US-0290975.
 PR 13-FEB-1989; 89US-0310252.
 PR 28-SEP-1990; 90US-0590274.
 PR 19-DEC-1990; 90US-0634278.
 XX
 PA (PROT-) PROTEIN DESIGN LABS INC.
 XX
 PI Queen CL, Sellick HE;
 XX
 DR WPI; 2001-190856/19.
 XX
 PT Producing humanized immunoglobulin, involves producing a cell
 PT containing DNA segments encoding humanized heavy and light chain
 PT variable regions, and expressing the DNA segments in the cell -
 XX
 PS Example 8; Fig 40; 145pp; English.
 XX
 CC The present invention describes a method of producing humanised

CC immunoglobulins involving expressing in a cell a nucleic acid encoding a
 CC humanised version of an immunoglobulin. This is obtained by comparing a
 CC donor and human immunoglobulin and producing a combined antibody which
 CC contains part of each. These are useful in the treatment of
 CC graft-versus-host disease, transplant rejection, autoimmune diseases such
 CC as diabetes, rheumatoid arthritis, myasthenia gravis, multiple sclerosis
 CC and systemic lupus erythematosus, herpes infections, CMV virus infections
 CC and myeloid leukaemia. The present sequence is an antibody used to
 CC demonstrate the method of the invention.
 XX
 SQ Sequence 107 AA;
 Query Match 90.7%; Score 49; DB 22; Length 107;
 Best Local Similarity 88.9%; Pred. No. 0.23;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QQSTSWPHT 9
 DB 89 QQSNSWPHT 97
 III IIIII
 RESULT 10
 AAY06388
 ID AAY06388 standard; Protein; 109 AA.
 XX
 AC AAY06388;
 XX
 DT 06-SEP-1999 (first entry)
 XX
 DE Humanised LM609 antibody VL domain.
 XX
 KW Humanised antibody; antibody humanisation; antibody engineering;
 KW LM609; monoclonal antibody; complementarity determining region;
 KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
 KW cancer; therapy; diagnosis.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key
 FT Peptide
 FT 1..2
 FT Location/Qualifiers
 FT /note= "vector-encoded residues"
 FT Region 24..34
 FT /note= "CDR1"
 FT Region 50..56
 FT /note= "CDR2"
 FT Region 89..97
 FT /note= "CDR3"
 XX
 PN WO9929888-A1.
 XX
 PD 17-JUN-1999.
 XX
 PF 04-DEC-1998; 98WO-US25828.
 XX
 PR 05-DEC-1997; 97US-0986016.
 XX
 PA (SCRI) SCRIPPS RES INST.
 XX
 PI Barbas CF, Rader C;
 XX
 DR WPI; 1999-394979/33.
 XX
 PT Production of humanized mouse monoclonal antibodies
 XX
 PS Disclosure; Page 52; 55pp; English.
 XX
 CC This sequence represents the light chain variable region of a
 CC humanised LM609 antibody. LM609 is directed to human integrin
 CC alpha-v beta-3. It selectively promotes apoptosis of vascular
 CC cells that have been stimulated to undergo angiogenesis, making it
 CC a tool for cancer diagnosis and therapy. The invention provides
 CC humanised antibodies, especially humanised LM609. In such humanized

CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
 CC grafted onto a human light chain, and a heavy chain CDR from a mouse
 CC antibody is grafted onto a human antibody heavy chain to produce
 CC libraries from which a humanised murine antibody having the desired
 CC specificity is selected. By preserving the original CDR sequences
 CC such as the HCDR3 and LCDR3 sequences of LM609 (see AAY06371-72), the
 CC humanisation strategy ensures epitope conservation.

XX Sequence 109 AA;

Query Match 90.7%; Score 49; DB 20; Length 109;

Best Local Similarity 88.9%; Pred. No. 0.23;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOSTSWPHT 9

Db 89 QQSNWPHT 97

RESULT 11

AAY06380

ID AAY06380 standard; Protein; 109 AA.

XX AC AAY06380;

XX DT 06-SEP-1999 (first entry)

XX DE Murine monoclonal antibody LM609 V lambda.

XX KW Humanised antibody; antibody humanisation; antibody engineering;

XX KW LM609; monoclonal antibody; complementarity determining region;

XX KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;

XX KW cancer; therapy; diagnosis.

XX OS Mus musculus.

XX FH Key

XX FT Peptide

XX FT Location/Qualifiers

XX FT 1..2 /note= "vector-encoded residues"

XX FT Region 24..34

XX FT /note= "CDR1"

XX FT Region 50..56

XX FT /note= "CDR2"

XX FT Region 89..97

XX FT /note= "CDR3"

XX PN WO9929888-A1.

XX PD 17-JUN-1999.

XX PF 04-DEC-1998; 98WO-US25828.

XX PR 05-DEC-1997; 97US-0986016.

XX PA (SCRI) SCRIPPS RES INST.

XX PI Barbas CF, Rader C;

XX PT WPI; 1999-394979/33.

XX DR Production of humanized mouse monoclonal antibodies

XX PS Disclosure; Page 49-50; 55pp; English.

XX CC This sequence represents the light chain V lambda region of
 CC murine monoclonal antibody LM609. LM609 is directed to integrin
 CC alpha-v beta-3. It selectively promotes apoptosis of vascular
 CC cells that have been stimulated to undergo angiogenesis, making it
 CC a tool for cancer diagnosis and therapy. The invention provides
 CC humanised antibodies, especially humanised LM609. In such humanized
 CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
 CC grafted onto a human light chain, and a heavy chain CDR from a mouse
 CC antibody is grafted onto a human antibody heavy chain to produce

CC libraries from which a humanised murine antibody having the desired
 CC specificity is selected. By preserving the original CDR sequences
 CC such as the HCDR3 and LCDR3 sequences of LM609 (see AAY06371-72), the
 CC humanisation strategy ensures epitope conservation.

XX Sequence 109 AA;

Query Match 90.7%; Score 49; DB 20; Length 109;

Best Local Similarity 88.9%; Pred. No. 0.23;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOSTSWPHT 9

Db 89 QQSNWPHT 97

RESULT 12

AAY06382

ID AAY06382 standard; Protein; 109 AA.

XX AC AAY06382;

XX DT 06-SEP-1999 (first entry)

XX DE Humanised LM609 antibody VL domain.

XX KW Humanised antibody; antibody humanisation; antibody engineering;

XX KW LM609; monoclonal antibody; complementarity determining region;

XX KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;

XX KW cancer; therapy; diagnosis.

XX OS Homo sapiens.

XX OS Synthetic.

XX FH Key

XX FT Peptide

XX FT Location/Qualifiers

XX FT 1..2 /note= "vector-encoded residues"

XX FT Region 24..34

XX FT /note= "CDR1"

XX FT Region 50..56

XX FT /note= "CDR2"

XX FT Region 89..97

XX FT /note= "CDR3"

XX PN WO9929888-A1.

XX PD 17-JUN-1999.

XX PF 04-DEC-1998; 98WO-US25828.

XX PR 05-DEC-1997; 97US-0986016.

XX PA (SCRI) SCRIPPS RES INST.

XX PI Barbas CF, Rader C;

XX PT WPI; 1999-394979/33.

XX DR Production of humanized mouse monoclonal antibodies

XX PS Disclosure; Page 50; 55pp; English.

XX CC This sequence represents the light chain variable region of a
 CC humanised LM609 antibody. LM609 is directed to human integrin
 CC alpha-v beta-3. It selectively promotes apoptosis of vascular
 CC cells that have been stimulated to undergo angiogenesis, making it
 CC a tool for cancer diagnosis and therapy. The invention provides
 CC humanised antibodies, especially humanised LM609. In such humanized
 CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
 CC grafted onto a human light chain, and a heavy chain CDR from a mouse
 CC antibody is grafted onto a human antibody heavy chain to produce
 CC libraries from which a humanised murine antibody having the desired
 CC specificity is selected. By preserving the original CDR sequences

CC such as the HCDR3 and LCDR3 sequences of LM609 (see AAY06371-72), the
 CC humanisation strategy ensures epitope conservation.

XX Sequence 109 AA;

Query Match 90.7%; Score 49; DB 20; Length 109;
 Best Local Similarity 88.9%; Pred. No. 0.23;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSTSWPHT 9
 ||| |||||
 Db 89 QQSNWPHT 97

RESULT 13

AAR54093
 ID AAR54093 standard; Protein; 127 AA.

XX AAR54093;

DT 29-DEC-1994 (first entry)

XX Sequence of mouse V-kappa showing the sequences of recombinant
 DE anti-FHV-1 antibody CDRs 1, 2 and 3.

XX Feline herpes virus; FHV-1; monoclonal antibody; CDR;

KW complementarity determining region.

XX Mus musculus.

PH Key Location/Qualifiers
 FT Peptide 1..20
 FT /label= leader
 FT Region 21..43
 FT /label= FR1
 FT Region 44..54
 FT /label= CDR1
 FT Region 55..70
 FT /label= FR2
 FT Region 71..76
 FT /label= CDR2
 FT Region 77..108
 FT /label= FR3
 FT Region 109..117
 FT /label= CDR3
 FT Region 118..127
 FT /label= FR4

XX WO9412661-A.

PN 09-JUN-1994.

XX 25-NOV-1993; 93WO-JP01724.

XX 28-NOV-1992; 92JP-0341255.

XX (KAGA) CHEMA SERO THERAPEUTIC RES INST.

XX Kimachi K, Meeda H, Nishiyama K, Tokiyoshi S;

XX WPI; 1994-200288/24.

DR N-PSDB; AAQ64167.

XX Feline monoclonal antibody and recombinant antibodies specific
 PT for FHV-1 - for detection, treatment and prevention of FHV-1
 PT infection.

XX Disclosure; Page 18-19; 53pp; Japanese.

XX The inventors claim a monoclonal antibody against feline herpes
 CC virus (FHV-1). They also claim a recombinant antibody against FHV-1
 CC and fragments of VH and VL CDR1, CDR2 and CDR3. The antibodies are
 CC used in the detection, treatment and prevention of FHV-1. The

CC sequences of the CDRs in the VH of the recombinant anti-FHV-1
 CC antibody are given in AAR54092. The sequences of the CDRs in the VL of
 CC the recombinant anti-FHV-1 antibody are given in AAR54093. These CDR
 CC sequences are claimed.

SQ Sequence 127 AA;

Query Match 90.7%; Score 49; DB 15; Length 127;
 Best Local Similarity 88.9%; Pred. No. 0.27;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSTSWPHT 9
 ||| |||||
 Db 109 QQSNWPHT 117

RESULT 14

AAB69687

ID AAB69687 standard; Protein; 127 AA.

XX AAB69687;

DT 30-APR-2001 (first entry)

XX Murine CMV5 antibody light chain SEQ ID NO: 83.

DE Humanised immunoglobulin; mouse; human; antibody; heavy chain; diabetes;
 KW light chain; graft versus host disease; transplant; autoimmune disease;
 KW multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus;
 KW myasthenia gravis; herpes infection; myeloid leukaemia; CMV infection.

OS Mus sp.

PN US6180370-B1.

XX 30-JAN-2001.

XX 07-JUN-1995; 95US-0484537.

XX 28-DEC-1988; 88US-0290975.

XX 13-FEB-1989; 89US-0310252.

XX 28-SEP-1990; 90US-0590274.

XX 19-DEC-1990; 90US-0634278.

XX (PROT-) PROTEIN DESIGN LABS INC.

XX Queen CL, Selick HE;

XX WPI; 2001-190856/19.

XX N-PSDB; AAF58747.

XX Producing humanized immunoglobulin, involves producing a cell
 PT containing DNA segments encoding humanized heavy and light chain
 PT variable regions, and expressing the DNA segments in the cell -

XX Example 8; Fig 39; 145pp; English.

XX The present invention describes a method of producing humanised
 CC immunoglobulins involving expressing in a cell a nucleic acid encoding a
 CC humanised version of an immunoglobulin. This is obtained by comparing a
 CC donor and human immunoglobulin and producing a combined antibody which
 CC contains part of each. These are useful in the treatment of
 CC graft-versus-host disease, transplant rejection, autoimmune diseases such
 CC as diabetes, rheumatoid arthritis, myasthenia gravis, multiple sclerosis
 CC and systemic lupus erythematosus, herpes infections, CMV virus infections
 CC and myeloid leukaemia. The present sequence is an antibody used to
 CC demonstrate the method of the invention.

SQ Sequence 127 AA;

Query Match 90.7%; Score 49; DB 22; Length 127;
 Best Local Similarity 88.9%; Pred. No. 0.27;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSTSWPHT 9
 ||| |||||
 Db 109 QQNSWPHT 117

RESULT 15

AAW76013
 ID AAW76013 standard; Protein; 9 AA.

XX
 AC AAW76013;

XX
 DT 02-NOV-1998 (first entry)

XX
 DE LM609 grafted antibody V-L region CDR3 protein fragment #1.

XX
 DE Vitaxin; antibody; variable region; heavy chain; light chain; integrin;

XX
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;

XX
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;

XX
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;

XX
 KW macular degeneration; osteoporosis; primer; V-L region; CDR;

XX
 KW complementarity determining region.

XX
 OS Mus sp.

XX
 PN WO9833919-A2.

XX
 PD 06-AUG-1998.

XX
 PF 30-JAN-1998; 98WO-US01826.

XX
 PR 30-JAN-1997; 97US-0791391.

XX
 PA (IXSY-) IXSYS INC.

XX
 PI Glaser SM, Huse WD;

XX
 DR NPI; 1998-437472/37.

XX
 DR N-PSDB; AAV49850.

XX
 PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3

XX
 PT integrin - and related grafted antibodies based on murine monoclonal

XX
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose

XX
 PT angiogenesis or restenosis

XX
 PS Disclosure; Page 40; 129pp; English.

XX
 CC AAW76007-W76040 are protein fragments of the grafted monoclonal antibody

XX
 CC LM609 heavy and light chain variable region. LM609 and the antibody

XX
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to

XX
 CC inhibit binding of alphavbeta3 to a ligand and thus block

XX
 CC integrin-mediated signal transduction. This is useful in the treatment,

XX
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically

XX
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,

XX
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,

XX
 CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The

XX
 CC antibodies contain non-murine framework regions so are suitable for use

XX
 CC in humans. Enhanced types of LM609 have affinity more than 90 times

XX
 CC greater than that of parent the parent antibody.

XX
 SQ Sequence 9 AA;

XX
 Query Match 87.0%; Score 47; DB 19; Length 9;

XX
 Best Local Similarity 88.9%; Pred. No. 7.8e+05;

XX
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

XX
 QY 1 QQSTSWPHT 9

XX
 Db 1 QQSGSWPHT 9

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 Search completed: November 18, 2002, 17:50:48

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 Job time : 26.4079 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 18, 2002, 18:45:22 ; Search time 4.14474 Seconds
(without alignments)
32.704 Million cell updates/sec

Title: us-09-016-061-88
Perfect score: 54
Sequence: 1 QQSTSWPHT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 97044 seqs, 15060890 residues

Total number of hits satisfying chosen parameters: 97044

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*

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- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB pep:*
- 7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB pep:*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB pep:*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB pep:*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	47	87.0	107	8	US-08-790-540A-4
2	47	87.0	107	8	US-08-790-540A-8
3	47	87.0	107	8	US-08-791-391A-4
4	47	87.0	107	8	US-08-791-391A-8
5	47	87.0	107	8	US-08-791-391A-32
6	43	79.6	33	9	US-09-956-206A-12
7	38	70.4	107	10	US-09-756-301A-3
8	38	70.4	107	10	US-09-927-703-3
9	38	70.4	107	10	US-09-766-535A-3
10	38	70.4	107	10	US-09-756-161A-3
11	38	70.4	107	12	US-10-010-229-3
12	38	70.4	107	12	US-10-043-450-3
13	38	70.4	107	12	US-10-044-534-3
14	38	70.4	128	12	US-10-006-773-6
15	38	70.4	235	12	US-10-020-139-3
16	35	64.8	111	10	US-09-840-459-11
17	35	64.8	154	10	US-09-759-143-383
18	35	64.8	154	10	US-09-780-669-383
19	35	64.8	154	10	US-09-822-827-383

20	35	64.8	161	10	US-09-759-143-846	Sequence 846, Appl
21	35	64.8	161	10	US-09-780-669-846	Sequence 846, Appl
22	35	64.8	161	10	US-09-822-827-846	Sequence 846, Appl
23	35	64.8	235	12	US-10-020-139-4	Sequence 4, Appl
24	34	63.0	9	9	US-09-968-561A-72	Sequence 72, Appl
25	34	63.0	9	9	US-09-968-561A-240	Sequence 240, Appl
26	34	63.0	9	10	US-09-192-854-48	Sequence 48, Appl
27	34	63.0	90	10	US-09-764-860-458	Sequence 458, Appl
28	34	63.0	100	10	US-09-899-896-2	Sequence 2, Appl
29	34	63.0	112	10	US-09-840-459-56	Sequence 58, Appl
30	34	63.0	112	10	US-09-840-459-61	Sequence 61, Appl
31	34	63.0	112	10	US-09-840-459-70	Sequence 70, Appl
32	33	61.1	20	10	US-09-205-658-281	Sequence 281, Appl
33	33	61.1	51	10	US-09-864-761-37934	Sequence 37934, A
34	33	61.1	100	10	US-09-899-896-4	Sequence 4, Appl
35	33	61.1	741	10	US-09-925-301-930	Sequence 930, Appl
36	33	61.1	1417	10	US-09-753-143-78	Sequence 78, Appl
37	32	59.3	72	10	US-09-764-869-744	Sequence 744, Appl
38	32	59.3	106	10	US-09-864-761-41749	Sequence 41749, A
39	32	59.3	135	9	US-09-957-995A-10	Sequence 10, Appl
40	32	59.3	154	10	US-09-764-864-814	Sequence 814, Appl
41	32	59.3	155	10	US-09-764-864-825	Sequence 825, Appl
42	32	59.3	222	8	US-08-424-550B-609	Sequence 609, Appl
43	32	59.3	264	8	US-08-424-550B-76	Sequence 76, Appl
44	32	59.3	272	10	US-09-782-980-30	Sequence 30, Appl
45	32	59.3	307	10	US-09-864-761-36802	Sequence 36802, A

ALIGNMENTS

RESULT 1
US-08-790-540A-4
; Sequence 4, Application US/08790540A
; Patent No. US20010011125A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; CITY: 4370 La Jolla Village Drive, Suite 700
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,540A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-790-540A-4

Query Match 87.0%; Score 47; DB 8; Length 107;
Best Local Similarity 88.9%; Pred. No. 0.18;

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Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSTSWPHT 9
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Db 89 QOSGWPHT 97

RESULT 2
US-08-790-540A-8
; Sequence 8, Application US/08790540A
; Patent No. US20010011125A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TELECOMMUNICATION INFORMATION:
; REFERENCE/DOCKET NUMBER: 31,815
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,540A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 8
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-790-540A-8

Query Match 87.0%; Score 47; DB 8; Length 107;
Best Local Similarity 88.9%; Pred. No. 0.18;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSTSWPHT 9
   ||| |||||
Db 89 QOSGWPHT 97

RESULT 3
US-08-791-391A-4
; Sequence 4, Application US/08791391A
; Patent No. US20010016645A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TELECOMMUNICATION INFORMATION:
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/791,391A
FILING DATE: 30-JAN-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX 1482
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-791-391A-4

Query Match 87.0%; Score 47; DB 8; Length 107;
Best Local Similarity 88.9%; Pred. No. 0.18;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSTSWPHT 9
   ||| |||||
Db 89 QOSGWPHT 97

RESULT 4
US-08-791-391A-8
; Sequence 8, Application US/08791391A
; Patent No. US20010016645A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TELECOMMUNICATION INFORMATION:
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,391A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 8
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-791-391A-8
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Query Match      87.0%; Score 47; DB 8; Length 107;
Best Local Similarity 88.9%; Pred. No. 0.18;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSTSWPHT 9
Db 89 QOSGSWPHT 97

RESULT 5
US-08-791-391A-32
; Sequence 32, Application US/08791391A
; Patent No. US20010016645A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791.391A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-391A-32

Query Match      87.0%; Score 47; DB 8; Length 107;
Best Local Similarity 88.9%; Pred. No. 0.18;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSTSWPHT 9
Db 89 QOSGSWPHT 97

RESULT 6
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; Sequence 12, Application US/09956206A
; Patent No. US20020164339A1
; GENERAL INFORMATION:
; APPLICANT: DO COUTO, FERNANDO J.R.
; APPLICANT: CERIANI, ROBERTO L.
; APPLICANT: PETERSON, JERRY A.
; TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
; TITLE OF INVENTION: M3 ANTI-BA46 ANTIBODY. METHODS OF USE THEREOF, AND
; METHODS OF HUMANIZING ANTIBODY PEPTIDES
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
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ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/956,206A
FILING DATE: 19-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/525,539
FILING DATE: 14-SEP-1995
APPLICATION NUMBER: PCT/US95/11683
FILING DATE: 14-SEP-1995
APPLICATION NUMBER: 08/487,598
FILING DATE: 7-JUNE-1995
APPLICATION NUMBER: 08/307,868
FILING DATE: 16-SEPT-1994
ATTORNEY/AGENT INFORMATION:
NAME: WITT, ERIC
REGISTRATION NUMBER: 44,408
REFERENCE/DOCKET NUMBER: 2763320000101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-956-206A-12

Query Match      79.6%; Score 43; DB 9; Length 33;
Best Local Similarity 77.8%; Pred. No. 0.28;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSTSWPHT 9
Db 21 QOSNSWPYT 29

RESULT 7
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; Sequence 3, Application US/09756301A
; Patent No. US20010027249A1
; GENERAL INFORMATION:
; APPLICANT: Le, Junming
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Ghayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
; TITLE OF INVENTION: Human Tumor Necrosis Factor
; FILE REFERENCE: 0975.1005-008
; CURRENT APPLICATION NUMBER: US/09/756,301A
; CURRENT FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: U.S. 09/133,119
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1994-10-18
; PRIOR APPLICATION NUMBER: U.S. 08/192,102
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; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,861
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,093
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/010,406
; PRIOR FILING DATE: 1993-01-29
; PRIOR APPLICATION NUMBER: U.S. 08/013,413
; PRIOR FILING DATE: 1993-02-02
; PRIOR APPLICATION NUMBER: U.S. 07/943,852
; PRIOR FILING DATE: 1992-09-11
; PRIOR APPLICATION NUMBER: U.S. 07/853,606
; PRIOR FILING DATE: 1992-03-18
; PRIOR APPLICATION NUMBER: U.S. 07/670,827
; PRIOR FILING DATE: 1991-03-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus Balb/c
US-09-756-301A-3
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Query Match 70.4%; Score 38; DB 10; Length 107;
Best Local Similarity 77.8%; Pred. No. 5.4;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 1 QOQSTSWPHT 9
||| ||| |
DB 89 QQSHSWPFT 97
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RESULT 8

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US-09-927-703-3
; Sequence 3, Application US/09927703
; Patent No. US2002022720A1
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; GENERAL INFORMATION:
; APPLICANT: Le, Junming
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Grayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
; TITLE OF INVENTION: Human Tumor Necrosis Factor
; FILE REFERENCE: 0575.1005-013
; CURRENT APPLICATION NUMBER: US/09/927,703
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: U.S. 09/756,398
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: U.S. 09/133,119
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1994-10-18
; PRIOR APPLICATION NUMBER: U.S. 08/192,102
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,861
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,093
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/010,406
; PRIOR FILING DATE: 1993-01-29
; PRIOR APPLICATION NUMBER: U.S. 08/013,413
; PRIOR FILING DATE: 1993-02-02
; PRIOR APPLICATION NUMBER: U.S. 07/943,852
; PRIOR FILING DATE: 1992-09-11
; PRIOR APPLICATION NUMBER: U.S. 07/853,606
; PRIOR FILING DATE: 1992-03-18
; PRIOR APPLICATION NUMBER: U.S. 07/670,827
; PRIOR FILING DATE: 1991-03-18
; NUMBER OF SEQ ID NOS: 19
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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus Balb/c
US-09-927-703-3
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Query Match 70.4%; Score 38; DB 10; Length 107;
Best Local Similarity 77.8%; Pred. No. 5.4;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 1 QOQSTSWPHT 9
||| ||| |
DB 89 QQSHSWPFT 97
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RESULT 9

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US-09-766-535A-3
; Sequence 3, Application US/09766535A
; Patent No. US20020106372A1
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; GENERAL INFORMATION:
; APPLICANT: Le, Junming
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Grayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
; TITLE OF INVENTION: Human Tumor Necrosis Factor
; FILE REFERENCE: 0975.1005-010
; CURRENT APPLICATION NUMBER: US/09/766,535A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: U.S. 09/133,119
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1994-10-18
; PRIOR APPLICATION NUMBER: U.S. 08/192,102
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,861
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,093
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/010,406
; PRIOR FILING DATE: 1993-01-29
; PRIOR APPLICATION NUMBER: U.S. 08/013,413
; PRIOR FILING DATE: 1993-02-02
; PRIOR APPLICATION NUMBER: U.S. 07/943,852
; PRIOR FILING DATE: 1992-09-11
; PRIOR APPLICATION NUMBER: U.S. 07/853,606
; PRIOR FILING DATE: 1992-03-18
; PRIOR APPLICATION NUMBER: U.S. 07/670,827
; PRIOR FILING DATE: 1991-03-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus Balb/c
US-09-766-535A-3
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```
Query Match 70.4%; Score 38; DB 10; Length 107;
Best Local Similarity 77.8%; Pred. No. 5.4;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 1 QOQSTSWPHT 9
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DB 89 QQSHSWPFT 97
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RESULT 10

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US-09-756-161A-3
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; Sequence 3, Application US/09756161A
; Patent No. US20020132307A1
; GENERAL INFORMATION:
; APPLICANT: Le, Junming
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Grayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
; TITLE OF INVENTION: Human Tumor Necrosis Factor
; FILE REFERENCE: 0975.1005-007
; CURRENT APPLICATION NUMBER: US/09/756,161A
; CURRENT FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: U.S. 09/133,119
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1994-10-18
; PRIOR APPLICATION NUMBER: U.S. 08/192,102
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,861
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,093
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/010,406
; PRIOR FILING DATE: 1993-01-29
; PRIOR APPLICATION NUMBER: U.S. 08/013,413
; PRIOR FILING DATE: 1993-02-02
; PRIOR APPLICATION NUMBER: U.S. 07/943,852
; PRIOR FILING DATE: 1992-09-11
; PRIOR APPLICATION NUMBER: U.S. 07/853,606
; PRIOR FILING DATE: 1992-03-18
; PRIOR APPLICATION NUMBER: U.S. 07/670,827
; PRIOR FILING DATE: 1991-03-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus Balb/c
US-09-756-161A-3
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Query Match 70.4%; Score 38; DB 10; Length 107;
Best Local Similarity 77.8%; Pred. No. 5.4;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy 1 QOSTSWPHT 9
Db 89 QQSHSWPFT 97
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RESULT 11

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US-10-010-229-3
; Sequence 3, Application US/10010229
; Patent No. US20020114805A1
; GENERAL INFORMATION:
; APPLICANT: Le, Junming
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Grayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
; TITLE OF INVENTION: Human Tumor Necrosis Factor
; FILE REFERENCE: 0975.1005-013
; CURRENT APPLICATION NUMBER: US/10/010,229
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US/09/927,703
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 3
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus Balb/c
US-10-010-229-3
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Query Match 70.4%; Score 38; DB 12; Length 107;
Best Local Similarity 77.8%; Pred. No. 5.4;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy 1 QOSTSWPHT 9
Db 89 QQSHSWPFT 97
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RESULT 12

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US-10-043-450-3
; Sequence 3, Application US/10043450
; Patent No. US20020141996A1
; GENERAL INFORMATION:
; APPLICANT: Le, Junming
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Grayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
; TITLE OF INVENTION: Human Tumor Necrosis Factor
; FILE REFERENCE: 0975.1005-013
; CURRENT APPLICATION NUMBER: US/10/043,450
; CURRENT FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: 09/927,703
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: U.S. 09/756,398
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: U.S. 09/133,119
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1994-10-18
; PRIOR APPLICATION NUMBER: U.S. 08/192,102
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,861
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,093
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/010,406
; PRIOR FILING DATE: 1993-01-29
; PRIOR APPLICATION NUMBER: U.S. 08/013,413
; PRIOR FILING DATE: 1993-02-02
; PRIOR APPLICATION NUMBER: U.S. 07/943,852
; PRIOR FILING DATE: 1992-09-11
; PRIOR APPLICATION NUMBER: U.S. 07/853,606
; PRIOR FILING DATE: 1992-03-18
; PRIOR APPLICATION NUMBER: U.S. 07/670,827
; PRIOR FILING DATE: 1991-03-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 3
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; LENGTH: 107
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; TYPE: PRT
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; ORGANISM: Mus Balb/c
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US-10-043-450-3
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Query Match 70.4%; Score 38; DB 12; Length 107;
Best Local Similarity 77.8%; Pred. No. 5.4;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy 1 QOSTSWPHT 9
Db 89 QQSHSWPFT 97
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RESULT 13
US-10-044-534-3
; Sequence 3, Application US/10044534
; Patent No. US20020146419A1
; GENERAL INFORMATION:
; APPLICANT: Le, Junming
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Grayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
; TITLE OF INVENTION: Human Tumor Necrosis Factor
; FILE REFERENCE: 0975.1005-013
; CURRENT APPLICATION NUMBER: US/10/044,534
; CURRENT FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: 09/927,703
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: U.S. 09/756,398
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: U.S. 09/133,119
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1994-10-18
; PRIOR APPLICATION NUMBER: U.S. 08/192,102
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,861
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,093
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/010,406
; PRIOR FILING DATE: 1993-01-29
; PRIOR APPLICATION NUMBER: U.S. 08/013,413
; PRIOR FILING DATE: 1993-02-02
; PRIOR APPLICATION NUMBER: U.S. 07/943,852
; PRIOR FILING DATE: 1992-09-11
; PRIOR APPLICATION NUMBER: U.S. 07/853,606
; PRIOR FILING DATE: 1992-03-18
; PRIOR APPLICATION NUMBER: U.S. 07/670,827
; PRIOR FILING DATE: 1991-03-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus Balb/c
US-10-044-534-3
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Query Match 70.4%; Score 38; DB 12; Length 107;
Best Local Similarity 77.8%; Pred. No. 5.4;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQSTSWPHT 9
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Db 89 QQSHSWPFT 97
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RESULT 14
US-10-006-773-6
; Sequence 6, Application US/10006773
; Patent No. US20020132983A1
; GENERAL INFORMATION:
; APPLICANT: Jungmans, Richard P.
; TITLE OF INVENTION: Antibodies as Chimeric Effector Cell Receptors Against Tumor Anti
; FILE REFERENCE: 003
; CURRENT APPLICATION NUMBER: US/10/006,773
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: 60/250,089
; PRIOR FILING DATE: 2000-11-30
; NUMBER OF SEQ ID NOS: 19
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-006-773-6

Query Match 70.4%; Score 38; DB 12; Length 128;
Best Local Similarity 77.8%; Pred. No. 6.4;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQSTSWPHT 9
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Db 109 QQSNWPLT 117

RESULT 15
US-10-020-139-3
; Sequence 3, Application US/10020139
; Patent No. US20020132304A1
; GENERAL INFORMATION:
; APPLICANT: DUAN, ROXANNE
; APPLICANT: RUBEN, STEVEN
; TITLE OF INVENTION: Parotid Secretory Protein
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/020,139
; FILING DATE: 18-Dec-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/993,529
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ANDERS A.
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF348
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 301-8439
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-020-139-3

Query Match 70.4%; Score 38; DB 12; Length 235;
Best Local Similarity 85.7%; Pred. No. 11;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQSTSWP 7
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Db 54 QQATSWP 60
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Search completed: November 18, 2002, 19:04:22
Job time : 5.14474 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:43:42 ; Search time 8.52632 Seconds
(without alignments)
31.058 Million cell updates/sec

Title: us-09-016-061-88
Perfect score: 54
Sequence: 1 QOSTSWPHT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	49	90.7	100	1	US-08-436-463-19
2	49	90.7	107	1	US-07-634-278-62
3	49	90.7	107	1	US-07-634-278-63
4	49	90.7	107	1	US-07-634-278-87
5	49	90.7	107	1	US-08-477-728-62
6	49	90.7	107	1	US-08-477-728-63
7	49	90.7	107	1	US-08-477-728-87
8	49	90.7	107	1	US-08-474-040-62
9	49	90.7	107	1	US-08-474-040-63
10	49	90.7	107	1	US-08-474-040-87
11	49	90.7	107	1	US-08-487-200-62
12	49	90.7	107	1	US-08-487-200-63
13	49	90.7	107	1	US-08-487-200-87
14	49	90.7	107	4	US-08-484-537-62
15	49	90.7	107	4	US-08-484-537-63
16	49	90.7	107	4	US-08-484-537-87
17	49	90.7	127	1	US-07-634-278-83
18	49	90.7	127	1	US-08-477-728-83
19	49	90.7	127	1	US-08-474-040-83
20	49	90.7	127	1	US-08-487-200-83
21	49	90.7	127	1	US-08-436-463-4
22	49	90.7	127	1	US-08-484-537-83
23	43	79.6	33	4	US-08-525-539A-12
24	43	79.6	107	1	US-08-436-463-20
25	43	79.6	107	1	US-08-107-669D-1
26	43	79.6	107	1	US-08-472-788A-1
27	43	79.6	107	2	US-08-477-531B-1

28	43	79.6	107	2	US-08-082-842A-1	Sequence 1, Appl
29	43	79.6	109	1	US-07-942-245-4	Sequence 4, Appl
30	43	79.6	143	2	US-08-653-402B-8	Sequence 8, Appl
31	39	72.2	9	2	US-08-232-081B-6	Sequence 6, Appl
32	39	72.2	107	2	US-08-232-081B-9	Sequence 9, Appl
33	39	72.2	107	2	US-08-232-081B-40	Sequence 40, Appl
34	38	70.4	9	2	US-08-476-176B-55	Sequence 55, Appl
35	38	70.4	9	3	US-08-127-721A-55	Sequence 55, Appl
36	38	70.4	9	3	US-08-485-246A-55	Sequence 55, Appl
37	38	70.4	13	1	US-08-221-580-7	Sequence 7, Appl
38	38	70.4	13	5	PCT-US95-04018-69	Sequence 21, Appl
39	38	70.4	103	1	US-08-436-463-21	Sequence 4, Appl
40	38	70.4	106	2	US-08-800-198-4	Sequence 4, Appl
41	38	70.4	106	3	US-09-296-593-4	Sequence 3, Appl
42	38	70.4	107	1	US-08-192-102-3	Sequence 3, Appl
43	38	70.4	107	1	US-08-324-799-3	Sequence 3, Appl
44	38	70.4	107	2	US-08-192-861A-3	Sequence 4, Appl
45	38	70.4	107	2	US-08-476-176B-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-08-436-463-19
; Sequence 19, Application US/08436463
; Patent No. 5760185
; GENERAL INFORMATION:
; APPLICANT: KIMACHI, Kazuhiko
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: NISHIYAMA, Kiyoto
; APPLICANT: TOKIYOSHI, Sachio
; TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT
; TITLE OF INVENTION: ANTIBODY AND GENE FRAGMENT CODING FOR SAID ANTIBODY
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,463
FILING DATE: 26-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 341255/1992
FILING DATE: 28-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: KIMACHI-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 100 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-436-463-19

Query Match 90.7%; Score 49; DB 1; Length 100;
Best Local Similarity 88.9%; Pred. No. 0.12;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 87:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-634-278-87

Query Match 90.7%; Score 49; DB 1; Length 107;
Best Local Similarity 88.9%; Pred. No. 0.13;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOQSTSWPHT 9
||| |||||
Db 89 QOQNSWPHT 97

RESULT 5
US-08-477-728-62
Sequence 62, Application US/08477728
Patent No. 5585089
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,728

FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-477-728-62

Query Match 90.7%; Score 49; DB 1; Length 107;
Best Local Similarity 88.9%; Pred. No. 0.13;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOQSTSWPHT 9
||| |||||
Db 89 QOQNSWPHT 97

RESULT 6
US-08-477-728-63
Sequence 63, Application US/08477728
Patent No. 5585089
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,728
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252

;; FILING DATE: 13-FEB-1989
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/290,975
;; FILING DATE: 28-DEC-1988
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Smith, William M
;; REGISTRATION NUMBER: 30,223
;; REFERENCE/DOCKET NUMBER: 11823-002600
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 326-2400
;; TELEFAX: (415) 326-2422
;; INFORMATION FOR SEQ ID NO: 63:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 107 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-477-728-63

Query Match 90.7%; Score 49; DB 1; Length 107;
Best Local Similarity 88.9%; Pred. No. 0.13;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSTSWPHT 9
Db 89 QQNSWPHT 97

RESULT 7

US-08-477-728-87
; Sequence 87, Application US/08477728
; Patent No. 5585089
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,728
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

;; TELEFAX: (415) 326-2422
;; INFORMATION FOR SEQ ID NO: 87:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 107 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-477-728-87

Query Match 90.7%; Score 49; DB 1; Length 107;
Best Local Similarity 88.9%; Pred. No. 0.13;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSTSWPHT 9
Db 89 QQNSWPHT 97

RESULT 8

US-08-474-040-62
; Sequence 62, Application US/08474040
; Patent No. 5693761
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,040
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-474-040-62

Query Match 90.7%; Score 49; DB 1; Length 107;
Best Local Similarity 88.9%; Pred. No. 0.13;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSTSWPHT 9
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Db 89 QQSNWPHT 97

RESULT 9

US-08-474-040-63
; Sequence 63, Application US/08474040
; Patent No. 5693761
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO. Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474, 040
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634, 278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590, 274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310, 252
; FILING DATE: 13-FEB-1989
; APPLICATION NUMBER: US 07/290, 975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-474-040-63

Query Match 90.7%; Score 49; DB 1; Length 107;
Best Local Similarity 88.9%; Pred. No. 0.13;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSTSWPHT 9
||| |||||

Db 89 QQSNWPHT 97

RESULT 10

US-08-474-040-87
; Sequence 87, Application US/08474040
; Patent No. 5693761
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO. Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474, 040
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634, 278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590, 274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310, 252
; FILING DATE: 13-FEB-1989
; APPLICATION NUMBER: US 07/290, 975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 87:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-474-040-87

Query Match 90.7%; Score 49; DB 1; Length 107;
Best Local Similarity 88.9%; Pred. No. 0.13;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSTSWPHT 9
||| |||||

Db 89 QQSNWPHT 97

RESULT 11

US-08-487-200-62
; Sequence 62, Application US/08487200
; Patent No. 5693762
; GENERAL INFORMATION:

APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,200
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-487-200-62

Query Match 90.7%; Score 49; DB 1; Length 107;
Best Local Similarity 88.9%; Pred. No. 0.13;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSTSWPHT 9
||| |||||
Db 89 QQSNWPHT 97

RESULT 12
US-08-487-200-63
Sequence 63, Application US/08487200
Patent No. 5693762
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS

NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,200
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-487-200-63

Query Match 90.7%; Score 49; DB 1; Length 107;
Best Local Similarity 88.9%; Pred. No. 0.13;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSTSWPHT 9
||| |||||
Db 89 QQSNWPHT 97

RESULT 13
US-08-487-200-87
Sequence 87, Application US/08487200
Patent No. 5693762
GENERAL INFORMATION:

APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US


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; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,200
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002610
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 87:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-487-200-87

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Query Match 90.7%; Score 49; DB 1; Length 107;
Best Local Similarity 88.9%; Pred. No. 0.13;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 QOSTSWPHT 9
Db 89 QOSNSWPHT 97

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RESULT 14
US-08-484-537-62
; Sequence 62, Application US/08484537
; Patent No. 6180370
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/484,537
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-484-537-62

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Query Match 90.7%; Score 49; DB 4; Length 107;
Best Local Similarity 88.9%; Pred. No. 0.13;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 QOSTSWPHT 9
Db 89 QOSNSWPHT 97

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RESULT 15
US-08-484-537-63
; Sequence 63, Application US/08484537
; Patent No. 6180370
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,537
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-484-537-63

Query Match 90.7%; Score 49; DB 4; Length 107;
Best Local Similarity 88.9%; Pred No. 0.13;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSTSWPHT 9
 | | | | | | | |
Db 89 QQSNSWPHT 97

Search completed: November 18, 2002, 17:55:51
Job time : 8.52632 secs

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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:47:14 ; Search time 9.5921 Seconds
(without alignments)
90.200 Million cell updates/sec

Title: US-09-016-061-90

Perfect score: 51

Sequence: 1 QQSGSWPLT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	88.2	104	2 B43413	Ig kappa chain V r
2	45	88.2	138	2 A26471	Ig kappa chain pre
3	40	78.4	106	2 PL0267	Ig kappa chain V r
4	40	78.4	106	2 PC4282	Ig kappa chain (an
5	40	78.4	107	2 C45722	anti-glycoprotein
6	39	76.5	67	2 PH1081	Ig light chain V r
7	39	76.5	69	2 PH1080	Ig light chain V r
8	39	76.5	553	2 T15220	hypothetical prote
9	38	74.5	107	2 A45722	anti-glycoprotein
10	38	74.5	133	2 S35479	Ig kappa chain pre
11	38	74.5	506	2 AH3252	dTMP kinase (EC 2.
12	37	72.5	102	2 C26346	Ig kappa chain V r
13	37	72.5	128	2 PN0445	Ig kappa chain pre
14	37	72.5	144	2 PL0106	Ig kappa chain pre
15	37	72.5	154	2 T17816	hypothetical prote
16	37	72.5	642	2 H69466	conserved hypotet
17	37	72.5	677	2 D97335	hypothetical prote
18	37	72.5	764	2 T48446	hypothetical prote
19	36	70.6	87	2 PH1082	Ig light chain V r
20	36	70.6	91	2 S37525	Ig kappa chain V r
21	36	70.6	108	2 C30502	Ig kappa chain V r
22	36	70.6	115	1 KVMSL7	Ig kappa chain pre
23	36	70.6	117	2 S40362	Ig kappa chain - h
24	36	70.6	169	2 D65126	probable general s
25	36	70.6	204	2 T32062	hypothetical prote
26	36	70.6	275	2 T70737	hypothetical prote
27	36	70.6	543	2 T06523	cytochrome P450 mo
28	36	70.6	1221	2 E83327	conserved hypotet
29	35	68.6	100	2 G81749	hypothetical prote

30 35 68.6 107 2 B45722 anti-glycoprotein
31 35 68.6 146 2 AD0929 conserved hypotet
32 35 68.6 181 2 A10861 syd protein limor
33 35 68.6 235 1 SQMS parotid secretory
34 35 68.6 317 2 B82084 probable cobalamin
35 35 68.6 365 1 SAVLWE large surface anti
36 35 68.6 366 1 SAVLBD large surface anti
37 35 68.6 366 1 SAVLWD large surface anti
38 35 68.6 499 2 A27198 cellulase (EC 3.2.
39 35 68.6 508 2 A26874 cellulase (EC 3.2.
40 35 68.6 939 2 H81686 valyl-tRNA synthet
41 35 68.6 939 2 H71532 valine-tRNA ligase
42 35 68.6 940 2 F86502 alvl tRNA syntheta
43 35 68.6 940 2 B72120 valine-tRNA ligase
44 34 66.7 91 2 S37511 Ig kappa chain V r
45 34 66.7 96 2 JC5945 regulatory protein

ALIGNMENTS

RESULT 1

B43413
Ig kappa chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: B43413
R:Toniyaama, Y.; Brojer, E.; Ruggeri, Z.M.; Shattil, S.J.; Smiltneck, J.; Gorski, J.;
J. Biol. Chem. 267, 18085-18092, 1992
A:Title: A molecular model of RGD ligands. Antibody D gene segments that direct speci
A:Reference number: A43413; MUID:92388177; PMID:1517241
A:Accession: B43413
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-104 <TOM>
A:Note: sequence extracted from NCBI backbone (NCBIP:112818)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:13-87/Domain: immunoglobulin homology <IMM>

Query Match 88.2%; Score 45; DB 2; Length 104;
Best Local Similarity 88.9%; Pred. No. 0.59;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSGSWPLT 9
||| |||||
Db 86 QQSNWPLT 94

RESULT 2

A26471
Ig kappa chain precursor V region (MAK33) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 23-Jul-1999
C:Accession: A26471
R:Buckel, P.; Hubner-Parajsz, C.; Mattes, R.; Lenz, H.; Haug, H.; Beaucamp, K.
Gene 51, 13-19, 1987
A:Title: Cloning and nucleotide sequence of heavy- and light-chain cDNAs from a creat
A:Reference number: A91572; MUID:87248058; PMID:3110009
A:Accession: A26471
A:Molecule type: mRNA
A:Residues: 1-138 <BUC>
A:Cross-references: GB:M16162; NID:gl96893; PIDN:AAA38823.1; PID:gl96894
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-138/Product: Ig kappa chain V region #status predicted <MAT>

Query Match 88.2%; Score 45; DB 2; Length 138;
Best Local Similarity 88.9%; Pred. No. 0.79;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSGSWPLT 9

Db 109 QQSNWPLT 117
||| |||||

RESULT 3

PL0267

Ig kappa chain V region (anti-DNA, DP12VK) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000

C:Accession: PL0267

R:Shionochik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A

J. Exp. Med. 171, 265-297, 1990

A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic

A:Reference number: PL0231; MUID:90111618; PMID:2104919

A:Accession: PL0267

A:Molecule type: mRNA

A:Residues: 1-106 <SHL>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-23/Region: framework 1

F:16-90/Domain: immunoglobulin homology <IMM>

F:24-34/Region: complementarity-determining 1

F:35-49/Region: framework 2

F:50-56/Region: complementarity-determining 2

F:57-88/Region: framework 3

F:89-97/Region: complementarity-determining 3

F:98-106/Region: framework 4

Query Match 78.4%; Score 40; DB 2; Length 106;

Best Local Similarity 77.8%; Pred. No. 4.4;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQSGSWPLT 9

||| ||| |

Db 89 QQSNWPLT 97

RESULT 4

PC4282

Ig kappa chain (anti-SS-A/Ro 60K peptide) (E-42 and E-56) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 07-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 21-Jan-2000

C:Accession: PC4282; PC4284

R:Suzuki, H.; Takemura, H.; Suzuki, M.; Sekine, Y.; Kashiwagi, H.

Biochem. Biophys. Res. Commun. 232, 101-106, 1997

A:Title: Molecular cloning of anti-ss-A/Ro 60-kDa peptide fab fragments from infiltration

A:Reference number: PC4279; MUID:97236289; PMID:9125110

A:Accession: PC4282

A:Molecule type: protein

A:Residues: 1-106 <SUZ>

A>Note: E-42

A:Accession: PC4284

A:Molecule type: protein

A:Residues: 1-106 <SUZ>

A>Note: E-56

C:Comment: This antibody is commonly found in systemic autoimmune diseases such as Sjogren

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:14-88/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 78.4%; Score 40; DB 2; Length 106;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQSGSWPLT 9

||| |||||

Db 87 QQRASWPLT 95

RESULT 5

C45722

anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 115) - mouse (f

C:Species: Mus musculus (house mouse)

C>Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000

C:Accession: C45722

R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Va

J. Virol. 67, 489-496, 1993

A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on

A:Reference number: A45722; MUID:93100833; PMID:7677958

A:Accession: C45722

A>Status: Preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-107 <SIM>

A>Note: sequence extracted from NCBI backbone (NCBIP:120591)

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: glycoprotein

F:16-90/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 78.4%; Score 40; DB 2; Length 107;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSGSWPLT 9

||| |||||

Db 89 QQSNWPLT 97

RESULT 6

PH1081

Ig light chain V region (clone 165.6) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 15-Jun-1996

C:Accession: PH1081

R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective

A:Reference number: PH0971; MUID:92381444; PMID:1512540

A:Accession: PH1081

A>Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-67 <TIL>

A:Experimental source: B cell, strain [NZB x NZW]F1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

Query Match

Best Local Similarity 76.5%; Score 39; DB 2; Length 67;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQSGSWPLT 9

||| |||||

Db 58 QQSNWPLT 66

RESULT 7

PH1080

Ig light chain V region (clone 165.60) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 15-Jun-1996

C:Accession: PH1080

R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective

A:Reference number: PH0971; MUID:92381444; PMID:1512540

A:Accession: PH1080

A>Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-69 <TIL>

A:Experimental source: B cell, strain [NZB x NZW]F1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

Query Match

Best Local Similarity 76.5%; Score 39; DB 2; Length 69;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQSGSWPLT 9

Db 60 QQSNWPQT 68

RESULT 8

T15220
hypothetical protein F57C9.8 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T15220
R:Gelsel, C.; Kramer, J.; Gibson, A.
Submitted to the EMBL Data Library, May 1997
A:Description: The sequence of C. elegans cosmid F57C9.
A:Reference number: Z18309
A:Accession: T15220
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-553 <GEI>
A:Cross-references: EMBL:AF003142; NID:q2088743; PID:q2088751; PIDN:AAB54191.1; GSPDB:GN
A:Experimental source: strain Bristol N2; clone F57C9
C:Genetics:
A:Gene: CESP:F57C9.8
A:Map position: 1
A:Introns: 184/1; 233/3; 286/3; 496/1

Query Match 76.5%; Score 39; DB 2; Length 553;
Best Local Similarity 66.7%; Pred. No. 35;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSGSWPLT 9
Db 373 QRSGSWPFS 381

RESULT 9

A45722
anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 5) - mouse (fra
C:Species: Mus musculus (house mouse)
C:Date: 03-Mar-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: A45722
R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Vasqu
J. Virol. 67, 489-496, 1993
A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on hu
A:Reference number: A45722; MUID:93100833; PMID:7677958
A:Accession: A45722
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-107 <SIM>
A:Note: sequence extracted from NCBI backbone (NCBIP:120589)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: glycoprotein
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 74.5%; Score 38; DB 2; Length 107;
Best Local Similarity 77.8%; Pred. No. 9;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQSGSWPLT 9
Db 89 QQSNWPHT 97

RESULT 10

S35479
Ig kappa chain precursor V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-Mar-1997 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: S35479
R:Takeda, Y.; Wise, K.S.; Hoffman, R.W.
Nucleic Acids Res. 20, 4099, 1992
A:Title: Nucleotide sequences of immunoglobulin heavy and light chain V-regions from a m
A:Reference number: S35479; MUID:92375706; PMID:1387203
A:Accession: S35479

A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-123 <TAK>
A:Cross-references: EMBL:M93959; NID:gl97572; PIDN:AAA39079.1; PID:g554148
C:Genetics:
A:Map position: 6

C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-12/Domain: signal sequence (fragment) #status predicted <SIG>
F:13-123/Product: Ig kappa chain V region (fragment) #status predicted <MAT>
F:28-102/Domain: immunoglobulin homology <IMM>

Query Match 74.5%; Score 38; DB 2; Length 123;
Best Local Similarity 77.8%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQSGSWPLT 9
Db 101 QQSNWPHT 109

RESULT 11

AH3252
dTMP kinase (EC 2.7.4.9) [imported] - Brucella melitensis (strain 16M)
C:Species: Brucella melitensis
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 19-Apr-2002
C:Accession: AH3252
R:DelVecchio, V.G.; Kaputral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanov
.; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Let
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melit
A:Reference number: AH3252; PMID:11756688
A:Accession: AH3252
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-506 <KUP>
A:Cross-references: GB:AE008917; PIDN:AAL51187.1; PID:gl7981871; GSPDB:GN00190
A:Experimental source: strain 16M
C:Genetics:
A:Gene: BMEI0005
A:Map position: 1
C:Keywords: phosphotransferase

Query Match 74.5%; Score 38; DB 2; Length 506;
Best Local Similarity 75.0%; Pred. No. 48;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 QQSGSWPLT 9
Db 135 QQGGWPLT 142

RESULT 12

S26346
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C:Accession: S26346
R:Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A:Title: Antibodies that are specific for a single amino acid interchange in a protei
A:Reference number: S26309; MUID:91341421; PMID:1908510
A:Accession: S26346
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-102 <STA>
A:Cross-references: EMBL:X59211; NID:g52338; PIDN:CAA41921.1; PID:gl334075
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:14-88/Domain: immunoglobulin homology <IMM>

Query Match 72.5%; Score 37; DB 2; Length 102;
Best Local Similarity 66.7%; Pred. No. 14;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQSGSWPLT 9

||| :|||

Db 87 QQSNTPVT 95

RESULT 13

PN0445

Ig kappa chain precursor V-I region - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000

C:Accession: PN0445

R:Kaluzs, B.; Betzl, G.; Shao, H.; Diamantstein, T.; Weidle, U.H.

Gene 122, 321-328, 1992

A:Title: A general method for chimerization of monoclonal antibodies by inverse polymerase

A:Reference number: PN0444; MUID:93138402; PMID:1339379

A:Accession: PN0445

A:Molecule type: mRNA

A:Residues: 1-128 <KAL>

A:Cross-references: GB:L02347

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-10/Domain: signal sequence #status predicted <SIG>

F:11-128/Product: Ig light chain kappa-1 V region #status predicted <MAT>

F:26-100/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 72.5%; Score 37; DB 2; Length 128;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQSGSWPLT 9

||| :|||

Db 99 QQTNSWPT 107

RESULT 14

PL0106

Ig kappa chain precursor V-J-C region (LSI) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000

C:Accession: PL0106

R:Silberstein, L.E.; Litwin, S.; Carmack, C.E.

J. Exp. Med. 169, 1631-1643, 1989

A:Title: Relationship of variable region genes expressed by a human B cell lymphoma sec

A:Reference number: PL0106; MUID:99235583; PMID:2541221

A:Accession: PL0106

A:Molecule type: mRNA

A:Residues: 1-144 <SL>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-115/Domain: V region <VRE>

F:36-110/Domain: immunoglobulin homology <IMM>

F:44-54/Region: complementarity-determining 1

F:70-76/Region: complementarity-determining 2

F:109-115/Region: complementarity-determining 3

F:116-127/Domain: J region <JRG>

F:128-144/Domain: C region (fragment) <CRE>

Query Match

Best Local Similarity 72.5%; Score 37; DB 2; Length 144;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQSGSWPLT 9

||| :|||

Db 109 QQRNSWPLT 117

RESULT 15

TI7816

hypotheical protein a317L - Chlorella virus PBCV-1

C:Species: Chlorella virus PBCV-1

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: TI7816

R:Graves, M.V.; Van Etten, J.L.

submitted to the EMBL Data Library, May 1999

A:Reference number: Z18806

A:Accession: TI7816

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-154 <GRA>

A:Cross-references: EMBL:U42580; NID:g4028896; PIDN:AAC96685.1

A:Experimental source: specific host Chlorella strain NC64A

C:Genetics:

A>Note: a317L

Query Match

Best Local Similarity 72.5%; Score 37; DB 2; Length 154;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSGSWPL 8

|||||

Db 33 QQTSGSWPV 40

Search completed: November 18, 2002, 17:57:20

Job time : 9.5921 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:33:36 ; Search time 4.85526 Seconds
(without alignments)
76.883 Million cell updates/sec

Title: US-09-016-061-90
Perfect score: 51
Sequence: 1 QQSGSNPLT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	40	78.4	745	1	CUL2_HUMAN
2	38	74.5	418	1	OR13_DROME
3	38	74.5	471	1	PX22_HUMAN
4	36	70.6	115	1	KV51_MOUSE
5	36	70.6	169	1	GSFH_ECOLI
6	36	70.6	544	1	C821_PEA
7	35	68.6	235	1	PSP_MOUSE
8	35	68.6	365	1	VNSA_HPBD
9	35	68.6	366	1	VNSA_HPBD
10	35	68.6	366	1	VNSA_HPBD
11	35	68.6	499	1	GUN1_BACSU
12	35	68.6	939	1	SVV_CHLMU
13	35	68.6	939	1	SVV_CHLTR
14	35	68.6	940	1	SVV_CHLTP
15	34	66.7	92	1	CATC_RHOOP
16	34	66.7	96	1	CTC1_ACIIM
17	34	66.7	146	1	YFDC_ECOLI
18	34	66.7	147	1	IE63_HSVB
19	34	66.7	470	1	IE63_HSVK
20	34	66.7	540	1	NUSA_MYCPN
21	34	66.7	777	1	BISC_ECOLI
22	34	66.7	1047	1	R1R1_CHLMU
23	34	66.7	1456	1	RRPO_PVX
24	34	66.7	1456	1	RRPO_PVXCP
25	34	66.7	1456	1	RRPO_PVXHB
26	34	66.7	1456	1	RRPO_PVXX3
27	34	66.7	3178	1	YS89_CAEEL
28	33	64.7	226	1	NUKM_NEUCR
29	33	64.7	251	1	BIOC_ECOLI
30	33	64.7	300	1	GP40_HUMAN
31	33	64.7	432	1	NFF1_RAT
32	33	64.7	468	1	NIFB_KLEPN
33	33	64.7	516	1	Y4NML_RHISN

ALIGNMENTS

RESULT 1

ID	CUL2_HUMAN	STANDARD;	PRT;	745 AA.
AC	Q13617; Q00200; Q9UNF9;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Cullin homolog 2 (CUL-2).			
GN	CUL2.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
[1]				
RP	SEQUENCE FROM N.A., AND VARIANT SER-109.			
RX	TISSUE=Kidney;			
RC	MEDLINE=97225922; PubMed=9122164;			
RA	Pause A., Lee S., Worrel R., Chen D.Y.T., Burgess W.H.,			
RA	Linehan W.M., Klausner R.D.;			
RT	"The von Hippel-Lindau tumor-suppressor gene product forms a stable			
RT	complex with human CUL-2, a member of the cdc53 family of proteins.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 94:2156-2161(1997).			
[2]				
RP	SEQUENCE FROM N.A., VARIANT SER-109, AND NEDDYLYATION.			
RC	TISSUE=Brain;			
RX	MEDLINE=99194561; PubMed=10092517;			
RA	Wada H., Yeh E.T.H., Kamitani T.;			
RT	"Identification of NEDD8-conjugation site in human cullin-2.";			
RL	Biochem. Biophys. Res. Commun. 257:100-105(1999).			
[3]				
RP	SEQUENCE OF 95-745 FROM N.A.			
RX	MEDLINE=96279828; PubMed=8681378;			
RA	Kipreos E.T., Lander L.E., Wing J.P., He W.W., Hedgecock E.M.;			
RT	"cul-1 is required for cell cycle exit in C. elegans and identifies a			
RT	novel gene family.";			
RL	Cell 85:829-839(1996).			
CC	-!- FUNCTION: FORMS A STABLE COMPLEX WITH THE VHL TUMOR SUPPRESSOR.			
CC	-!- SIMILARITY: BELONGS TO THE CULLIN FAMILY.			
CC				
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC				
CC	EMBL; U83410; AAC51190.1; -			
DR	EMBL; AF126404; AAD23581.1; -			
DR	EMBL; U58088; AAC50545.1; -			
DR	Gene; HGNC:2552; CUL2.			
DR	MIM: 603135; -			
DR	InterPro: IPR001373; Cullin.			
DR	Pfam; PF00888; Cullin; 1.			
DR	SMART; SM00182; CULLIN; 1.			
DR	PROSITE; PS01256; CULLIN_1; 1.			

O00515 homo sapien
Q03348 rattus norv
P18433 homo sapien
P18052 mus musculu
P97929 mus musculu
P51587 homo sapien
P57499 buchnera ap
P21156 escherichia
P25765 oryza sativ
O88621 mus musculu
Q01602 pseudomonas
P48723 homo sapien

34 33 64.7 517 1 LAD1_HUMAN
35 33 64.7 796 1 PTR_A_RAT
36 33 64.7 802 1 PTR_A_HUMAN
37 33 64.7 829 1 PTR_A_MOUSE
38 33 64.7 3329 1 BRC2_MOUSE
39 33 64.7 3418 1 BRC2_HUMAN
40 32 62.7 302 1 CYSD_BUCAI
41 32 62.7 302 1 CYSD_ECOLI
42 32 62.7 336 1 FXH2_ORYSA
43 32 62.7 401 1 OPDE_PSEAE
44 32 62.7 402 1 STCH_HUMAN
45 32 62.7 471 1

```

DR PROSITE; PS00069; CULLIN_2; 1.
KW Ubl conjugation; Polymorphism.
FT BINDING 689 NEDB8.
FT VARIANT 109 N -> S.
FT 109 /FTid=VAR_011374.
FT CONFLICT 95 98 SKGA -> IRHE (IN REF. 3).
FT CONFLICT 681 681 Q -> H (IN REF. 3).
SQ SEQUENCE 745 AA; 86393 MW; 30647248F671AB0E CRC64;

Query Match 78.4%; Score 40; DB 1; Length 745;
Best Local Similarity 75.0%; Pred. No. 13;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QSGSWPLT 9
I:|:|:|:|
DB 513 QAGAWPLT 520

RESULT 2
OR13_DROME STANDARD; PRT; 418 AA.
AC Q9VXLO:
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Putative odorant receptor 13a.
GN OR13A OR CG12697.
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
[1]
SEQUENCE FROM N.A.
SR STRAIN-Berkeley;
RA MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Gallo R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champagne M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrieria S., Fleischmann W.,
RA Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.P.,
RA Markulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J., Yao Q.A.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou S., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
```

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Science 287:2185-2195(2000).
[2]
CONCEPTUAL TRANSLATION.
RA Robertson H.M.;
RL Unpublished observations (MAY-2001).
CC -!- FUNCTION: PROBABLE ROLE IN THE ODORANT RESPONSE, BEING AN ODORANT
CC RECEPTOR.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: BELONGS TO FAMILY DR-OR OF G-PROTEIN COUPLED
CC RECEPTORS.
CC -!- CAUTION: Ref.1 sequence differs from that shown due to erroneous
CC gene model prediction.
-----
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-----
CC EMBL; AF003500; AAF48549.1; ALT_SEQ.
CC FlyBase; FBgn0030715; Ori3a.
CC InterPro; IPR004117; 7tm_6.
CC Pfam; PF02949; 7tm_6; 1.
CC DR Hypothetical protein; Transmembrane; G-protein coupled receptor;
CC KW Glycoprotein; Olfaction; Multigene family.
CC DOMAIN 1 38 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 39 59 1 (POTENTIAL).
CC DOMAIN 60 70 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 71 91 2 (POTENTIAL).
CC DOMAIN 92 140 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 141 161 3 (POTENTIAL).
CC DOMAIN 162 195 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 196 216 4 (POTENTIAL).
CC DOMAIN 217 273 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 274 294 5 (POTENTIAL).
CC DOMAIN 295 320 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 300 320 6 (POTENTIAL).
CC DOMAIN 321 385 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 386 406 7 (POTENTIAL).
CC DOMAIN 407 418 CYTOPLASMIC (POTENTIAL).
CC CARBOHYD 22 22 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 109 109 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 118 118 N-LINKED (GLCNAC. .) (POTENTIAL).
CC SEQUENCE 418 AA; 48263 MW; 6E8EC466CF246F0E CRC64;

Query Match 74.5%; Score 38; DB 1; Length 418;
Best Local Similarity 85.7%; Pred. No. 16;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 QSGSWPLT 9
I:|:|:|:|
DB 22 NGSWPLT 28

RESULT 3
P2X2_HUMAN STANDARD; PRT; 471 AA.
ID P2X2_HUMAN Q9Y637; Q9Y638; Q9UHD5; Q9UHD6; Q9UHD7; Q9NR37; Q9NR38;
AC Q9UHL9; Q9Y637; Q9Y638; Q9UHD5; Q9UHD6; Q9UHD7; Q9NR37; Q9NR38;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE P2X purinoceptor 2 (ATP receptor) (P2X2) (Purinergic receptor).
GN P2X2 OR P2X2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_Taxid=9606;
[1]
SEQUENCE FROM N.A. (ISOFORMS A; B; C AND D).
RC TISSUE=Pituitary;
RX MEDLINE=20040550; PubMed=10570044;
```


DE transport protein hofH).
GN HOFH OR HOFH OR B3329.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12";
RN Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE OF 1-30 FROM N.A.
RX STRAIN=K12;
RX MEDLINE=95204361; PubMed=7896718;
RA Stojiljkovic I., Schoenher R., Kusters J.G.;
RT "Identification of the hopG gene, a component of Escherichia coli
RT K-12 type II export system, and its conservation among different
RT pathogenic Escherichia coli and Shigella isolates";
RN J. Bacteriol. 177:1892-1895(1995).
CC -!- FUNCTION: INVOLVED IN A GENERAL SECRETION PATHWAY (GSP) FOR THE
CC EXPORT OF PROTEINS (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE PULH/OUTH/XPSH/EXEH/XCPU FAMILY.
CC -----
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CC -----
DR EMBL; U18997; AAA58126.1; -;
DR EMBL; AE000409; AAC76354.1; -;
DR EMBL; U20786; AAA69032.1; -;
DR EcoGene; EG12887; hofH.
DR InterPro; IPR002416; Bac_GSPH.
DR InterPro; IPR001120; Prok_N_methylto.
DR PRINTS; PR00885; BCTERIALGSPH.
DR PROSITE; PS00409; PROKAR_NTER_METHYL; 1.
KW Transport; Methylation; Complete proteome.
FT PROPEP 1 6 BY SIMILARITY.
FT CHAIN 7 169 PUTATIVE GENERAL SECRETION PATHWAY
FT PROTEIN H.
FT MOD_RES 7 7 METHYLATION (BY SIMILARITY).
SQ SEQUENCE 169 AA; 18565 MW; 18565 MW; D42B1127FBB81A09 CRC64;

Query Match 70.68; Score 36; DB 1; Length 169;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SGSWPL 8
Db 154 SGSWPL 159
| | | | | | | |

RESULT 6
C821_PEA
ID C821_PEA STANDARD; PRT; 544 AA.
AC Q43068;
DT 13-DEC-1998 (Rel. 37, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cytochrome P450 82A1 (EC 1.14.-.-) (CYPLXXII) (Fragment).
GN CYP82A1 OR CYP82.
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
OX NCBI_TaxID=3888;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Stem;
RX MEDLINE=96417083; PubMed=8819874;
RA Frank M.R., Deyneka J.M., Schuler M.A.;
RT "Cloning of wound-induced cytochrome P450 monooxygenases expressed in
RT pea";
RN Plant Physiol. 110:1035-1046(1996).
RN [2]
RP REVISIONS TO 47-48; 127; 198-199; 304; 311; 333-335 AND 454.
RA Frank M.R.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -!- INDUCTION: By wounding.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
CC -----
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CC -----
DR EMBL; U29333; AAC49188.2; -;
DR InterPro; IPR001128; Cytochrome_P450.
DR Pfam; PF00067; p450; 1.
DR PRINTS; PR00385; P450.
DR PROSITE; PS00086; CYTOCHROME_P450; 1.
KW Oxidoreductase; Monooxygenase; Membrane; Heme.
FT NON_TER 1 1
FT BINDING 480 480 HEME (BY SIMILARITY).
SQ SEQUENCE 544 AA; 62055 MW; DE006067C33DADE5 CRC64;

Query Match 70.68; Score 36; DB 1; Length 544;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SGSWPL 8
Db 39 SGSWPL 44
| | | | | | | |

RESULT 7
PSP_MOUSE
ID PSP_MOUSE STANDARD; PRT; 235 AA.
AC P07743;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Parotid secretory protein precursor (PSP).
GN PSP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Parotid gland;
RX MEDLINE=85215456; PubMed=2582349;
RA Madsen H.O., Hjorth J.P.;
RT "Molecular cloning of mouse PSP mRNA";
RL Nucleic Acids Res. 13:1-13(1985).
RN [2]
RP SEQUENCE OF 1-87 FROM N.A.
RC STRAIN=C3H; TISSUE=Spleen;
RX MEDLINE=87004556; PubMed=2428613;
RA Poulsen K., Jakobsen B.K., Mikkelsen B.M., Harnmark K.,
RA Nielsen J.F., Hjorth J.P.;
RT "Coordination of murine parotid secretory protein and salivary
RT amylase expression";
RN EMBO J. 5:1891-1896(1986).

```
CC -1- FUNCTION: PSP IS THE MOST ABUNDANT PROTEIN IN THE PAROTID GLAND.
CC ITS FUNCTION IS NOT KNOWN; HOWEVER, ITS PRODUCTION IS COORDINATED
CC WITH THAT OF SALIVARY AMYLASE.
CC -----
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CC -----
DR EMBL: X01697; CAA25846.1; -
DR EMBL: M26807; AAA40009.1; -
DR EMBL: M26806; AAA40009.1; JOINED.
DR PIR: A23031; SQMS.
DR MGD; MGI:97787; Psp.
KW Parotid gland; Signal.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 235 PAROTID SECRETORY PROTEIN.
SQ SEQUENCE 235 AA; 24753 MW; 23311BAE1E6E2EF3 CRC64;
Query Match 68.6%; Score 35; DB 1; Length 235;
Best Local Similarity 75.0%; Pred. No. 31;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 QQSGSWPL 8
DB 54 QQATSWPL 61
RESULT 8
VMSA_HPBDC STANDARD; PRT; 365 AA.
AC P3029;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Major surface antigen precursor.
GN S.
OS Duck hepatitis B virus (strain China) (DHBV).
OC Viruses; Retroid viruses; Hepadnaviridae; Avihepadnavirus.
OX NCBI_TaxID=31510;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=91045091; PubMed=2235506;
RA Tong S., Mattes F., Teubner K., Blum H.E.;
RT "Complete nucleotide sequence of a Chinese duck hepatitis B virus.";
RL Nucleic Acids Res. 18:6139-6139(1990).
CC -----
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CC -----
DR EMBL: M21953; AAA45746.1; -
DR PIR: S12842; SAVLWE.
DR InterPro: IPR000349; Hepvir_surfag.
DR Pfam: PF00695; VMSA; 1.
KW Antigen.
FT CHAIN 1 198 MAJOR SURFACE ANTIGEN.
FT CARBOHYD 297 297 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 365 AA; 40511 MW; 67F3A4174CB7D884 CRC64;
Query Match 68.6%; Score 35; DB 1; Length 365;
Best Local Similarity 71.4%; Pred. No. 47;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 QQSGSWP 7
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DB 96 QQQGAWP 102
RESULT 9
VMSA_HPBDB STANDARD; PRT; 366 AA.
AC P17194;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-MAY-1991 (Rel. 18, Last annotation update)
DE Major surface antigen precursor.
GN S.
OS Duck hepatitis B virus (brown Shanghai duck isolate S5) (DHBV).
OC Viruses; Retroid viruses; Hepadnaviridae; Avihepadnavirus.
OX NCBI_TaxID=10439;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=90085807; PubMed=2596031;
RA Uchida M., Esumi M., Shikata T.;
RT "Molecular cloning and sequence analysis of duck hepatitis B virus
RL Virolgy 173:600-606(1989).
CC -----
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CC -----
DR EMBL: M32990; AAA45755.1; ALT_INIT.
DR PIR: C33746; SAVLBD.
DR InterPro: IPR000349; Hepvir_surfag.
DR Pfam: PF00695; VMSA; 1.
KW Antigen.
FT PROPEP 1 199 MAJOR SURFACE ANTIGEN.
FT CHAIN 200 366 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 298 298 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 366 AA; 40897 MW; 5B72879A182EF38 CRC64;
Query Match 68.6%; Score 35; DB 1; Length 366;
Best Local Similarity 71.4%; Pred. No. 47;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 QQSGSWP 7
DB 96 QQQGAWP 102
RESULT 10
VMSA_HPBDB STANDARD; PRT; 366 AA.
AC P17195;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-MAY-1991 (Rel. 18, Last annotation update)
DE Major surface antigen precursor.
GN S.
OS Duck hepatitis B virus (white Shanghai duck isolate S31) (DHBV).
OC Viruses; Retroid viruses; Hepadnaviridae; Avihepadnavirus.
OX NCBI_TaxID=10440;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=90085807; PubMed=2596031;
RA Uchida M., Esumi M., Shikata T.;
RT "Molecular cloning and sequence analysis of duck hepatitis B virus
RL Virolgy 173:600-606(1989).
CC -----
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 CC -----
 DR EMBL; M32991; AAA45752.1; ALT_INIT.
 DR PIR; D33746; SAVLWD.
 DR InterPro; IPR000349; Hepvir_surfa.
 DR Pfam; PF00695; vmsa; 1.
 KW Antigen.
 FT PROPEP 1 199
 FT CHAIN 200 366 MAJOR SURFACE ANTIGEN.
 FT CARBOHYD 170 170 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 298 298 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 366 AA; 40858 MW; CF60E78B7B2FCD52 CRC64;
 Query Match 68.6%; Score 35; DB 1; Length 366;
 Best Local Similarity 71.4%; Pred. No. 47;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QQGSWP 7
 Db 96 QQGAWP 102
 RESULT 11
 GUNL_BACSU STANDARD; PRT; 499 AA.
 ID GUNL_BACSU STANDARD; PRT; 499 AA.
 AC P07983;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 01-OCT-1994 (Rel. 30, Last annotation update)
 DE Endoglucanase precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase)
 DE (Cellulase).
 GN BGIC OR GLD.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 ON NCBI_TaxID=1423;
 RX MEDLINE=87194581; PubMed=3106328;
 RA Robson L.M., Chambliss G.H.;
 RT "Endo-beta-1,4-glucanase gene of Bacillus subtilis DLG.";
 RL J. Bacteriol. 169:2017-2025(1987).
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic
 CC linkages in cellulose.
 CC -!- SIMILARITY: BELONGS TO CELLULASE FAMILY A (FAMILY 5 OF GLYCOSYL
 CC HYDROLASES).
 CC -----
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 CC -----
 DR EMBL; M16185; AAA22496.1; ALT_INIT.
 DR PIR; A26874; A26874.
 DR HSSP; O85465; 1A3H.
 DR InterPro; IPR001956; CBD_3.
 DR InterPro; IPR001547; GH_5.
 DR Pfam; PF00150; cellulase; 1.
 DR Pfam; PF00942; CBM_3; 1.
 DR ProDom; PD001947; CBD_3; 1.
 DR PROSITE; PS00659; GLYCOSYL_HYDROL_F5; 1.
 KW Cellulose degradation; Hydrolase; Glycosidase; Signal.
 FT SIGNAL 1 29
 FT CHAIN 30 499 ENDOGLUCANASE.
 FT ACT_SITE 169 169 PROTON DONOR (BY SIMILARITY).
 Query Match 68.6%; Score 35; DB 1; Length 939;
 Best Local Similarity 85.7%; Pred. No. 1.2e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 3 QSGSWPLT 9

FT ACT_SITE 257 257 NUCLEOPHILE (BY SIMILARITY).
 FT DOMAIN 350 499 CELLULOSE-BINDING (BY SIMILARITY).
 SQ SEQUENCE 499 AA; 55187 MW; 339D04EE95A63EE1 CRC64;
 Query Match 68.6%; Score 35; DB 1; Length 499;
 Best Local Similarity 62.5%; Pred. No. 63;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 2 QSGSWPLT 9
 Db 309 KTGWPLT 316
 RESULT 12
 SYV_CHLMU STANDARD; PRT; 939 AA.
 ID SYV_CHLMU STANDARD; PRT; 939 AA.
 AC Q9PK91;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Valyl-tRNA synthetase (EC 6.1.1.9) (Valine--tRNA ligase) (VAIRS).
 GN VALS OR TC0576.
 OS Chlamydia muridarum.
 OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
 ON NCBI_TaxID=83560;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MoPn / Nig9;
 RX MEDLINE=20150255; PubMed=10684935;
 RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
 RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
 RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
 RA Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
 RA Eisen J., Fraser C.M.;
 RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
 RT pneumoniae AR39.";
 RL Nucleic Acids Res. 28:1397-1406(2000).
 CC -!- CATALYTIC ACTIVITY: ATP + L-valine + tRNA(Val) = AMP + diphosphate
 CC + L-valyl-tRNA(Val).
 CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
 CC -----
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 CC -----
 DR EMBL; AE002326; AAF39411.1; -.
 DR HSSP; P96142; 1GAX.
 DR TIGR; TC0576; -.
 DR InterPro; IPR002300; tRNA-synt_1a.
 DR InterPro; IPR001412; tRNA-synt_1.
 DR InterPro; IPR002303; tRNA-synt_val.
 DR Pfam; PF00133; tRNA-synt_1; 1.
 DR PRINTS; PR00986; TRNASYNTHVAL.
 DR TIGRFAMS; TIGR00422; vals; 1.
 DR PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
 KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
 KW Complete proteome.
 FT SITE 47 57 "HIGH" REGION.
 FT SITE 564 568 "KMSKS" REGION.
 FT BINDING 567 567 ATP (BY SIMILARITY).
 SQ SEQUENCE 939 AA; 107121 MW; 1D141FA682187869 CRC64;
 Query Match 68.6%; Score 35; DB 1; Length 939;
 Best Local Similarity 85.7%; Pred. No. 1.2e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 3 QSGSWPLT 9

```

Db 460 SGLWPLT 466

RESULT 13
SVV_CHLTR STANDARD; PRT; 939 AA.
AC 084304;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Valyl-tRNA synthetase (EC 6.1.1.9) (Valine--trNA ligase) (ValRS).
VALS OR CT302.
GN Chlamydia trachomatis.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D/UV-3/Cx;
RX MEDLINE=99000809; PubMed=9784136;
RA Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
RA Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
RA Davis R.W.;
RT "Genome sequence of an obligate intracellular pathogen of humans:
RT Chlamydia trachomatis."
RL Science 282:754-759(1998).
CC -!- CATALYTIC ACTIVITY: ATP + L-valine + tRNA(Val) = AMP + diphosphate
CC + L-valyl-tRNA(Val).
CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
-----
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-----
CC EMBL; AE001302; AAC67895.1; -
CC HSSP; P96142; 1GAX.
CC InterPro; IPR002300; tRNA-synt_1a.
CC InterPro; IPR001412; tRNA-synt_1.
CC InterPro; IPR002303; tRNA-synt_val.
CC Pfam; PF00133; tRNA-synt_1; 1.
CC PRINTS; PR00986; TRNASYNTHVAL.
CC TIGRfams; TIGR00422; vals; 1.
CC PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
Complete proteome.
FT SITE 47 57 "HIGH" REGION.
FT SITE 563 567 "KMSKS" REGION.
FT BINDING 566 566 ATP (BY SIMILARITY).
SQ SEQUENCE 939 AA; 107036 MW; CEB849DC7BB9066 CRC64;

Query Match 68.6%; Score 35; DB 1; Length 939;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 SGLWPLT 9
DB 459 SGLWPLT 465

RESULT 14
SVV_CHLTPN STANDARD; PRT; 940 AA.
AC Q92987; Q9J0A5;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Valyl-tRNA synthetase (EC 6.1.1.9) (Valine--trNA ligase) (ValRS).
VALS OR CT302.
GN Chlamydia trachomatis.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D/UV-3/Cx;
RX MEDLINE=99000809; PubMed=9784136;
RA Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
RA Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
RA Davis R.W.;
RT "Genome sequence of an obligate intracellular pathogen of humans:
RT Chlamydia trachomatis."
RL Science 282:754-759(1998).
CC -!- CATALYTIC ACTIVITY: ATP + L-valine + tRNA(Val) = AMP + diphosphate
CC + L-valyl-tRNA(Val).
CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
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-----
CC EMBL; AE001302; AAC67895.1; -
CC HSSP; P96142; 1GAX.
CC InterPro; IPR002300; tRNA-synt_1a.
CC InterPro; IPR001412; tRNA-synt_1.
CC InterPro; IPR002303; tRNA-synt_val.
CC Pfam; PF00133; tRNA-synt_1; 1.
CC PRINTS; PR00986; TRNASYNTHVAL.
CC TIGRfams; TIGR00422; vals; 1.
CC PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
Complete proteome.
FT SITE 47 57 "HIGH" REGION.
FT SITE 563 567 "KMSKS" REGION.
FT BINDING 566 566 ATP (BY SIMILARITY).
SQ SEQUENCE 939 AA; 107036 MW; CEB849DC7BB9066 CRC64;

Query Match 68.6%; Score 35; DB 1; Length 939;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 SGLWPLT 9
DB 459 SGLWPLT 465

VALS OR CPN0094 OR CP0680.
GN Chlamydia pneumoniae (Chlamydophila pneumoniae).
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
OX NCBI_TaxID=83558;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CWL029;
RX MEDLINE=99206606; PubMed=10192388;
RA Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis."
Nat. Genet. 21:385-389(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AR39;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
RA Eisen J., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
RT pneumoniae AR39."
RL Nucleic Acids Res. 28:1397-1406(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=J138;
RX MEDLINE=20330349; PubMed=10871362;
RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
RT from Japan and CWL029 from USA."
RL Nucleic Acids Res. 28:2311-2314(2000).
CC -!- CATALYTIC ACTIVITY: ATP + L-valine + tRNA(Val) = AMP + diphosphate
CC + L-valyl-tRNA(Val).
CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
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-----
CC EMBL; AE001595; AAD18247.1; -
CC EMBL; AE002226; AAF38490.1; -
CC EMBL; AP002545; BAA98304.1; -
CC HSSP; P96142; 1GAX.
CC TIGR; CP0680; -
CC InterPro; IPR002300; tRNA-synt_1a.
CC InterPro; IPR001412; tRNA-synt_1.
CC InterPro; IPR002303; tRNA-synt_val.
CC Pfam; PF00133; tRNA-synt_1; 1.
CC PRINTS; PR00986; TRNASYNTHVAL.
CC TIGRfams; TIGR00422; vals; 1.
CC PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
Complete proteome.
FT SITE 47 57 "HIGH" REGION.
FT SITE 564 568 "KMSKS" REGION.
FT BINDING 567 567 ATP (BY SIMILARITY).
SQ SEQUENCE 940 AA; 107111 MW; 28054683FB9D0404 CRC64;

Query Match 68.6%; Score 35; DB 1; Length 940;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 SGLWPLT 9
DB 460 SGLWPLT 466

```

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RESULT 15
CATC_RHOOP          STANDARD;          PRT;          92 AA.
ID   CATC_RHOOP
AC   P95609;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DE   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Muconolactone delta-isomerase (EC 5.3.3.4) (Miaase).
GN   CATC.
OS   Rhodococcus opacus (Nocardia opaca).
OC   Bacteria; Actinobacteria; Actinobacteridae (class); Actinobacteridae;
OC   Actinomycetales; Corynebacterineae; Nocardiaceae; Rhodococcus.
OX   NCBI_TaxID=37919;
RN   [1]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 1-20.
RC   STRAIN=ICP;
RX   MEDLINE=97144521; PubMed=8990288;
RA   Eulberg D., Golovleva L.A., Schloemann M.;
RT   "Characterization of catechol catabolic genes from Rhodococcus
RL   J. Bacteriol. 179:370-381(1997).
CC   -1- CATALYTIC ACTIVITY: 2,5-dihydro-5-oxofuran-2-acetate = 3,4-
CC   dihydro-5-oxofuran-2-acetate.
CC   -1- PATHWAY: THIRD STEP IN THE CATABOLISM OF CATECHOL TO SUCCINATE-
CC   AND ACETYL-COA IN THE BETA-KETOADIPATE PATHWAY.
CC   -1- SUBUNIT: HOMODECAMER (BY SIMILARITY).
CC   -----
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CC   or send an email to license@isb-sib.ch).
CC   -----
DR   EMBL; X99622; CAA67935.1; -.
DR   InterPro; IPR003464; Miaase.
DR   Pfam; PF02426; Miaase; 1.
KW   Aromatic hydrocarbons catabolism; Isomerase.
FT   INIT_MET          0
SQ   SEQUENCE          92 AA; 10780 MW; 9CCE5A17DED4B153 CRC64;

Query Match          66.7%; Score 34; DB 1; Length 92;
Best Local Similarity 71.4%; Pred. No. 18;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY   1 QQSGSWP 7
Db    35 QRSQKWP 41

```

Search completed: November 18, 2002, 17:51:39
 Job time : 5.85526 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:40:56 ; Search time 20.1316 Seconds
(without alignments)
92.115 Million cell updates/sec

Title: US-09-016-061-90
Perfect score: 51
Sequence: 1 QQSGSWPLT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_undefined:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	41	80.4	153	Q9YH52	Q9YH52 gallus gall
2	40	78.4	706	Q9D4H8	Q9D4H8 mus musculu
3	40	78.4	1194	Q9VSI2	Q9VSI2 drosophila
4	39	76.5	986	Q01443	Q01443 caenorhabdi
5	38	74.5	506	Q8YJS7	Q8YJS7 brucella me
6	37	72.5	154	Q84631	Q84631 paraneurium
7	37	72.5	612	Q941S9	Q941S9 oryza sativ
8	37	72.5	612	Q8RUM5	Q8RUM5 oryza sativ
9	37	72.5	642	Q28537	Q28537 archaeoglob
10	37	72.5	677	Q97DD2	Q97DD2 clostridium
11	37	72.5	737	Q9U9P1	Q9U9P1 drosophila
12	37	72.5	764	Q9LZ75	Q9LZ75 arabidopsis
13	37	72.5	781	Q9VRA2	Q9VRA2 drosophila
14	37	72.5	1346	Q98IR5	Q98IR5 rhizobium l
15	36	70.6	204	Q95X90	Q95X90 caenorhabdi
16	36	70.6	275	Q50711	Q50711 mycobacteri

17	36	70.6	396	16	Q9RDF1	Q9RDF1 streptomyc
18	36	70.6	540	10	Q9FVK6	Q9FVK6 pisum sativ
19	36	70.6	613	5	Q9VHU1	Q9VHU1 drosophila
20	36	70.6	841	10	Q8RWY4	Q8RWY4 arabidopsis
21	36	70.6	847	10	Q9SGW2	Q9SGW2 arabidopsis
22	36	70.6	1221	16	Q9T0U2	Q9T0U2 pseudomonas
23	36	70.6	1903	5	Q9U5D6	Q9U5D6 plautia sta
24	35	68.6	100	16	Q9PLT4	Q9PLT4 chlamydia m
25	35	68.6	123	4	Q9UKB9	Q9UKB9 homo sapien
26	35	68.6	146	16	Q8Z341	Q8Z341 salmonella
27	35	68.6	181	16	Q8XFC9	Q8XFC9 salmonella
28	35	68.6	235	11	Q9D734	Q9D734 mus musculu
29	35	68.6	317	16	Q9KPI7	Q9KPI7 vibrio chol
30	35	68.6	320	16	Q8XWH9	Q8XWH9 raiistonia s
31	35	68.6	327	12	Q67852	Q67852 duck hepati
32	35	68.6	329	12	Q91HP5	Q91HP5 duck hepati
33	35	68.6	330	12	Q72885	Q72885 duck hepati
34	35	68.6	330	12	Q66405	Q66405 duck hepati
35	35	68.6	366	12	Q66404	Q66404 duck hepati
36	35	68.6	407	2	Q9R904	Q9R904 brachyspira
37	35	68.6	413	2	Q9R905	Q9R905 brachyspira
38	35	68.6	415	2	Q9R908	Q9R908 treponema h
39	35	68.6	415	2	Q9ZHI1	Q9ZHI1 brachyspira
40	35	68.6	415	2	Q9R902	Q9R902 brachyspira
41	35	68.6	416	2	Q9ZHI3	Q9ZHI3 brachyspira
42	35	68.6	418	2	Q9ZHI6	Q9ZHI6 brachyspira
43	35	68.6	420	2	Q9R907	Q9R907 treponema h
44	35	68.6	420	2	Q9ZHI7	Q9ZHI7 serpulina s
45	35	68.6	421	2	Q9R906	Q9R906 brachyspira

ALIGNMENTS

RESULT 1

Q9YH52 ID Q9YH52 PRELIMINARY: PRT; 153 AA.

AC Q9YH52;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE Hypothetical 17.4 kDa protein.

OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;

RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=H.B19;
RX MEDLINE=90077532; PubMed=2592020;
RA Kaufman J., Salomonsen J., Skjoldt K.;
RT "B-G cDNA clones have multiple small repeats and hybridize to both
chicken MHC regions.";
RL Immunogenetics 30:440-451(1989).
DR EMBL; M27666; AAA69840.1; -;
KW Hypothetical protein.
SQ SEQUENCE 153 AA; 17404 MW; 6D344F572FA7EE48 CRC64;

Query Match 80.4%; Score 41; DB 13; Length 153;
Best Local Similarity 87.5%; Pred. No. 8.1;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QSGSWPLT 9

DB 65 QSGHWPLT 72

RESULT 2

Q9D4H8 ID Q9D4H8 PRELIMINARY: PRT; 706 AA.
AC Q9D4H8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DE 4932411N15R1k protein.
 GN 4932411N15R1K.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=TESTIS;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.,
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 DR EMBL; AK016520; BAB30283.1; -
 DR MGD; MGI:1922970; 4932411N15R1k.
 DR InterPro: IPR001373; Cullin.
 DR Pfam: PF00888; Cullin; 1.
 DR SMART; SM00182; CULLIN; 1.
 DR PROSITE; PS01256; CULLIN_1; 1.
 DR PROSITE; PS00069; CULLIN_2; 1.
 SQ SEQUENCE 706 AA; 82298 MW; CBB796B20CA6A6E2B4 CRC64;

 Query Match 78.4%; Score 40; DB 11; Length 706;
 Best Local Similarity 75.0%; Pred. No. 57;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

 QY 2 QSGSWPLT.9
 Db 513 QAGAWPLT 520
 1:1:11111

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA April J.F., Agayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Flosser C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ijedenwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195(2000).
 DR EMBL; AE003555; AAF50437.1; -
 DR FlyBase; FBgn0035879; CG7112.
 DR InterPro: IPR000050; PID_domain.
 DR InterPro: IPR000195; RabGAP_TBC.
 DR Pfam; PF00566; TBC; 1.
 DR SMART; SM00462; PTB; 1.
 DR SMART; SM00164; TBC; 1.
 SQ SEQUENCE 1194 AA; 133393 MW; E0E3DB547B4924E0 CRC64;

 Query Match 78.4%; Score 40; DB 5; Length 1194;
 Best Local Similarity 77.8%; Pred. No. 98;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

 QY 1 QSGSWPLT.9
 Db 461 QOSSSWPYT 469
 11111111

RESULT 4
 Q01443 PRELIMINARY; PRT; 986 AA.
 ID 001443
 AC 001443; 001444;
 DT 01-JUL-1997 (TrEMBLrel. 04; Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Hypothetical 108.1 kDa protein.
 GN C01F4.2.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA Waterston R.;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium."
 RL Science 282:2012-2018(1998).
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Wamsley P., Geisel C.;
 RT "The sequence of *C. elegans* cosmid C01F4.";
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Waterston R.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U97192; AAB52434.2; -;
 KW Hypothetical protein.
 SQ SEQUENCE 986 AA; 108136 MW; E8076DD8DB6DE7A5 CRC64;

Query Match 76.5%; Score 39; DB 5; Length 986;
 Best Local Similarity 66.7%; Pred. No. 1.2e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QSGSWPLT 9
 I:|||||;
 DB 806 QSGSWPFS 814

RESULT 5
 Q8YJS7 PRELIMINARY; PRT; 506 AA.
 ID Q8YJS7
 AC Q8YJS7;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Thymidylate kinase (EC 2.7.4.9).
 GN BME10005.
 OS Brucella melitensis.
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Brucellaceae; Brucella.
 OX NCBI_TaxID=29459;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=16M / ATCC 23456 / BIOTYPE 1;
 RX MEDLINE=20020109; PubMed=11756688;
 RA DelVecchio V.G., Kapral V., Redkar R.J., Patra G., Mujar C., Los T.,
 RA Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,
 RA Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltzman E.,
 RA Salkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
 RA Haselkorn R., Kyrpides N., Overbeek R.;
 RT "The genome sequence of the facultative intracellular pathogen
 RT Brucella melitensis.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
 DR EMBL; AE009444; AAL51187.1; -;
 DR InterPro; IPR004879; DUF255.
 DR InterPro; IPR001599; MacroglblnA2.
 DR Pfam; PF00207; A2M; 1.
 DR Pfam; PF03190; DUF255; 1.
 KW Transferase; Complete proteome.
 SQ SEQUENCE 506 AA; 57315 MW; 2A2914478FF81F43 CRC64;

Query Match 74.5%; Score 38; DB 16; Length 506;
 Best Local Similarity 75.0%; Pred. No. 92;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QSGSWPLT 9
 I:|||||
 DB 135 QSGSWPLT 142

RESULT 6
 Q84631 PRELIMINARY; PRT; 154 AA.
 ID Q84631
 AC Q84631;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE A317L protein.

GN A317L.
 OS Paramesidium bursaria chlorella virus 1 (PBCV-1).
 OC Viruses; dsDNA viruses, no RNA stage; Phycodnaviridae; Chlorovirus.
 OX NCBI_TaxID=10506;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96187795; PubMed=8614977;
 RA Lu Z., Li Y., Que Q., Kutish G.F., Rock D.L., Van Etten J.L.;
 RT "Analysis of 94 kb of the chlorella virus PBCV-1 330-kb genome: map
 RT positions 88 to 182.";
 RL Virology 216:102-123(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20013326; PubMed=10544099;
 RA Kaiser A., Vollmert M., Tholl D., Graves M.V., Gurnon J.R., Xing W.,
 RA Liscic A.D., Nickerson K.W., Van Etten J.L.;
 RT "Chlorella virus PBCV-1 encodes a functional homospesmidine
 RT synthase.";
 RL Virology 263:254-262(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20478054; PubMed=11021991;
 RA Sun L., Gurnon J.R., Adams B.J., Graves M.V., Van Etten J.L.;
 RT "Characterization of a beta-1,3-glucanase encoded by chlorella virus
 RT PBCV-1.";
 RL Virology 276:27-36(2000).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Van Etten J.L.;
 RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Van Etten J.L.;
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RA Van Etten J.L.;
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RA Graves M.V., Van Etten J.L.;
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 RN [8]
 RP SEQUENCE FROM N.A.
 RA Graves M.V., Van Etten J.L.;
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 RN [9]
 RP SEQUENCE FROM N.A.
 RA Gurnon J.R., Graves M.V., Van Etten J.L.;
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U42580; AAC96685.1; -;
 SQ SEQUENCE 154 AA; 18564 MW; 7B45EE2E7F518E15 CRC64;

Query Match 72.5%; Score 37; DB 12; Length 154;
 Best Local Similarity 75.0%; Pred. No. 42;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QSGSWPL 8
 I:|||||
 DB 33 QSGSWPV 40

RESULT 7
 Q941S9 PRELIMINARY; PRT; 612 AA.
 ID Q941S9
 AC Q941S9;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Putative homeodomain protein (QSH-1).
 GN P005H10.19 OR QSH-1.
 OS Oryza sativa (Rice), and
 OS Oryza sativa (japonica cultivar-group).

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OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzae; Oryza.
ON NCBI_TaxID=4530, 39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
RT clone: P0005H10.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Konishi S., Yano M., Lin S., Fukuta Y., Sasaki T.;
RT "Map-based cloning of qsh-1 controlling seed shattering habit in
RT rice.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP004127; BAB64282.1; -.
DR EMBL; AB071331; BAB85943.1; -.
DR EMBL; AB071333; BAB85945.1; -.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
DR ProDom; PD000010; Homeobox; 1.
DR PROSITE; PS00027; HOMEBOX_1; UNKNOWN_1.
DR PROSITE; PS50071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
SQ SEQUENCE 612 AA; 65175 MW; A5B7AA5281CD28E4 CRC64;

Query Match 72.5%; Score 37; DB 10; Length 612;
Best Local Similarity 85.7%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSGSWP 7
|||
Db 93 QQHGSWP 99

RESULT 8
Q8RUM5 PRELIMINARY; PRT; 612 AA.
AC Q8RUM5;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE QSH-1.
DE QSH-1.
GN QSH-1.
OS Oryza sativa (indica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzae; Oryza.
OX NCBI_TaxID=39946;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. KASALATH;
RA Konishi S., Yano M., Lin S., Fukuta Y., Sasaki T.;
RT "Map-based cloning of qsh-1 controlling seed shattering habit in
RT rice.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB071330; BAB85942.1; -.
DR EMBL; AB071332; BAB85944.1; -.
SQ SEQUENCE 612 AA; 65205 MW; A5A6FF1690986CE4 CRC64;

Query Match 72.5%; Score 37; DB 10; Length 612;
Best Local Similarity 85.7%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSGSWP 7
|||
Db 93 QQHGSWP 99

RESULT 9

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O28537 PRELIMINARY; PRT; 642 AA.
AC O28537;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical protein AF1737.
GN AF1737.
OS Archaeoglobus fulgidus.
OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
OC Archaeoglobaceae; Archaeoglobus.
OX NCBI_TaxID=2234;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RX MEDLINE=98049343; PubMed=9389475;
RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
RA Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
RA Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RA Venter J.C.;
RT "The complete genome sequence of the hyperthermophilic, sulphate-
RT reducing archaeon Archaeoglobus fulgidus.";
RL Nature 390:364-370(1997).
DR EMBL; AE000983; AAB89512.1; -.
DR TIGR; AF1737; -.
DR InterPro; IPR004879; DUF255.
DR Pfam; PF03190; DUF255; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 642 AA; 74057 MW; 3E80BA624D747B5 CRC64;

Query Match 72.5%; Score 37; DB 17; Length 642;
Best Local Similarity 85.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 SGSWPLT 9
|||
Db 101 SGWPLT 107

RESULT 10
Q97DD2 PRELIMINARY; PRT; 677 AA.
AC Q97DD2;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Highly conserved protein containing a domain related to cellulase
DE catalytic domain and a thioredoxin domain.
GN CAC3546.
OS Clostridium acetobutylicum.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC Clostridiales; Clostridiaceae; Clostridium.
OX NCBI_TaxID=1488;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
RX MEDLINE=21359325; PubMed=11466286;
RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
RA Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
RA Bennett G.N., Koonin E.V., Smith D.R.;
RT "Genome sequence and comparative analysis of the solvent-producing
RT bacterium Clostridium acetobutylicum.";
RL J. Bacteriol. 183:4823-4838(2001).
DR EMBL; AE007851; AAK81471.1; -.
DR InterPro; IPR004879; DUF255.

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DR Pfam; PF03190; DUF255; 1.
KW Complete proteome.
SQ SEQUENCE 677 AA; 78241 MW; F8ED0443466830F3 CRC64;
Query Match 72.5%; Score 37; DB 16; Length 677;
Best Local Similarity 85.7%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3 SGSWPLT 9
Db 108 SGGWPLT 114
RESULT 11
Q909P1 PRELIMINARY; PRT; 737 AA.
AC Q909P1;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE MAROON-like protein.
GN MAL OR CG1692.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CANTON S;
RA Primus J., Arcangeli L., Finnerty V.;
RT "The maroon-like gene in Drosophila encodes a putative sulfurase."
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162681; AAD50777.1; -
DR FlyBase; FBgn0002641; mal.
DR InterPro; IPR005302; MOSC.
DR InterPro; IPR005303; MOSC_N.
DR Pfam; PF03473; MOSC; 1.
DR Pfam; PF03476; MOSC_N; 1.
SQ SEQUENCE 737 AA; 83139 MW; 76DFEE077E3F06D4 CRC64;
Query Match 72.5%; Score 37; DB 5; Length 737;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 GSWPLT 9
Db 533 GSWPLT 538
RESULT 12
Q9LZ75 PRELIMINARY; PRT; 764 AA.
AC Q9LZ75;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
DE Hypothetical 86.3 kDa protein.
GN T32M2100.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Bevan M., Terry N., Ardiles W., Buysshaert C., Dasseville R.,
RA De Clerck R., De Keyser A., Neyt P., Rouze P., Van Den Daele H.,
RA Villarroel R., Gielen J., Van Montagu M., Bancroft I., Mewes H.W.,
RA Rudd S., Lemcke K., Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.

RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL162875; CAB85556.1; -
KW Hypothetical protein.
SQ SEQUENCE 764 AA; 86299 MW; AFE0E482FF091CB8 CRC64;
Query Match 72.5%; Score 37; DB 10; Length 764;
Best Local Similarity 62.5%; Pred. No. 2.1e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 2 QSGSWPLT 9
Db 112 ESGWPLT 119
RESULT 13
Q9VRA2 PRELIMINARY; PRT; 781 AA.
AC Q9VRA2;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE MAL protein.
GN MAL OR CG1692.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Fandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Aqbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrier S., Fleischmann W.,
RA Fostler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jaitani M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muszy D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195 (2000).
DR EMBL; AE003571; AAF50901.1; -
DR FlyBase; FBgn0002641; mal.

DR InterPro: IPR005302; MOSC.
 DR InterPro: IPR005303; MOSC_N.
 DR Pfam: PF03473; MOSC; 1.
 DR Pfam: PF03476; MOSC_N; 1.
 SQ SEQUENCE 781 AA; 88103 MW; D2B2D5F52FDDF712 CRC64;

Query Match 72.5%; Score 37; DB 5; Length 781;

Best Local Similarity 100.0%; Pred. No. 2.2e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GSWPLT 9

|||||

Db 533 GSWPLT 538

RESULT 14

Q98IR5 PRELIMINARY; PRT; 1346 AA.

ID Q98IR5 PRELIMINARY; PRT; 1346 AA.

DT 01-OCT-2001 (TrEMBLrel. 18, Created)

DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)

DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)

DE Hypothetical protein ml2286.

GN ML2286.

OS Rhizobium loti (Mesorhizobium loti).

OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;

OC Phyllobacteriaceae; Mesorhizobium.

OX NCBI_TaxID=381;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=MAFF303099;

RX MEDLINE=21082930; PubMed=11214968;

RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,

RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,

RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,

RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,

RA Takeuchi C., Yamada M., Tabata S.;

RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium

RT Mesorhizobium loti.";

RL DNA Res. 7:331-338(2000).

DR EMBL: AF002999; BAB49451.1; -

DR InterPro: IPR003975; Shal_channel.

DR PRINTS: PR01497; SHALCHANNEL.

KW Hypothetical protein; Complete proteome.

SQ SEQUENCE 1346 AA; 148727 MW; 7D1288A3FC26E879 CRC64;

Query Match 72.5%; Score 37; DB 16; Length 1346;

Best Local Similarity 75.0%; Pred. No. 3.7e+02;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QSGSWPLT 9

|||||

Db 204 QSGSWPLT 211

RESULT 15

Q95X90

ID Q95X90 PRELIMINARY; PRT; 204 AA.

AC Q95X90;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE Hypothetical 22.8 kDa protein.

GN D2062.1.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;

OC Rhabditidae; Peloderinae; Caenorhabditis.

OX NCBI_TaxID=6239;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BRISTOL N2;

RX MEDLINE=99069613; PubMed=9851916;

RA None;

RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018(1998).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=BRISTOL N2;

RA Tin-Wollam A., Wohldmann P.;

RT "The sequence of C. elegans cosmid D2062.";

RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=BRISTOL N2;

RA Waterston R.;

RT "Direct Submission.";

RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF016664; AAK72083.1; -

DR InterPro: IPR001283; Allrgn_V5/TpX1.

DR Pfam: PF00188; SCP; 1.

DR PRODOM: PD000542; Allrgn_V5/TpX1; 1.

DR PROSITE: PS01009; SCP_AG5_PRI_SC7_1; UNKNOWN_1.

KW Hypothetical protein.

SQ SEQUENCE 204 AA; 22758 MW; 27753F06500B35C8 CRC64;

Query Match 70.6%; Score 36; DB 5; Length 204;

Best Local Similarity 85.7%; Pred. No. 83;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QSGSWPL 8

|||||

Db 107 QSGCWPL 113

Search completed: November 18, 2002, 17:54:36

Job time : 21.1316 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 18, 2002, 17:31:45 ; Search time 26.4079 Seconds
(without alignments)
45.413 Million cell updates/sec

Title: US-09-016-061-90

Perfect score: 51

Sequence: 1 QQSGSWPLT 9

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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20: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	51	100.0	9	19	AAW76035
2	51	100.0	9	22	AAW76035
3	45	88.2	9	14	AAW76035
4	45	88.2	9	19	AAW76035
5	45	88.2	9	22	AAW76035
6	45	88.2	107	14	AAW76035
7	45	88.2	107	14	AAW76035
8	44	86.3	9	19	AAW76035
9	44	86.3	9	22	AAW76035
10	44	86.3	107	19	AAW76035

11	44	86.3	107	19	AAW76002
12	44	86.3	107	19	AAW76004
13	44	86.3	107	22	AAW76004
14	44	86.3	107	22	AAW76004
15	44	86.3	107	22	AAW76004
16	44	86.3	107	22	AAW76004
17	44	86.3	107	22	AAW76004
18	42	82.4	9	21	AAW76004
19	42	82.4	9	22	AAW76004
20	42	82.4	9	22	AAW76004
21	42	82.4	9	23	AAW76004
22	42	82.4	9	23	AAW76004
23	42	82.4	107	21	AAW76004
24	42	82.4	107	22	AAW76004
25	42	82.4	107	22	AAW76004
26	42	82.4	107	23	AAW76004
27	42	82.4	107	23	AAW76004
28	42	82.4	127	21	AAW76004
29	42	82.4	127	21	AAW76004
30	42	82.4	510	23	AAW76004
31	42	82.4	510	23	AAW76004
32	41	80.4	105	20	AAW76004
33	41	80.4	105	20	AAW76004
34	41	80.4	107	20	AAW76004
35	41	80.4	108	20	AAW76004
36	41	80.4	112	20	AAW76004
37	40	78.4	107	14	AAW76004
38	40	78.4	107	19	AAW76004
39	40	78.4	108	12	AAW76004
40	40	78.4	109	15	AAW76004
41	40	78.4	143	18	AAW76004
42	40	78.4	240	12	AAW76004
43	40	78.4	1194	22	AAW76004
44	39	76.5	9	19	AAW76004
45	39	76.5	9	20	AAW76004

ALIGNMENTS

RESULT 1

AAW76035

ID AAW76035 standard; Protein; 9 AA.

XX

AC AAW76035;

XX

DT 02-NOV-1998 (first entry)

XX

DE LM609 grafted antibody V-L region CDR3 protein fragment #4.

XX

KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angioneurotic; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-L region; CDR;
 KW complementarity determining region.

XX

OS Mus sp.

XX

PN WO9833919-A2.

XX

PD 06-AUG-1998.

XX

PF 30-JAN-1998; 98WO-US01826.

XX

PR 30-JAN-1997; 97US-0791391.

XX

PA Mutant VL CDR3 pep

XX

PI B-B10 Mab L chain

XX

DR LM609 grafted anti

XX

DR LM609 grafted anti

XX

DR LM609 grafted anti

XX

XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
PS Claim 62; Page 44; 129pp; English.
XX
CC AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphaVbeta3 and can be used to
CC inhibit binding of alphaVbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphaVbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
CC antibodies contain non-murine framework regions so are suitable for use
CC in humans. Enhanced types of LM609 have affinity more than 90 times
CC greater than that of parent the parent antibody.
XX
SQ Sequence 9 AA;
Query Match 100.0%; Score 51; DB 19; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 QQSGSWPLT 9
Db 1 QQSGSWPLT 9
|||||||
RESULT 2
AAB61393
ID AAB61393 standard; peptide; 9 AA.
XX
AC AAB61393;
XX
DT 03-APR-2001 (first entry)
XX
DE Mutant VL CDR3 peptide #3.
XX
XX LM609; grafted antibody; alphaVbeta3 integrin; angiogenesis;
KW inflammatory; cancer; retina; restenosis; osteoporosis.
XX
OS Unidentified.
XX
XX WO200078815-A1.
PN
XX
PD 28-DEC-2000.
XX
XX 23-JUN-2000; 2000WO-US17454.
PF
XX 24-JUN-1999; 99US-0339922.
PR
XX (MOLE-) APPLIED MOLECULAR EVOLUTION.
PA
XX
XX Huse WD, Wu H;
PI
XX WPI; 2001-050110/06.
DR
XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
PT osteoporosis -
XX
XX Claim 4; Page 41; 132pp; English.
PS
XX The present invention relates to enhanced LM609 grafted antibodies
CC exhibiting selective binding affinity to alphaVbeta3 integrin or
CC their functional fragments. The antibodies or their functional
CC fragments can be used in the diagnosis and treatment of
CC alphaVbeta3-mediated diseases such as angiogenesis, inflammatory

CC diseases (such as psoriasis and chronic articular rheumatism),
CC disorders associated with inappropriate or inopportune invasion of
CC vessels (such as diabetic retinopathy, neovascular glaucoma and
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
CC diseases (such as macular degeneration), restenosis and
CC osteoporosis.
XX
SQ Sequence 9 AA;
Query Match 100.0%; Score 51; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 QQSGSWPLT 9
Db 1 QQSGSWPLT 9
|||||||
RESULT 3
AAR37604
ID AAR37604 standard; peptide; 9 AA.
XX
AC AAR37604;
XX
DT 13-OCT-1993 (first entry)
XX
DE hIL2R Ab L chain V region CDR3.
XX
XX Complementarity-determining region; CDR: humanised; antibody; hIL2R;
KW human; interleukin; IL-2; receptor; murine; anti-human; Ab; T-cell;
KW monoclonal antibody; B-B10; mixed lymphocyte reaction; variable; V;
KW region; PCR; framework; plasmid.
XX
OS Mus musculus.
XX
XX WO9311238-A.
PN
XX 10-JUN-1993.
PD
XX 03-DEC-1992; 92WO-JP01583.
PF
XX 06-DEC-1991; 91JP-0323319.
PR
XX (BIOT) BIOTEST PHARMA GMBH.
PA (INNO-) INNOTHERAPIE LAB.
PA (SUMU) SUMITOMO PHARM CO LTD.
XX
XX Gomi H, Nakatani T, Noguchi H, Wijdenes J;
PI
XX WPI; 1993-197057/24.
DR
XX Humanised antibody comprising - CDR region of mouse MAB B-B10
PT specific for IL-2 receptor useful for treating carcinoma
PT expressing IL-2 receptor
XX
XX Claim 1; Page 43; 62pp; English.
PS
XX The sequences given in AAR37599-604 represent the complementarity-
CC determining regions (CDRs) of a humanised antibody (Ab) which binds
CC specifically to human interleukin (IL)-2 receptor (hIL2R). These
CC CDRs were derived from the murine anti-human IL-2 receptor monoclonal
CC Ab (MAB) B-B10 (see also AAQ43242-43). This MAB is antagonistic to the
CC binding of IL-2 to the IL-2 receptor on human T-cells. It also
CC inhibits the human mixed lymphocyte reaction. The CDNA encoding the
CC variable (V) region of the B-B10 Ab was cloned by PCR and sequenced
CC (see also AAQ43226-32 and AAQ43233-36). A human Ab with high levels of
CC amino acid sequence homology to the murine sequence was selected and
CC the framework of this Ab was bound with the B-B10 V region CDR and a
CC part of the framework to design several kinds of the humanised B-B10 V
CC region (see also AAQ43244-45). The DNA sequence coding this humanised
CC B-B10 was synthesised and a plasmid expressing humanised B-B10 was
CC constructed.
XX

```

SQ Sequence 9 AA;
  Query Match      88.2%; Score 45; DB 14; Length 9;
  Best Local Similarity 88.9%; Pred. No. 7.8e+05;
  Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSGSWPLT 9
    III IIIII
DB 1 QQSSSWPLT 9

RESULT 4
AAW76036
ID AAW76036 standard; Protein; 9 AA.
XX
AC AAW76036;
XX
DT 02-NOV-1998 (first entry)
XX
DE LM609 grafted antibody V-L region CDR3 protein fragment #5.
XX
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-L region; CDR;
KW complementarity determining region.
XX
OS Mus sp.
XX
PN WO9833919-A2.
XX
PD 06-AUG-1998.
XX
PF 30-JAN-1998; 98WO-US01826.
XX
PR 30-JAN-1997; 97US-0791391.
XX
PA (IXSY-) IXSYS INC.
XX
PI Glaser SM, Huse WD;
XX
XX WPI; 1998-437472/37.
DR N-PSDB; AAV49873.
XX
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
PS Claim 62; Page 44; 129pp; English.
XX
CC AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically,
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
CC antibodies contain non-murine framework regions so are suitable for use
CC in humans. Enhanced types of LM609 have affinity more than 90 times
CC greater than that of parent the parent antibody.
XX
SQ Sequence 9 AA;
  Query Match      88.2%; Score 45; DB 19; Length 9;
  Best Local Similarity 88.9%; Pred. No. 7.8e+05;
  Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSGSWPLT 9
    IIIIIII
DB 1 QQSSSWPLT 9

RESULT 5
AAW76036
ID AAW76036 standard; peptide; 9 AA.
XX
AC AAW76036;
XX
DT 03-APR-2001 (first entry)
XX
DE Mutant VL CDR3 peptide #4.
XX
KW LM609; grafted antibody; alphaVbeta3 integrin; angiogenesis;
KW inflammatory; cancer; retina; restenosis; osteoporosis.
XX
OS Unidentified.
XX
PN WO200078815-A1.
XX
PD 28-DEC-2000.
XX
PF 23-JUN-2000; 2000WO-US17454.
XX
PR 24-JUN-1999; 99US-0339922.
XX
PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX
PI Huse WD, Wu H;
XX
XX WPI; 2001-050110/06.
XX
PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity
PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
PT osteoporosis -
XX
PS Disclosure; Page 41; 132pp; English.
XX
CC The present invention relates to enhanced LM609 grafted antibodies
CC exhibiting selective binding affinity to alphavbeta3 integrin or
CC their functional fragments. The antibodies or their functional
CC fragments can be used in the diagnosis and treatment of
CC alphavbeta3-mediated diseases such as angiogenesis, inflammatory
CC diseases (such as psoriasis and chronic articular rheumatism),
CC disorders associated with inappropriate or inopportune invasion of
CC vessels (such as diabetic retinopathy, neovascular glaucoma and
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
CC diseases (such as macular degeneration), restenosis and
CC osteoporosis.
XX
SQ Sequence 9 AA;
  Query Match      88.2%; Score 45; DB 22; Length 9;
  Best Local Similarity 88.9%; Pred. No. 7.8e+05;
  Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSGSWPLT 9
    IIIIIII
DB 1 QQSSSWPLT 9

RESULT 6
AAW76036
ID AAW76036 standard; Protein; 107 AA.
XX
AC AAW76036;
XX
DT 13-OCT-1993 (first entry)
XX
DE hIL2R Ab L chain V region.
XX
KW Complementarity-determining region; CDR; humanised; antibody; hIL2R;

```

KW human; interleukin; IL-2; receptor; murine; anti-human; Ab; T-cell;
KW monoclonal antibody; B-B10; mixed lymphocyte reaction; variable; V;
XX region; PCR; framework; plasmid; heavy; H; light; L.
XX Mus musculus/Homo sapiens.
XX WO9311238-A.
XX 10-JUN-1993.
XX 03-DEC-1992; 92WO-JP01583.
XX 06-DEC-1991; 91JP-0323319.
XX (BIOT) BIOTEST PHARMA GMBH.
XX (INNO-) INNOTHERAPIE LAB.
XX (SUMU) SUMITOMO PHARM CO LTD.
XX Gomi H, Nakatani T, Noguchi H, Wijdenes J;
XX WPI; 1993-197057/24.
XX N-PSDB; AAQ43245.
XX Humanised antibody comprising - CDR region of mouse MAB B-B10
XX specific for IL-2 receptor useful for treating carcinoma
XX expressing IL-2 receptor
XX Claim 2; Fig 5; 62pp; English.
XX The sequences given in AAR37611-12 represent the heavy (H) and light (L)
XX chain variable (V) regions of a humanised antibody (Ab) which binds
XX specifically to human interleukin (IL)-2 receptor (hIL2R). The
XX complementarity-determining regions (CDRs) of these V regions were
XX derived from the murine anti-human IL-2 receptor monoclonal Ab (MAB)
XX B-B10 (see also AAR37599-04). This MAB is antagonistic to the binding
XX of IL-2 to the IL-2 receptor on human T-cells. It also inhibits
XX the human mixed lymphocyte reaction. The cDNA encoding the variable
XX (V) region of the B-B10 Ab was cloned by PCR and sequenced (see also
XX AAQ43226-32 and AAQ43233-36). A human Ab with high levels of amino acid
XX sequence homology to the murine sequence was selected and the
XX framework of this Ab was bound with the B-B10 V region CDR and a
XX part of the framework to design several kinds of the humanised B-B10
XX V region. The DNA sequence coding this humanised B-B10 was
XX synthesised and a plasmid expressing humanised B-B10 was constructed.
XX Sequence 107 AA;
XX
XX Query Match 88.2%; Score 45; DB 14; Length 107;
XX Best Local Similarity 88.9%; Pred. No. 1.3;
XX Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 QQSGSWPLT 9
XX III IIIII
XX Db 89 QQSSSWPLT 97
XX
XX RESULT 7
XX AAR37610
XX ID AAR37610 standard; Protein; 107 AA.
XX AC AAR37610;
XX
XX 13-OCT-1993 (first entry)
XX B-B10 MAB L chain V region.
XX Complementarity-determining region; CDR; humanised; antibody; hIL2R;
XX human; interleukin; IL-2; receptor; murine; anti-human; Ab; T-cell;
XX monoclonal antibody; B-B10; mixed lymphocyte reaction; variable; V;
XX region; PCR; framework; plasmid; heavy; H; light; L.
XX Mus musculus.
XX

PN WO9311238-A.
XX 10-JUN-1993.
XX 03-DEC-1992; 92WO-JP01583.
XX 06-DEC-1991; 91JP-0323319.
XX (BIOT) BIOTEST PHARMA GMBH.
XX (INNO-) INNOTHERAPIE LAB.
XX (SUMU) SUMITOMO PHARM CO LTD.
XX Gomi H, Nakatani T, Noguchi H, Wijdenes J;
XX WPI; 1993-197057/24.
XX N-PSDB; AAQ43243.
XX Humanised antibody comprising - CDR region of mouse MAB B-B10
XX specific for IL-2 receptor useful for treating carcinoma
XX expressing IL-2 receptor
XX Disclosure; Fig 2; 62pp; English.
XX The sequences given in AAR37609-10 represent the heavy (H) and light (L)
XX chain variable (V) regions of the murine anti-human IL-2 receptor
XX monoclonal antibody (MAB) B-B10, respectively. This MAB was used in
XX the construction of a humanised antibody (Ab) which binds specifically
XX to human interleukin (IL)-2 receptor (hIL2R). The complementarity-
XX determining regions (CDRs) for the hIL2R MAB were derived from B-B10
XX (see also AAR37599-04). The hIL2R MAB is antagonistic to the binding
XX of IL-2 to the IL-2 receptor on human T-cells. It also inhibits
XX the human mixed lymphocyte reaction. The cDNA encoding the variable
XX (V) region of the B-B10 Ab was cloned by PCR and sequenced (see also
XX AAQ43226-32 and AAQ43233-36). A human Ab with high levels of amino acid
XX sequence homology to the murine sequence was selected and the
XX framework of this Ab was bound with the B-B10 V region CDR and a
XX part of the framework to design several kinds of the humanised B-B10
XX V region. The DNA sequence coding this humanised B-B10 was
XX synthesised and a plasmid expressing humanised B-B10 was constructed.
XX Sequence 107 AA;
XX
XX Query Match 88.2%; Score 45; DB 14; Length 107;
XX Best Local Similarity 88.9%; Pred. No. 1.3;
XX Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 QQSGSWPLT 9
XX III IIIII
XX Db 89 QQSSSWPLT 97
XX
XX RESULT 8
XX AAR76013
XX ID AAR76013 standard; Protein; 9 AA.
XX AC AAR76013;
XX
XX 02-NOV-1998 (first entry)
XX LM609 grafted antibody V-L region CDR3 protein fragment #1.
XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
XX LM609; inhibitor; integrin-mediated signal transduction; treatment;
XX diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
XX neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
XX macular degeneration; osteoporosis; primer; V-L region; CDR;
XX complementarity determining region.
XX Mus sp.
XX WO9833919-A2.
XX 06-AUG-1998.

XX PF 30-JAN-1998; 98WO-US01826.
 XX PR 30-JAN-1997; 97US-0791391.
 XX PA (IXSY-) IXSYS INC.
 XX PI Glaser SM, Huse WD;
 XX PT WPI: 1998-437472/37.
 XX DR N-PSDB; AAV49850.
 XX PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX PT
 XX Disclosure: Page 40; 129pp; English.
 XX PS
 XX CC AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphaVbeta3 and can be used to
 CC inhibit binding of alphaVbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphaVbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
 CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
 CC antibodies contain non-murine framework regions so are suitable for use
 CC in humans. Enhanced types of LM609 have affinity more than 90 times
 CC greater than that of parent the parent antibody.
 XX PT
 XX SQ Sequence 9 AA;
 XX
 XX Query Match 86.3%; Score 44; DB 19; Length 9;
 XX Best Local Similarity 88.9%; Pred. No. 7.8e+05;
 XX Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX
 XX QY 1 QQSGSWPLT 9
 XX | | | | | | | |
 XX DB 1 QQSGSWPHT 9
 XX
 XX RESULT 9
 XX ID AAB61371 standard; peptide; 9 AA.
 XX AC AAB61371;
 XX DT 03-APR-2001 (first entry)
 XX DE LM609 VL CDR3 peptide.
 XX KW LM609; grafted antibody; alphaVbeta3 integrin; angiogenesis;
 XX KW Inflammatory; cancer; retina; restenosis; osteoporosis.
 XX OS Unidentified.
 XX PN WO200078815-A1.
 XX PD 28-DEC-2000.
 XX PF 23-JUN-2000; 2000WO-US17454.
 XX PR 24-JUN-1999; 99US-0339922.
 XX (MOLE-) APPLIED MOLECULAR EVOLUTION.
 XX PA Huse WD, Wu H;
 XX PI WPI: 2001-050110/06.
 XX DR Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 XX PT

PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -
 XX PS
 XX Disclosure: Page 39; 132pp; English.
 XX
 XX The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphaVbeta3 integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphaVbeta3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.
 XX PT
 XX SQ Sequence 9 AA;
 XX
 XX Query Match 86.3%; Score 44; DB 22; Length 9;
 XX Best Local Similarity 88.9%; Pred. No. 7.8e+05;
 XX Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX
 XX QY 1 QQSGSWPLT 9
 XX | | | | | | | |
 XX DB 1 QQSGSWPHT 9
 XX
 XX RESULT 10
 XX ID AAW76006 standard; Protein; 107 AA.
 XX AC AAW76006;
 XX DT 02-NOV-1998 (first entry)
 XX DE LM609 grafted antibody light chain variable region protein fragment.
 XX KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.
 XX OS Mus sp.
 XX
 XX FH Key Location/Qualifiers
 XX FT Misc-difference 49
 XX FT /label= Arg, Met
 XX
 XX PN WO9833919-A2.
 XX PD 06-AUG-1998.
 XX PF 30-JAN-1998; 98WO-US01826.
 XX PR 30-JAN-1997; 97US-0791391.
 XX (IXSY-) IXSYS INC.
 XX PI Glaser SM, Huse WD;
 XX PT WPI: 1998-437472/37.
 XX DR N-PSDB; AAV49843.
 XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX PT
 XX Claim 19; Fig 7; 129pp; English.
 XX

CC This sequence represents a LM609 grafted antibody variable light chain
 CC region. LM609 and the antibody vitaxin bind selectively to integrin
 CC alphavbeta3 and can be used to inhibit binding of alphavbeta3 to a ligand
 CC and thus block integrin-mediated signal transduction. This is useful in
 CC the treatment, prevention and diagnosis of alphavbeta3-mediated disease,
 CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
 CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
 CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
 CC etc.). The antibodies contain non-murine framework regions so are
 CC suitable for use in humans. Enhanced types of LM609 have affinity more
 CC than 90 times greater than that of parent the parent antibody.
 XX

SQ Sequence 107 AA;

Query Match 86.3%; Score 44; DB 19; Length 107;
 Best Local Similarity 88.9%; Pred. No. 2;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOQSGSWPLT 9

Db 89 QOQSGSWPHT 97

RESULT 11

AAW76002
 ID AAW76002 standard; Protein; 107 AA.

XX AAW76002;

XX 02-NOV-1998 (first entry)

DE Vitaxin antibody light chain variable region protein fragment.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.

XX Mus sp.

XX WO9833919-A2.

XX 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

XX Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

XX N-PSDB; AAV49821.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

XX Claim 1; Fig 1b; 129pp; English.

XX This sequence represents the vitaxin antibody variable light chain
 CC region. Vitaxin and the antibody LM609 bind selectively to integrin
 CC alphavbeta3 and can be used to inhibit binding of alphavbeta3 to a
 CC ligand and thus block integrin-mediated signal transduction. This is
 CC useful in the treatment, prevention and diagnosis of alphavbeta3-mediated
 CC disease, specifically angiogenesis and restenosis (but also e.g.
 CC (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,
 CC cancer, psoriasis, rheumatoid arthritis, macular degeneration,
 CC osteoporosis etc.). The antibodies contain non-murine framework regions
 CC so are suitable for use in humans. Enhanced types of LM609 have affinity

CC more than 90 times greater than that of parent the parent antibody.
 XX

SQ Sequence 107 AA;

Query Match 86.3%; Score 44; DB 19; Length 107;
 Best Local Similarity 88.9%; Pred. No. 2;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOQSGSWPLT 9

Db 89 QOQSGSWPHT 97

RESULT 12

AAW76004

ID AAW76004 standard; Protein; 107 AA.

XX AAW76004;

XX 02-NOV-1998 (first entry)

DE LM609 antibody light chain variable region protein fragment.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.

XX Mus sp.

XX WO9833919-A2.

XX 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

XX Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

XX N-PSDB; AAW76004.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

XX Claim 46; Fig 2b; 129pp; English.

XX This sequence represents the LM609 antibody variable light chain region.
 CC LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3
 CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus
 CC block integrin-mediated signal transduction. This is useful in the
 CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,
 CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
 CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
 CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
 CC etc.). The antibodies contain non-murine framework regions so are
 CC suitable for use in humans. Enhanced types of LM609 have affinity more
 CC than 90 times greater than that of parent the parent antibody.

XX Sequence 107 AA;

Query Match 86.3%; Score 44; DB 19; Length 107;
 Best Local Similarity 88.9%; Pred. No. 2;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOQSGSWPLT 9

XXXXXXXXXX

```

Db      89 QQSGSWPHT 97

RESULT 13
AAG63588
ID      AAG63588 standard; Protein; 107 AA.
XX
AC      AAG63588;
XX
DT      15-OCT-2001 (first entry)
XX
DE      A light chain variable region of LM609 grafted antibody.
XX
KW      Grafted antibody; LM609; integrin; alphavbeta3; inflammatory disorder;
KW      chronic articular rheumatism; psoriasis; diabetic retinopathy;
KW      neovascular glaucoma; capillary proliferation; atherosclerotic plaque;
KW      cancer.
XX
OS      Synthetic.
OS      Mus sp.
XX
FH      Key      Location/Qualifiers
FT      Misc-difference 49
FT      /note= "unspecified residue encoded by MKK"
XX
PN      US2001011125-A1.
XX
PD      02-AUG-2001.
XX
PF      30-JAN-1997; 97US-0790540.
XX
PR      30-JAN-1997; 97US-0790540.
XX
PA      (HUSE/) HUSE W D.
XX
PI      Huse WD;
XX
DR      WPI: 2001-496171/54.
DR      N-PSDB; AAH74624.
XX
PT      New LM609 grafted antibody exhibiting selective binding affinity to
PT      alphavbeta3, comprising at least one LM609 grafted heavy and light
PT      chain polypeptide, useful for diagnosing and treating e.g. inflammatory
PT      disorders or cancer.
XX
PS      Claim 1; Fig 1B; 25pp; English.
XX
CC      The present sequence represents the light chain variable region of the
CC      grafted monoclonal antibody LM609. LM609 is a murine antibody which
CC      specifically recognises the integrin alphavbeta3, and inhibits its
CC      functional activity. The LM609 grafted antibody has the
CC      complementarity determining regions (CDRs) substituted into a non-murine
CC      framework. Nucleic acids encoding LM609 grafted heavy and light chain
CC      polypeptides and fragments are useful in diagnostic and therapeutic
CC      purposes, such as in the production of LM609 grafted antibodies and
CC      fragments having binding specificity and inhibitory activity against
CC      the integrin alphavbeta3. The antibody can be used for the diagnosis
CC      or treatment of alphavbeta3-mediated diseases (e.g. inflammatory
CC      disorders, chronic articular rheumatism, psoriasis, disorders
CC      associated with inappropriate or inopportune invasion of vessels such
CC      as diabetic retinopathy, neovascular glaucoma and capillary
CC      proliferation in atherosclerotic plaques, or cancers), and to inhibit
CC      binding activity of alphavbeta3 that are necessary for progression of
CC      an alphavbeta3-mediated disease.
XX
SQ      Sequence 107 AA;

Query Match      86.3%; Score 44; DB 22; Length 107;
Best Local Similarity 88.9%; Pred. No. 2;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      1 QQSGSWPLT 9
        | | | | | | | |

Db      89 QQSGSWPHT 97

RESULT 15
AAB61360

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Db      89 QQSGSWPHT 97

RESULT 14
AAG63590
ID      AAG63590 standard; Protein; 107 AA.
XX
AC      AAG63590;
XX
DT      15-OCT-2001 (first entry)
XX
DE      A light chain variable region of LM609 antibody.
XX
KW      Grafted antibody; LM609; integrin; alphavbeta3; inflammatory disorder;
KW      chronic articular rheumatism; psoriasis; diabetic retinopathy;
KW      neovascular glaucoma; capillary proliferation; atherosclerotic plaque;
KW      cancer.
XX
OS      Mus sp.
XX
PN      US2001011125-A1.
XX
PD      02-AUG-2001.
XX
PF      30-JAN-1997; 97US-0790540.
XX
PR      30-JAN-1997; 97US-0790540.
XX
PA      (HUSE/) HUSE W D.
XX
PI      Huse WD;
XX
DR      WPI: 2001-496171/54.
DR      N-PSDB; AAH74626.
XX
PT      New LM609 grafted antibody exhibiting selective binding affinity to
PT      alphavbeta3, comprising at least one LM609 grafted heavy and light
PT      chain polypeptide, useful for diagnosing and treating e.g. inflammatory
PT      disorders or cancer.
XX
PS      Disclosure; Fig 2B; 25pp; English.
XX
CC      The present sequence represents the light chain variable region of the
CC      monoclonal antibody LM609. LM609 is a murine antibody which specifically
CC      recognises the integrin alphavbeta3, and inhibits its functional activity.
CC      The specification describes a LM609 grafted antibody which has the
CC      complementarity determining regions (CDRs) substituted into a non-murine
CC      framework. Nucleic acids encoding LM609 grafted heavy and light chain
CC      polypeptides and fragments are useful in diagnostic and therapeutic
CC      purposes, such as in the production of LM609 grafted antibodies and
CC      fragments having binding specificity and inhibitory activity against
CC      the integrin alphavbeta3. The antibody can be used for the diagnosis
CC      or treatment of alphavbeta3-mediated diseases (e.g. inflammatory
CC      disorders, chronic articular rheumatism, psoriasis, disorders
CC      associated with inappropriate or inopportune invasion of vessels such
CC      as diabetic retinopathy, neovascular glaucoma and capillary
CC      proliferation in atherosclerotic plaques, or cancers), and to inhibit
CC      binding activity of alphavbeta3 that are necessary for progression of
CC      an alphavbeta3-mediated disease.
XX
SQ      Sequence 107 AA;

Query Match      86.3%; Score 44; DB 22; Length 107;
Best Local Similarity 88.9%; Pred. No. 2;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      1 QQSGSWPLT 9
        | | | | | | | |

Db      89 QQSGSWPHT 97

RESULT 15
AAB61360

```

ID AAB61360 standard; protein; 107 AA.
XX
AC AAB61360;
XX
DT 03-APR-2001 (first entry)
XX
DE Vitaxin light chain variable region protein.
XX
KW LM609; grafted antibody; alphaVbeta_3 integrin; angiogenesis;
XX inflammatory; cancer; retina; restenosis; osteoporosis.
XX
OS Unidentified.
XX
PN WO200078815-A1.
XX
PD 28-DEC-2000.
XX
XX 23-JUN-2000; 2000WO-US17454.
XX
XX 24-JUN-1999; 99US-0339922.
PR
XX (MOLE-) APPLIED MOLECULAR EVOLUTION.
PA
XX Huse WD, Wu H;
XX
XX WPI: 2001-050110/06.
DR
XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
PT osteoporosis -
XX
PS Disclosure; Fig 1; 132pp; English.
XX
XX The present invention relates to enhanced LM609 grafted antibodies
CC exhibiting selective binding affinity to alphaVbeta_3 integrin or
CC their functional fragments. The antibodies or their functional
CC fragments can be used in the diagnosis and treatment of
CC alphaVbeta_3-mediated diseases such as angiogenesis, inflammatory
CC diseases (such as psoriasis and chronic articular rheumatism),
CC disorders associated with inappropriate or inopportune invasion of
CC vessels (such as diabetic retinopathy, neovascular glaucoma and
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
CC diseases (such as macular degeneration), restenosis and
CC osteoporosis.
XX
SQ Sequence 107 AA;

Query Match 86.3%; Score 44; DB 22; Length 107;
Best Local Similarity 88.9%; Pred. No. 2;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOQSGSWPLT 9
DB 89 QOQSGSWPHT 97
|||||||

Search completed: November 18, 2002, 17:50:49
Job time : 27.4079 secs

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OM protein - protein search, using sw model

Run on: November 18, 2002, 18:45:22 ; Search time 4.14474 Seconds
(without alignments)
32.704 Million cell updates/sec

Title: US-09-016-061-90
Perfect score: 51
Sequence: 1 QOSGSWPLT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 97044 seqs, 15060890 residues

Total number of hits satisfying chosen parameters: 97044

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
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14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	88.2	128	12	US-10-006-773-6
2	44	86.3	107	8	US-08-790-540A-4
3	44	86.3	107	8	US-08-790-540A-8
4	44	86.3	107	8	US-08-791-391A-4
5	44	86.3	107	8	US-08-791-391A-8
6	44	86.3	107	8	US-08-791-391A-32
7	40	78.4	33	9	US-09-956-206A-12
8	39	76.5	100	10	US-09-899-896-4
9	39	76.5	107	10	US-09-756-301A-3
10	39	76.5	107	10	US-09-927-703-3
11	39	76.5	107	10	US-09-766-539A-3
12	39	76.5	107	10	US-09-756-161A-3
13	39	76.5	107	12	US-10-010-229-3
14	39	76.5	107	12	US-10-043-450-3
15	39	76.5	107	12	US-10-044-534-3
16	38	74.5	251	10	US-09-764-853-686
17	35	68.6	59	9	US-10-108-605-353
18	35	68.6	109	9	US-09-144-886-77
19	35	68.6	122	12	US-10-042-417-38

20	35	68.6	235	12	US-10-020-139-3	Sequence 3, Appli
21	34	66.7	80	10	US-09-864-761-13817	Sequence 43817, A
22	34	66.7	113	10	US-09-925-301-1064	Sequence 1064, Ap
23	34	66.7	166	12	US-10-142-373-4	Sequence 4, Appli
24	34	66.7	244	10	US-09-764-864-1075	Sequence 1075, Ap
25	33	64.7	50	10	US-09-864-761-45004	Sequence 45004, A
26	33	64.7	281	10	US-09-788-626-28	Sequence 28, Appl
27	33	64.7	426	10	US-09-292-973-19	Sequence 19, Appl
28	33	64.7	432	10	US-09-292-973-2	Sequence 2, Appli
29	33	64.7	558	9	US-09-850-991-2	Sequence 67, Appl
30	33	64.7	1148	9	US-10-108-605-67	Sequence 173, App
31	33	64.7	1148	9	US-10-108-605-173	Sequence 275, App
32	33	64.7	1148	9	US-10-108-605-275	Sequence 45844, A
33	32	62.7	33	10	US-09-864-761-45844	Sequence 45844, A
34	32	62.7	37	10	US-09-864-761-44048	Sequence 1108, Ap
35	32	62.7	39	10	US-09-925-299-1108	Sequence 7, Appli
36	32	62.7	52	10	US-09-832-197-7	Sequence 46439, A
37	32	62.7	66	10	US-09-864-761-46439	Sequence 2, Appli
38	32	62.7	100	10	US-09-899-896-2	Sequence 42799, A
39	32	62.7	103	10	US-09-864-761-42799	Sequence 93, Appl
40	32	62.7	107	10	US-09-850-165-93	Sequence 168, Appl
41	32	62.7	159	9	US-09-984-245-168	Sequence 6, Appli
42	32	62.7	215	10	US-09-946-805-6	Sequence 36116, A
43	32	62.7	221	10	US-09-864-761-36116	Sequence 1, Appli
44	32	62.7	244	10	US-09-940-391-1	Sequence 7, Appli
45	32	62.7	284	12	US-10-041-400A-7	

ALIGNMENTS

RESULT 1
US-10-006-773-6
; Sequence 6, Application US/10006773
; Patent No. US20020132983A1
; GENERAL INFORMATION:
; APPLICANT: Junghans, Richard P.
; TITLE OF INVENTION: Antibodies as Chimeric Effector Cell Receptors Against Tumor A
; FILE REFERENCE: 003
; CURRENT APPLICATION NUMBER: US/10/006,773
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: 60/250,089
; PRIOR FILING DATE: 2000-11-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-006-773-6

Query Match 88.2%; Score 45; DB 12; Length 128;
Best Local Similarity 88.9%; Pred. No. 0.5;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOSGSWPLT 9
Db 109 QOSNSWPLT 117

RESULT 2
US-08-790-540A-4
; Sequence 4, Application US/08790540A
; Patent No. US20010011125A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego

; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,540A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-790-540A-4
Query Match 86.3%; Score 44; DB 8; Length 107;
Best Local Similarity 88.9%; Pred. No. 0.62;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSGSWPLT 9
Db 89 QQSGSWPHT 97

RESULT 3
US-08-790-540A-8
; Sequence 8, Application US/08790540A
; Patent No. US2001001125A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,540A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

; MOLECULE TYPE: protein
; US-08-790-540A-8
Query Match 86.3%; Score 44; DB 8; Length 107;
Best Local Similarity 88.9%; Pred. No. 0.62;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 QQSGSWPLT 9
Db 89 QQSGSWPHT 97
RESULT 4
US-08-791-391A-4
; Sequence 4, Application US/08791391A
; Patent No. US20010016645A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,391A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-791-391A-4

Query Match 86.3%; Score 44; DB 8; Length 107;
Best Local Similarity 88.9%; Pred. No. 0.62;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSGSWPLT 9
Db 89 QQSGSWPHT 97

RESULT 5
US-08-791-391A-8
; Sequence 8, Application US/08791391A
; Patent No. US20010016645A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Campbell & Flores LLP
;; STREET: 4370 La Jolla Village Drive, Suite 700
;; CITY: San Diego
;; STATE: California
;; COUNTRY: United States
;; ZIP: 92122
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/791,391A
;; FILING DATE: 30-JAN-1997
;; CLASSIFICATION: 424
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Campbell, Cathryn A.
;; REGISTRATION NUMBER: 31,815
;; REFERENCE/DOCKET NUMBER: P-IX 1482
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (619) 535-9001
;; TELEFAX: (619) 535-8949
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 107 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-791-391A-8

Query Match 86.3%; Score 44; DB 8; Length 107;
Best Local Similarity 88.9%; Pred. No. 0.62;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 QQSGSWPLT 9
Db 89 QQSGSWPHT 97

RESULT 6

US-08-791-391A-32
; Sequence 32, Application US/08791391A
; Patent No. US20010016645A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,391A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 32:

;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 107 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-791-391A-32

Query Match 86.3%; Score 44; DB 8; Length 107;
Best Local Similarity 88.9%; Pred. No. 0.62;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 QQSGSWPLT 9
Db 89 QQSGSWPHT 97

RESULT 7

US-09-956-206A-12
; Sequence 12, Application US/09956206A
; Patent No. US20020164339A1
; GENERAL INFORMATION:
; APPLICANT: DO COUTO, FERNANDO J.R.
; CERIANI, ROBERTO L.
; PETERSON, JERRY A.
; TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
; MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND
; METHODS OF HUMANIZING ANTIBODY PEPTIDES

NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/956,206A
FILING DATE: 19-Apr-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/525,539
FILING DATE: 14-SEP-1995
APPLICATION NUMBER: PCT/US95/11683
FILING DATE: 14-SEP-1995
APPLICATION NUMBER: 08/487,598
FILING DATE: 7-JUNE-1995
APPLICATION NUMBER: 08/307,868
FILING DATE: 16-SEPT-1994
ATTORNEY/AGENT INFORMATION:
NAME: WITT, ERIC

REGISTRATION NUMBER: 44,408
REFERENCE/DOCKET NUMBER: 276332000101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
TELEX: 706141

INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 12:

US-09-956-206A-12

Query Match 78.4%; Score 40; DB 9; Length 33;
Best Local Similarity 77.8%; Pred. No. 0.97;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQSGSWPLT 9
||| ||| |
Db 21 QQSNSWPEY 29

RESULT 8

US-09-899-896-4
; Sequence 4, Application US/09899896
; Patent No. US20020072588A1
; GENERAL INFORMATION:
; APPLICANT: von Bdingen, Hans-Christian
; APPLICANT: Genain, Claude P.
; APPLICANT: Hauser, Stephen L.
; TITLE OF INVENTION: Recombinant Antibody Fragments as Autoantibody
; TITLE OF INVENTION: Antagonists
; FILE REFERENCE: SF01-025-2
; CURRENT APPLICATION NUMBER: US/09/899,896
; CURRENT FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 09/691,654
; PRIOR FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 100
; TYPE: PRT
; ORGANISM: human
US-09-899-896-4

Query Match 76.5%; Score 39; DB 10; Length 100;
Best Local Similarity 77.8%; Pred. No. 3.9; Mismatches 0; Gaps 0;
Matches 7; Conservative 0; Indels 2; Indels 0; Gaps 0;

QY 1 QQSGSWPLT 9
|| | |||||
Db 89 QQYSSWPLT 97

RESULT 9

US-09-756-301A-3
; Sequence 3, Application US/09756301A
; Patent No. US20010027249A1
; GENERAL INFORMATION:
; APPLICANT: Le, Junming
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Grayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
; TITLE OF INVENTION: Human Tumor Necrosis Factor
; FILE REFERENCE: 0975.1005-008
; CURRENT APPLICATION NUMBER: US/09/756,301A
; CURRENT FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: U.S. 09/133,119
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1994-10-18
; PRIOR APPLICATION NUMBER: U.S. 08/192,102
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,861
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,093
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/010,406
; PRIOR FILING DATE: 1993-01-29
; PRIOR APPLICATION NUMBER: U.S. 08/013,413
; PRIOR FILING DATE: 1993-02-02
; PRIOR APPLICATION NUMBER: U.S. 07/943,852
; PRIOR FILING DATE: 1992-09-11
; PRIOR APPLICATION NUMBER: U.S. 07/853,606
; PRIOR FILING DATE: 1992-03-18
; PRIOR APPLICATION NUMBER: U.S. 07/670,827
; PRIOR FILING DATE: 1991-03-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus Balb/c
US-09-756-301A-3

Query Match 76.5%; Score 39; DB 10; Length 107;
Best Local Similarity 77.8%; Pred. No. 4.1; Mismatches 0; Gaps 0;
Matches 7; Conservative 0; Indels 2; Indels 0; Gaps 0;

QY 1 QQSGSWPLT 9

; PRIOR FILING DATE: 1992-03-18
; PRIOR APPLICATION NUMBER: U.S. 07/670,827
; PRIOR FILING DATE: 1991-03-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus Balb/c
US-09-756-301A-3

Query Match 76.5%; Score 39; DB 10; Length 107;
Best Local Similarity 77.8%; Pred. No. 4.1; Mismatches 0; Gaps 0;
Matches 7; Conservative 0; Indels 2; Indels 0; Gaps 0;

QY 1 QQSGSWPLT 9
||| ||| |
Db 89 QQSHSWPFT 97

RESULT 10

US-09-927-703-3
; Sequence 3, Application US/09927703
; Patent No. US20020022720A1
; GENERAL INFORMATION:
; APPLICANT: Le, Junming
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Grayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
; TITLE OF INVENTION: Human Tumor Necrosis Factor
; FILE REFERENCE: 0975.1005-013
; CURRENT APPLICATION NUMBER: US/09/927,703
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: U.S. 09/756,398
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: U.S. 09/133,119
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1994-10-18
; PRIOR APPLICATION NUMBER: U.S. 08/192,102
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,861
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,093
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/010,406
; PRIOR FILING DATE: 1993-01-29
; PRIOR APPLICATION NUMBER: U.S. 08/013,413
; PRIOR FILING DATE: 1993-02-02
; PRIOR APPLICATION NUMBER: U.S. 07/943,852
; PRIOR FILING DATE: 1992-09-11
; PRIOR APPLICATION NUMBER: U.S. 07/853,606
; PRIOR FILING DATE: 1992-03-18
; PRIOR APPLICATION NUMBER: U.S. 07/670,827
; PRIOR FILING DATE: 1991-03-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus Balb/c
US-09-927-703-3

Query Match 76.5%; Score 39; DB 10; Length 107;
Best Local Similarity 77.8%; Pred. No. 4.1; Mismatches 0; Gaps 0;
Matches 7; Conservative 0; Indels 2; Indels 0; Gaps 0;


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Db      89 QQSHSWPFT 97
      ||| ||| |
      ; CURRENT APPLICATION NUMBER: US/09/756,161A
      ; CURRENT FILING DATE: 2001-01-08
      ; PRIOR APPLICATION NUMBER: U.S. 09/133,119
      ; PRIOR FILING DATE: 1998-08-12
      ; PRIOR APPLICATION NUMBER: U.S. 08/570,674
      ; PRIOR FILING DATE: 1995-12-11
      ; PRIOR APPLICATION NUMBER: U.S. 08/324,799
      ; PRIOR FILING DATE: 1994-10-18
      ; PRIOR APPLICATION NUMBER: U.S. 08/192,102
      ; PRIOR FILING DATE: 1994-02-04
      ; PRIOR APPLICATION NUMBER: U.S. 08/192,861
      ; PRIOR FILING DATE: 1994-02-04
      ; PRIOR APPLICATION NUMBER: U.S. 08/192,093
      ; PRIOR FILING DATE: 1994-02-04
      ; PRIOR APPLICATION NUMBER: U.S. 08/010,406
      ; PRIOR FILING DATE: 1993-01-29
      ; PRIOR APPLICATION NUMBER: U.S. 08/013,413
      ; PRIOR FILING DATE: 1993-02-02
      ; PRIOR APPLICATION NUMBER: U.S. 07/943,852
      ; PRIOR FILING DATE: 1992-09-11
      ; PRIOR APPLICATION NUMBER: U.S. 07/853,606
      ; PRIOR FILING DATE: 1992-03-18
      ; PRIOR APPLICATION NUMBER: U.S. 07/670,827
      ; PRIOR FILING DATE: 1991-03-18
      ; NUMBER OF SEQ ID NOS: 19
      ; SOFTWARE: FastSeq for Windows Version 4.0
      ; SEQ ID NO 3
      ; LENGTH: 107
      ; TYPE: PRT
      ; ORGANISM: Mus Balb/c
      ; US-09-756-161A-3

Query Match      76.5%; Score 39; DB 10; Length 107;
Best Local Similarity 77.8%; Pred. No. 4.1;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 QQSGSWPFT 9
      ||| ||| |
Db      89 QQSHSWPFT 97

RESULT 13
US-10-010-229-3
; Sequence 3, Application US/10010229
; Patent No. US20020114805A1
; GENERAL INFORMATION:
; APPLICANT: Le, Junming
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Ghayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
; TITLE OF INVENTION: Human Tumor Necrosis Factor
; FILE REFERENCE: 0975.1005-013
; CURRENT APPLICATION NUMBER: US/10/010,229
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US/09/927,703
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus Balb/c
; US-10-010-229-3

Query Match      76.5%; Score 39; DB 12; Length 107;
Best Local Similarity 77.8%; Pred. No. 4.1;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 QQSGSWPFT 9
      ||| ||| |
Db      89 QQSHSWPFT 97

RESULT 12
US-09-756-161A-3
; Sequence 3, Application US/09756161A
; Patent No. US20020132307A1
; GENERAL INFORMATION:
; APPLICANT: Le, Junming
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Ghayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
; TITLE OF INVENTION: Human Tumor Necrosis Factor
; FILE REFERENCE: 0975.1005-007
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Db 89 QQSHSWPFT 97

RESULT 14

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US-10-043-450-3
; Sequence 3, Application US/10043450
; Patent No. US20020141996A1
; GENERAL INFORMATION:
; APPLICANT: Le, Junming
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Ghayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
; FILE OF INVENTION: Human Tumor Necrosis Factor
; FILE REFERENCE: 0975.1005-013
; CURRENT APPLICATION NUMBER: US/10/043.450
; CURRENT FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: 09/927,703
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: U.S. 09/756,398
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: U.S. 09/133,119
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,102
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,861
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,093
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/010,406
; PRIOR FILING DATE: 1993-01-29
; PRIOR APPLICATION NUMBER: U.S. 08/013,413
; PRIOR FILING DATE: 1993-02-02
; PRIOR APPLICATION NUMBER: U.S. 07/943,852
; PRIOR FILING DATE: 1992-09-11
; PRIOR APPLICATION NUMBER: U.S. 07/853,606
; PRIOR FILING DATE: 1992-03-18
; PRIOR APPLICATION NUMBER: U.S. 07/670,827
; PRIOR FILING DATE: 1991-03-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus Balb/c
US-10-043-450-3

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Query Match 76.5%; Score 39; DB 12; Length 107;
 Best Local Similarity 77.8%; Pred. No. 4.1;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQSGSWPFT 9

Db 89 QQSHSWPFT 97

RESULT 15

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US-10-044-534-3
; Sequence 3, Application US/10044534
; Patent No. US20020146419A1
; GENERAL INFORMATION:
; APPLICANT: Le, Junming
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Ghayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott

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; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
; FILE OF INVENTION: Human Tumor Necrosis Factor
; FILE REFERENCE: 0975.1005-013
; CURRENT APPLICATION NUMBER: US/10/044.534
; CURRENT FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: 09/927,703
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: U.S. 09/756,398
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: U.S. 09/133,119
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1994-10-18
; PRIOR APPLICATION NUMBER: U.S. 08/192,102
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,861
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,093
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/010,406
; PRIOR FILING DATE: 1993-01-29
; PRIOR APPLICATION NUMBER: U.S. 08/013,413
; PRIOR FILING DATE: 1993-02-02
; PRIOR APPLICATION NUMBER: U.S. 07/943,852
; PRIOR FILING DATE: 1992-09-11
; PRIOR APPLICATION NUMBER: U.S. 07/853,606
; PRIOR FILING DATE: 1992-03-18
; PRIOR APPLICATION NUMBER: U.S. 07/670,827
; PRIOR FILING DATE: 1991-03-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus Balb/c
US-10-044-534-3

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Query Match 76.5%; Score 39; DB 12; Length 107;
 Best Local Similarity 77.8%; Pred. No. 4.1;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQSGSWPFT 9

Db 89 QQSHSWPFT 97

Search completed: November 18, 2002, 19:04:22
 Job time : 4.14474 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:43:42 ; Search time 8.52632 Seconds
(without alignments)
31.058 Million cell updates/sec

Title: US-09-016-061-90
Perfect score: 51
Sequence: 1 QOSGSWPLT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	88.2	9	2	US-08-232-081B-6
2	45	88.2	103	1	US-08-436-463-21
3	45	88.2	107	2	US-08-232-081B-9
4	45	88.2	107	2	US-08-232-081B-40
5	45	88.2	127	1	US-08-436-463-18
6	40	78.4	33	4	US-08-525-539A-12
7	40	78.4	107	1	US-08-436-463-20
8	40	78.4	107	1	US-08-107-669D-1
9	40	78.4	107	1	US-08-472-788A-1
10	40	78.4	107	2	US-08-477-531B-1
11	40	78.4	107	2	US-08-082-842A-1
12	40	78.4	109	1	US-07-942-245-4
13	40	78.4	143	2	US-08-653-402B-8
14	40	78.4	745	4	US-09-177-165A-25
15	39	76.5	9	2	US-08-476-176B-55
16	39	76.5	9	3	US-08-127-721A-55
17	39	76.5	9	3	US-08-485-246A-55
18	39	76.5	13	1	US-08-221-580-7
19	39	76.5	13	5	PCT-US93-04018-69
20	39	76.5	106	2	US-08-800-198-4
21	39	76.5	106	3	US-09-296-595-4
22	39	76.5	107	1	US-08-192-102-3
23	39	76.5	107	1	US-08-324-799-3
24	39	76.5	107	2	US-08-152-861A-3
25	39	76.5	107	2	US-08-476-176B-4
26	39	76.5	107	3	US-08-127-721A-4
27	39	76.5	107	3	US-08-485-246A-4

28	39	76.5	107	4	US-09-133-119-3	Sequence 3, Appl
29	39	76.5	107	4	US-08-192-093A-3	Sequence 3, Appl
30	39	76.5	127	2	US-08-476-176B-6	Sequence 6, Appl
31	39	76.5	127	2	US-08-476-176B-8	Sequence 8, Appl
32	39	76.5	127	2	US-08-476-176B-10	Sequence 10, Appl
33	39	76.5	127	3	US-08-127-721A-6	Sequence 6, Appl
34	39	76.5	127	3	US-08-127-721A-8	Sequence 8, Appl
35	39	76.5	127	3	US-08-127-721A-10	Sequence 10, Appl
36	39	76.5	127	3	US-08-485-246A-6	Sequence 6, Appl
37	39	76.5	127	3	US-08-485-246A-8	Sequence 8, Appl
38	39	76.5	127	3	US-08-485-246A-10	Sequence 10, Appl
39	39	76.5	240	2	US-08-800-198-8	Sequence 8, Appl
40	39	76.5	240	3	US-09-296-595-8	Sequence 8, Appl
41	38	74.5	100	1	US-08-436-463-19	Sequence 19, Appl
42	38	74.5	107	1	US-07-634-278-62	Sequence 62, Appl
43	38	74.5	107	1	US-07-634-278-63	Sequence 63, Appl
44	38	74.5	107	1	US-07-634-278-87	Sequence 87, Appl
45	38	74.5	107	1	US-08-477-728-62	Sequence 62, Appl

ALIGNMENTS

RESULT 1
US-08-232-081B-6
; Sequence 6, Application US/08232081B
; Patent No. 5886152
; GENERAL INFORMATION:
; APPLICANT: NAKATANI, TOMOYUKI
; APPLICANT: GOMI, HIDEYUKI
; APPLICANT: WAJDENES, JOHN
; APPLICANT: NOGUCHI, HIROSHI
; TITLE OF INVENTION: HUMANIZED B-B10
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
; STREET: PO BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: .Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,081B
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: SVENSSON, LEONARD R
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 20-3484
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-232-081B-6

Query Match 88.2%; Score 45; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 2e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 QOSGSWPLT 9
|||||
DB 1 QOSGSWPLT 9

```
RESULT 2
US-08-436-463-21
; Sequence 21, Application US/08436463
; Patent No. 5760185
; GENERAL INFORMATION:
; APPLICANT: KIMACHI, Kazuhiko
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: NISHIYAMA, Kiyoto
; APPLICANT: TOKIYOSHI, Sachio
; TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT
; TITLE OF INVENTION: ANTIBODY AND GENE FRAGMENT CODING FOR SAID ANTIBODY
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,463
; FILING DATE: 26-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 341255/1992
; FILING DATE: 28-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: KIMACHI-1
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 103 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-436-463-21

Query Match 88.2%; Score 45; DB 1; Length 103;
Best Local Similarity 88.9%; Pred. No. 0.55;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSGSWPLT 9
Db 86 QQNSWPLT 94

RESULT 3
US-08-232-081B-9
; Sequence 9, Application US/08232081B
; Patent No. 5886152
; GENERAL INFORMATION:
; APPLICANT: NAKATANI, TOMOYUKI
; APPLICANT: GOMI, HIDEYUKI
; APPLICANT: WIJDENES, JOHN
; APPLICANT: NOGUCHI, HIROSHI
; TITLE OF INVENTION: HUMANIZED B-B10
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
; STREET: PO BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,081B
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: SVENSSON, LEONARD R
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 20-3484
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
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STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,081B
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SVENSSON, LEONARD R
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 20-3484
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-232-081B-9

Query Match 88.2%; Score 45; DB 2; Length 107;
Best Local Similarity 88.9%; Pred. No. 0.58;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSGSWPLT 9
Db 89 QQSSSWPLT 97

RESULT 4
US-08-232-081B-40
; Sequence 40, Application US/08232081B
; Patent No. 5886152
; GENERAL INFORMATION:
; APPLICANT: NAKATANI, TOMOYUKI
; APPLICANT: GOMI, HIDEYUKI
; APPLICANT: WIJDENES, JOHN
; APPLICANT: NOGUCHI, HIROSHI
; TITLE OF INVENTION: HUMANIZED B-B10
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
; STREET: PO BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,081B
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: SVENSSON, LEONARD R
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 20-3484
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
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; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-232-081B-40

Query Match      88.2%; Score 45; DB 2; Length 107;
Best Local Similarity 88.9%; Pred. No. 0.56;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSGSWPLT 9
Db 89 QQSSSWPLT 97

RESULT 5
US-08-436-463-18
; Sequence 18, Application US/08436463
; Patent No. 5760185
; GENERAL INFORMATION:
; APPLICANT: KIMACHI, Kazuhiko
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: NISHIYAMA, Kiyoto
; APPLICANT: TOKIYOSHI, Sachio
; TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT
; TITLE OF INVENTION: ANTIBODY AND GENE FRAGMENT CODING FOR SAID ANTIBODY
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,463
; FILING DATE: 26-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 341255/1992
; FILING DATE: 28-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: KIMACHI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 127 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-436-463-18

Query Match      88.2%; Score 45; DB 1; Length 127;
Best Local Similarity 88.9%; Pred. No. 0.69;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSGSWPLT 9
Db 109 QQSNSWPLT 117

RESULT 6
US-08-525-539A-12
; Sequence 12, Application US/08525539A
; Patent No. 6309636
; GENERAL INFORMATION:
; APPLICANT: DO COUTO, FERNANDO J.R.
; APPLICANT: CERIANI, ROBERTO L.
; APPLICANT: PETERSON, JERRY A.
; TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
; TITLE OF INVENTION: MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND
; TITLE OF INVENTION: METHODS OF HUMANIZING ANTIBODY PEPTIDES
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/525,539A
; FILING DATE: 14-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DYLAN, TYLER
; REGISTRATION NUMBER: 37,612
; REFERENCE/DOCKET NUMBER: 27633-20001.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-525-539A-12

Query Match      78.4%; Score 40; DB 4; Length 33;
Best Local Similarity 77.8%; Pred. No. 1.2;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQSGSWPLT 9
Db 21 QQSNSWPVT 29

RESULT 7
US-08-436-463-20
; Sequence 20, Application US/08436463
; Patent No. 5760185
; GENERAL INFORMATION:
; APPLICANT: KIMACHI, Kazuhiko
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: NISHIYAMA, Kiyoto
; APPLICANT: TOKIYOSHI, Sachio
; TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT
; TITLE OF INVENTION: ANTIBODY AND GENE FRAGMENT CODING FOR SAID ANTIBODY
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/436.463
;; FILING DATE: 26-JUN-1995
;; CLASSIFICATION: 536
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: JP 341255/1992
;; FILING DATE: 28-NOV-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: YUN, Allen C.
;; REGISTRATION NUMBER: 37,971
;; REFERENCE/DOCKET NUMBER: KIMACHI-1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-628-5197
;; TELEFAX: 202-737-3528
;; INFORMATION FOR SEQ ID NO: 20:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 107 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-436-463-20

Query Match 78.4%; Score 40; DB 1; Length 107;
Best Local Similarity 77.8%; Pred. No. 4.1;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOQSGSWPLT 9
 | | | | | | | |
Db 89 QQSNWPYT 97

RESULT 8

US-08-107-669D-1
;; Sequence 1, Application US/08107669D
;; Patent No. 5766886
;; GENERAL INFORMATION:
;; APPLICANT: Studnicka, Gary M.
;; TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)
;; NUMBER OF SEQUENCES: 67
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
;; STREET: 1100 New York Ave., N.W., Suite 600
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: United States of America
;; ZIP: 20005-3934
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/107.669D
;; FILING DATE: 13-AUG-1993
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US92/10906
;; FILING DATE: 14-DEC-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/808,464
;; FILING DATE: 13-DEC-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Michele A. Cimbala
;; REGISTRATION NUMBER: 33,851
;; REFERENCE/DOCKET NUMBER: 0610.1000001/MAC
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202/371-2600
;; TELEFAX: 202/371-2540
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 107 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-107-669D-1

Query Match 78.4%; Score 40; DB 1; Length 107;
Best Local Similarity 77.8%; Pred. No. 4.1;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOQSGSWPLT 9
 | | | | | | | |
Db 89 QQSNWPYT 97

;; LENGTH: 107 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-107-669D-1
Query Match 78.4%; Score 40; DB 1; Length 107;
Best Local Similarity 77.8%; Pred. No. 4.1;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOQSGSWPLT 9
 | | | | | | | |
Db 89 QQSNWPYT 97

RESULT 9

US-08-472-788A-1
;; Sequence 1, Application US/08472788A
;; Patent No. 5770196
;; GENERAL INFORMATION:
;; APPLICANT: Studnicka, Gary M.
;; TITLE OF INVENTION: Modified Antibody Variable Domains
;; NUMBER OF SEQUENCES: 89
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
;; STREET: 1100 New York Ave., N.W., Suite 600
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: USA
;; ZIP: 20005-3934
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/472,788A
;; FILING DATE: 07-JUN-1995
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/082,842
;; FILING DATE: 23-JUN-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US92/10906
;; FILING DATE: 14-DEC-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/808,464
;; FILING DATE: 13-DEC-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Cimbala, Michele A.
;; REGISTRATION NUMBER: 33,851
;; REFERENCE/DOCKET NUMBER: 0610.1000003
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202/371-2600
;; TELEFAX: 202/371-2540
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 107 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-472-788A-1

Query Match 78.4%; Score 40; DB 1; Length 107;
Best Local Similarity 77.8%; Pred. No. 4.1;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOQSGSWPLT 9
 | | | | | | | |
Db 89 QQSNWPYT 97

RESULT 10
US-08-477-531B-1
; Sequence 1, Application US/08477531B
; Patent No. 5821123
; GENERAL INFORMATION:
; APPLICANT: Studnicka, Gary M.
; TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States of America
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,531B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/107,669
; FILING DATE: 13-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10906
; FILING DATE: 14-DEC-1992
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/808,464
; FILING DATE: 13-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Michele A. Cimbala
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 0610.1000004/MAC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/371-2600
; TELEFAX: 202/371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-477-531B-1

Query Match 78.4%; Score 40; DB 2; Length 107;
Best Local Similarity 77.8%; Pred. No. 4.1;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQSGSWPLT 9
Db 89 QQSNSWPYT 97

RESULT 11
US-08-082-842A-1
; Sequence 1, Application US/08082842A
; Patent No. 5869619
; GENERAL INFORMATION:
; APPLICANT: Studnicka, Gary M.
; TITLE OF INVENTION: Modified Antibody Variable Domains
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/082,842A
; FILING DATE: 23-JUN-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10906
; FILING DATE: 14-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/808,464
; FILING DATE: 13-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Cimbala, Michele A.
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 0610.1000002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/371-2600
; TELEFAX: 202/371-2540
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-082-842A-1

Query Match 78.4%; Score 40; DB 2; Length 107;
Best Local Similarity 77.8%; Pred. No. 4.1;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQSGSWPLT 9
Db 89 QQSNSWPYT 97

RESULT 12
US-07-942-245-4
; Sequence 4, Application US/07942245
; Patent No. 5639641
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, Jan T.
; APPLICANT: SEARLE, Stephen M.J.
; APPLICANT: REES, Anthony R.
; APPLICANT: ROGUSKA, Michael A.
; APPLICANT: GUILD, Braydon C.
; TITLE OF INVENTION: SURFACE RESIDUE VENEERING OF RODENT
; NUMBER OF SEQUENCES: 522
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: HP 9000/700 Workstation
; OPERATING SYSTEM: UNIX
; SOFTWARE: in house
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/942,245
; FILING DATE: 09-SEP-1992
; CLASSIFICATION: 530
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 293-7060
; TELEFAX: (202) 293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 4:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-942-245-4

Query Match      78.4%; Score 40; DB 1; Length 109;
Best Local Similarity 77.8%; Pred. No. 4.2;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQSGSWPLT 9
   |||||
Db 89 QQSNSWPLY 97

RESULT 13
US-08-653-402B-8
; Sequence 8, Application US/08653402B
; Patent No. 5969107
; GENERAL INFORMATION:
; APPLICANT: CARCELLER, Ana
; APPLICANT: ROSELL, Elisabet
; APPLICANT: GOMEZ, Alicia
; APPLICANT: ADEN, Jaume
; TITLE OF INVENTION: PIULATS, Jaume
; TITLE OF INVENTION: Anti-idiotypic antibodies which induce an
; TITLE OF INVENTION: immune response against epidermal growth factor receptor.
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
; STREET: 2200 Clarendon Boulevard, Suite 1400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/653.402B
; FILING DATE: 24-MAY-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95107967.2
; FILING DATE: 26-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lebovitz, Richard M.
; REGISTRATION NUMBER: 37,067
; REFERENCE/DOCKET NUMBER: MERCK 1781
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-243-6333
; TELEFAX: 703-243-6410
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 143 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-653-402B-8

Query Match      78.4%; Score 40; DB 2; Length 143;
Best Local Similarity 77.8%; Pred. No. 5.6;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQSGSWPLT 9
   |||||
Db 109 QQSNSWPLY 117

RESULT 14
US-09-177-165A-25
; Sequence 25, Application US/09177165A
; Patent No. 6426205
; GENERAL INFORMATION:
; APPLICANT: Tyers, Mike
; APPLICANT: Willem, Andrew
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING UBIQUITIN
; TITLE OF INVENTION: DEPENDENT PROTEOLYSIS
; FILE REFERENCE: 11757.10USU1
; CURRENT APPLICATION NUMBER: US/09/177,165A
; CURRENT FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/092,443
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/063,254
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 745
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-177-165A-25

Query Match      78.4%; Score 40; DB 4; Length 745;
Best Local Similarity 75.0%; Pred. No. 32;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QQSGSWPLT 9
   |||||
Db 513 QAGAWPLT 520

RESULT 15
US-08-476-176B-55
; Sequence 55, Application US/08476176B
; Patent No. 5958708
; GENERAL INFORMATION:
; APPLICANT: Hardman, No. 5958708man
; APPLICANT: Kolbinger, Frank
; APPLICANT: Saldanha, Jose
; TITLE OF INVENTION: Reshaped monoclonal antibodies against an
; TITLE OF INVENTION: immunoglobulin isotype
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5958708artis Patent Department
; STREET: 59 Route 10
; CITY: East Hanover
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07936-1080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,176B
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/127,721
; FILING DATE: 27-SEPTEMBER-1993
; APPLICATION NUMBER: US 07/952,802
; FILING DATE: 25-SEPTEMBER-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5958708ak, Henry P.
; REGISTRATION NUMBER: 33,200
; REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 277-5110
; TELEFAX: (908) 277-4306
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
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; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-476-176B-55

Query Match 76.5% Score 39; DB 2; Length 9;
Best Local Similarity 77.8%; Pred. No. 2e+05;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QSGSWPLT 9
||| ||| |
Db 1 QSDSWPTT 9

Search completed: November 18, 2002, 17:55:52
Job time : 9.52632 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:47:14 : Search time 9.5921 Seconds
(without alignments)
90.200 Million cell updates/sec

Title: US-09-016-061-92

Perfect score: 52

Sequence: 1 QQSGSNWPT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR_73:*

2: PIR:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	46	88.5	67	2 PH1081	Ig light chain V r
2	46	88.5	69	2 PH1080	Ig light chain V r
3	41	78.8	107	2 A5722	anti-glycoprotein
4	41	78.8	123	2 S35479	Ig kappa chain pre
5	40	76.9	106	2 PL0267	Ig kappa chain V r
6	39	75.0	104	2 B43413	Ig kappa chain V r
7	39	75.0	108	2 C30502	Ig kappa chain V r
8	39	75.0	138	2 A26471	Ig kappa chain pre
9	38	73.1	107	2 B45722	anti-glycoprotein
10	38	73.1	553	2 T15220	hypothetical prote
11	37	71.2	102	2 S26346	Ig kappa chain V r
12	37	71.2	128	2 PN0445	Ig kappa chain pre
13	36	69.2	87	2 PH1082	Ig light chain V r
14	36	69.2	115	1 KVM5L7	Ig kappa chain pre
15	36	69.2	134	2 T17816	hypothetical prote
16	36	69.2	331	2 T48867	drpGlucose 4,6-de
17	36	69.2	345	2 AG0366	thiosulfate-bindin
18	36	69.2	371	2 A87322	pentapeptide repea
19	36	69.2	775	2 F98136	hypothetical prote
20	36	69.2	800	2 AE3151	glucoamylase [impo
21	36	69.2	1456	1 WNGP9V	RNA-directed RNA p
22	36	69.2	1456	1 JQ2294	hypothetical 165.1
23	36	69.2	1456	2 S14005	hypothetical prote
24	35	67.3	146	2 AD0929	conserved hypotet
25	35	67.3	313	2 G95883	probable ABC trans
26	35	67.3	322	2 B96014	probable sugar upt
27	35	67.3	365	1 SAVLWE	large surface anti
28	35	67.3	366	1 SAVLBD	large surface anti
29	35	67.3	366	1 SAVLWD	large surface anti

30 35 67.3 366 2 A37374 Fc gamma (IqG) rec
31 35 67.3 470 1 WZBEA4 transcription acti
32 35 67.3 470 1 B42746 transcription acti
33 35 67.3 618 2 T49177 hypothetical prote
34 35 67.3 633 2 AC3634 nrd protein (impo
35 35 67.3 753 2 JC2099 glutenin, high mol
36 35 67.3 789 2 A30843 glutenin, high mole
37 35 67.3 791 2 JN0690 glutenin, high-mol
38 35 67.3 815 2 B30843 glutenin, high mole
39 35 67.3 815 2 JN0689 glutenin, high-mol
40 35 67.3 830 2 S15720 glutenin-high mole
41 35 67.3 1086 2 AF1662 cellobiose-phospho
42 35 67.3 1086 2 AH1290 cellobiose-phospho
43 34 65.4 96 2 JC5945 regulatory protein
44 34 65.4 98 2 H90882 ribosomal-protein-
45 34 65.4 98 2 G85735 ribosomal-protein-

ALIGNMENTS

RESULT 1

PH1081

Ig light chain V region (clone 165.6) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 15-Jun-1996

C:Accession: PH1081

R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective

A:Reference number: PH0971; MUID:92381444; PMID:1512540

A:Accession: PH1081

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-67 <TIL>

A:Experimental source: B cell, strain [NZB x NZWJF1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

Query Match 88.5%; Score 46; DB 2; Length 67;
Best Local Similarity 88.9%; Pred. No. 0.22;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSGSNWPT 9

Db 58 QQSGSNWPT 66

RESULT 2

PH1080

Ig light chain V region (clone 165.60) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 15-Jun-1996

C:Accession: PH1080

R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective

A:Reference number: PH0971; MUID:92381444; PMID:1512540

A:Accession: PH1080

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-69 <TIL>

A:Experimental source: B cell, strain [NZB x NZWJF1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

Query Match 88.5%; Score 46; DB 2; Length 69;
Best Local Similarity 88.9%; Pred. No. 0.23;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSGSNWPT 9

Db 60 QQSGSNWPT 68

```
RESULT 3
A45722
anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 5) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 03-Mar-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: A45722
R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Vasquez, J.; Virol, 67, 489-496, 1993
A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on human immunoglobulin V region; immunoglobulin homology
A:Reference number: A45722; MUID:93100833; PMID:7677958
A:Accession: A45722
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-107 <SIM>
A>Note: sequence extracted from NCBI backbone (NCBIP:120589)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: glycoprotein
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 78.8%; Score 41; DB 2; Length 107;
Best Local Similarity 77.8%; Pred. No. 2.7;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQSGSWPQT 9
   ||| ||| |
Db 89 QQSNSWPHT 97

RESULT 4
S35479
Ig kappa chain precursor V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 19-Mar-1997 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: S35479
R:Takeda, Y.; Wise, K.S.; Hoffman, R.W.
Nucleic Acids Res. 20, 4099, 1992
A:Title: Nucleotide sequences of immunoglobulin heavy and light chain V-regions from a mouse
A:Reference number: S35479; MUID:93375706; PMID:1387203
A:Accession: S35479
A>Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-123 <TAK>
A:Cross-references: EMBL:M93959; NID:gl97572; PIDN:AAA39079.1; PID:9554148
C:Genetics:
A:Map position: 6
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-12/Domain: signal sequence (fragment) #status predicted <SIG>
F:13-123/Product: Ig kappa chain V region (fragment) #status predicted <MAT>
F:28-102/Domain: immunoglobulin homology <IMM>

Query Match 78.8%; Score 41; DB 2; Length 123;
Best Local Similarity 77.8%; Pred. No. 3.1;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQSGSWPQT 9
   ||| ||| |
Db 101 QQSNSWPHT 109

RESULT 5
PL0267
Ig kappa chain V region (anti-DNA, DP12VK) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C:Accession: PL0267
R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.; Exp. Med. 171, 265-297, 1990
A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic mutation
A:Reference number: PL0231; MUID:90111618; PMID:2104919
A:Accession: PL0267
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A:Molecule type: mRNA
A:Residues: 1-106 <SHL>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-23/Region: framework 1
F:16-90/Domain: immunoglobulin homology <IMM>
F:24-34/Region: complementarity-determining 1
F:35-49/Region: framework 2
F:50-56/Region: complementarity-determining 2
F:57-88/Region: framework 3
F:89-97/Region: complementarity-determining 3
F:98-106/Region: framework 4

Query Match 76.9%; Score 40; DB 2; Length 106;
Best Local Similarity 77.8%; Pred. No. 4;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQSGSWPQT 9
   ||| ||| |
Db 89 QQSNSWPYT 97

RESULT 6
B43413
Ig kappa chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: B43413
R:Tomiya, Y.; Brojer, E.; Ruggeri, Z.M.; Shattil, S.J.; Smiltneck, J.; Gorski, J.; J. Biol. Chem. 267, 18085-18092, 1992
A:Title: A molecular model of RGD ligands. Antibody D gene segments that direct specific binding to alpha5 beta1 integrin
A:Reference number: A43413; MUID:92388177; PMID:1517241
A:Accession: B43413
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-104 <TOM>
A>Note: sequence extracted from NCBI backbone (NCBIP:112818)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:13-87/Domain: immunoglobulin homology <IMM>

Query Match 75.0%; Score 39; DB 2; Length 104;
Best Local Similarity 77.8%; Pred. No. 5.8;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQSGSWPQT 9
   ||| ||| |
Db 86 QQSNSWPLT 94

RESULT 7
C30502
Ig kappa chain V region (D444) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 03-Nov-1988 #sequence_revision 03-Nov-1988 #text_change 21-Jan-2000
C:Accession: C30502
R:Eilat, D.; Webster, D.M.; Rees, A.R.; J. Immunol. 141, 1745-1753, 1988
A:Title: V region sequences of anti-DNA and anti-RNA autoantibodies from NZB/NZW F-1 mice
A:Reference number: A30502; MUID:88315787; PMID:2457627
A:Accession: C30502
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-108 <EIL>
A:Cross-references: GB:M21907; NID:gl97071; PIDN:AAA38907.1; PID:gl97072
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 75.0%; Score 39; DB 2; Length 108;
Best Local Similarity 66.7%; Pred. No. 6.1;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

QY 1 QOQSGSWPQT 9

II: IIII I

Db 89 QQTNSWPRT 97

RESULT 8

A26471

Ig kappa chain precursor V region (MAX33) - mouse

C:Species: Mus musculus (house mouse)

C>Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 23-Jul-1999

C:Accession: A26471

R:Buckel, P.; Hubner-Parajsz, C.; Mattes, R.; Lenz, H.; Haug, H.; Beaucamp, K.

Gene 51, 13-19, 1987

A>Title: Cloning and nucleotide sequence of heavy- and light-chain cDNAs from a creatine

A:Reference number: A91572; MUID:87248058; PMID:3110009

A:Accession: A26471

A:Molecule type: mRNA

A:Residues: 1-138 <BUC>

A:Cross-references: GB:M16162; NID:g196893; PIDN:AAA38023.1; PID:g196894

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-138/Product: Ig kappa chain V region #status predicted <MAT>

Query Match

Best Local Similarity 75.0%; Score 39; DB 2; Length 138;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOQSGSWPQT 9

III: IIII I

Db 109 QQNSWPLT 117

RESULT 9

B45722

anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 33) - mouse (fr

C:Species: Mus musculus (house mouse)

C>Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000

C:Accession: B45722

R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Vasqu

J. Virol. 67, 489-496, 1993

A>Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on hu

A:Reference number: A45722; MUID:93100833; PMID:7677958

A:Accession: B45722

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-107 <STM>

A>Note: sequence extracted from NCBI backbone (NCBIP:120590)

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: glycoprotein

F:16-90/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 73.1%; Score 38; DB 2; Length 107;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOQSGSWPQT 9

II: IIII I

Db 89 QQTNSWPRT 97

RESULT 10

T15220

hypothetical protein F57C9.8 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C:Accession: T15220

R:Gelsel, C.; Kramer, J.; Gibson, A.

submitted to the EMBL Data Library, May 1997

A:Description: The sequence of C. elegans cosmid F57C9.

A:Reference number: Z18309

A:Accession: T15220

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-553 <GEI>

A:Cross-references: EMBL:AF003142; NID:g2088743; PID:g2088751; PIDN:AA854191.1; GSPDB

A:Experimental source: strain Bristol N2; clone F57C9

C:Genetics:

A:Gene: CESP:F57C9.8

A:Map position: 1

A:Introns: 184/1; 233/3; 286/3; 496/1

Query Match

Best Local Similarity 73.1%; Score 38; DB 2; Length 553;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOQSGSWP 7

I: IIIII

Db 373 QRSQSWP 379

RESULT 11

S26346

Ig kappa chain V region - mouse

C:Species: Mus musculus (house mouse)

C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000

C:Accession: S26346

R:Stark, S.E.; Caton, A.J.

J. Exp. Med. 174, 613-624, 1991

A>Title: Antibodies that are specific for a single amino acid interchange in a protei

A:Reference number: S26309; MUID:91341421; PMID:1908510

A:Accession: S26346

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-102 <STA>

A:Cross-references: EMBL:X59211; NID:g52338; PIDN:CAA41921.1; PID:g1334075

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:14-88/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 71.2%; Score 37; DB 2; Length 102;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOQSGSWPQT 9

III: IIII I

Db 87 QQSTWPTT 95

RESULT 12

PN0445

Ig kappa chain precursor V-I region - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000

C:Accession: PN0445

R:Kaluzs, B.; Betz, G.; Shao, H.; Diamantse, T.; Weidle, U.H.

Gene 122, 321-328, 1992

A>Title: A general method for chimerization of monoclonal antibodies by inverse polym

A:Reference number: PN0444; MUID:93138402; PMID:1339379

A:Accession: PN0445

A:Molecule type: mRNA

A:Residues: 1-128 <NAL>

A:Cross-references: GB:L02347

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-10/Domain: signal sequence #status predicted <SIG>

F:11-128/Product: Ig light chain kappa-1 V region #status predicted <MAT>

F:26-100/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 71.2%; Score 37; DB 2; Length 128;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOQSGSWPQT 9

II: IIII I

Db 99 QQTNSWPTT 107

RESULT 13

PH1082
Ig light chain V region (clone 165.54) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C:Accession: PH1082
R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marlon, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cell gene rearrangement
A:Reference number: PH0971; MUID:92381444; PMID:1512540
A:Accession: PH1082
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-87 <TIL>
A:Experimental source: B cell, strain [N2B x NZW]F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:6-80/Domain: immunoglobulin homology <IMM>

Query Match 69.2%; Score 36; DB 2; Length 87;
Best Local Similarity 85.7%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSGSWP 7
||| |||
Db 79 QQNSWP 85

RESULT 14

KVMSL7
Ig kappa chain precursor V region (L7) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 18-Dec-1981 #sequence_revision 18-Dec-1981 #text_change 22-Jun-1999
C:Accession: A01925
R:Peck, M.; Hochli, J.; Schnell, H.; Zachau, H.G.
Nature 291, 668-670, 1981
A:Title: Differences between germ-line and rearranged immunoglobulin V-kappa coding sequences
A:Reference number: A93259; MUID:81220975; PMID:6264318
A:Accession: A01925
A:Molecule type: DNA
A:Residues: 1-115 <PEC>
A:Cross-references: GB:V01564; GB:J00574; NID:g51718; PIDN:CAA24884.1; PID:g758153
A:Note: the sequence was determined from the germline gene
A:Note: there appear to be two possible splice junctions at the 3' end of the intron; the sequence shown is the first
C:Genetics: 17/1
A:Introns: 17/1
C:Complex: An immunoglobulin heterotrimer subunit consists of two identical light (kappa) and two heavy (lambda) chains held together by disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger oligomers.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-115/Product: Ig kappa chain V region (L7) #status predicted <MAT>
F:36-110/Domain: immunoglobulin homology <IMM>
F:43-108/Disulfide bonds: #status predicted

Query Match 69.2%; Score 36; DB 1; Length 115;
Best Local Similarity 85.7%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSGSWP 7
||| |||
Db 109 QQNSWP 115

RESULT 15

T17816
hypothetical protein a317L - Chlorella virus PBCV-1
C:Species: Chlorella virus PBCV-1
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T17816
R:Graves, M.V.; Van Etten, J.L.

submitted to the EMBL Data Library, May 1999

A:Reference number: Z18806
A:Accession: T17816
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-154 <GRA>
A:Cross-references: EMBL:U42580; NID:g4028896; PIDN:AAC96685.1
A:Experimental source: specific host Chlorella strain NC64A
C:Genetics:
A:Note: a317L

Query Match 69.2%; Score 36; DB 2; Length 154;
Best Local Similarity 85.7%; Pred. No. 29;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSGSWP 7
||| |||
Db 33 QQSGSWP 39

Search completed: November 18, 2002, 17:57:21
Job time : 10.5921 secs

GenCore version 5.1.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:33:36 ; Search time 4.85526 Seconds
(without alignments)
76.883 Million cell updates/sec

Title: US-09-016-061-92

Perfect score: 52

Sequence: 1 QOSGSWPQT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	69.2	92	1 CATC_RHOOP	P95609 rhodococcus
2	36	69.2	115	1 KV51_MOUSE	P01642 mus musculus
3	36	69.2	1456	1 RRPO_PVX	P09395 potato viru
4	36	69.2	1456	1 RRPO_PVXCP	P22591 potato viru
5	36	69.2	1456	1 RRPO_PVXH	Q07630 potato viru
6	36	69.2	1456	1 RRPO_PVXX3	P17779 potato viru
7	35	67.3	365	1 VMSA_HPBDC	P30029 duck hepati
8	35	67.3	366	1 FCN_RAT	P13599 rattus norv
9	35	67.3	366	1 VMSA_HPBDB	P17194 duck hepati
10	35	67.3	366	1 VMSA_HPBDB	P17195 duck hepati
11	35	67.3	470	1 IE63_HSVB	P28939 equine herp
12	35	67.3	470	1 IE63_HSVK	Q05906 equine herp
13	35	67.3	471	1 P2X2_HUMAN	Q9ub19 homo sapien
14	34	65.4	96	1 CTC1_ACILW	O33947 acinetobact
15	34	65.4	146	1 YFDK_ECOLI	P77656 escherichia
16	34	65.4	179	1 RIML_ECOLI	P13857 escherichia
17	34	65.4	231	1 HB2L_CHICK	P23068 gallus gall
18	34	65.4	318	1 GLUP_DROME	O18640 drosophila
19	34	65.4	318	1 PEX7_MOUSE	P97865 mus musculu
20	34	65.4	323	1 PEX7_HUMAN	O00628 homo sapien
21	34	65.4	491	1 TYTR_CRIFA	P39040 crithidia f
22	34	65.4	492	1 TYTR_TRYBB	P39051 trypanosoma
23	34	65.4	492	1 TYTR_TRYCO	P13110 trypanosoma
24	34	65.4	745	1 CUL2_HUMAN	Q13617 homo sapien
25	34	65.4	1335	1 RRPO_FAMV	P22168 foxtail mos
26	33	63.5	353	1 LEU3_BACFR	P54354 bacteroides
27	33	63.5	360	1 VG47_BPMU	Q9tlv2 bacterioph
28	33	63.5	436	1 VU10_HSV6U	Q01348 human herpe
29	33	63.5	443	1 YJJJ_ECOLI	P39410 escherichia
30	33	63.5	468	1 NIFB_KLEPN	P10390 klebsiella
31	33	63.5	528	1 HEXA_MOUSE	P29416 mus musculu
32	33	63.5	529	1 HEXA_HUMAN	P06865 homo sapien
33	33	63.5	658	1 EGLN_HUMAN	P17813 homo sapien

ALIGNMENTS

RESULT 1

ID	CATC_RHOOP	STANDARD;	PRT;	92 AA.
AC	P95609;			
DT	15-JUL-1999 (Rel. 38, Created)			
DT	15-JUL-1999 (Rel. 38, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Muconolactone delta-isomerase (EC 5.3.3.4) (Mise).			
GN	CATC.			
OS	Rhodococcus opacus (Nocardia opaca).			
OC	Bacteria; Actinobacteria; Actinobacteriia (Class); Actinobacteridae;			
OC	Actinomycetales; Corynebacterineae; Nocardiaceae; Rhodococcus.			
OX	NCBI_TaxID=37919;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 1-20.			
RC	STRAIN=ICP;			
RX	MEDLINE=97144521; PubMed=8990288;			
RA	Eulberg D., Golovleva L.A., Schloemann M.;			
RT	"Characterization of catechol catabolic genes from Rhodococcus erythropolis ICP.";			
RL	J. Bacteriol. 179:370-381(1997).			
CC	-I- CATALYTIC ACTIVITY: 2,5-dihydro-5-oxofuran-2-acetate = 3,4-dihydro-5-oxofuran-2-acetate.			
CC	-I- PATHWAY: THIRD STEP IN THE CATABOLISM OF CATECHOL TO SUCCINATE- AND ACETYL-COA IN THE BETA-KETOADIPATE PATHWAY.			
CC	-I- SUBUNIT: HOMODECAMER (BY SIMILARITY).			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announcement/ or send an email to license@isb-sib.ch).			
DR	EMBL: X99622; CAA67935.1; -.			
DR	InterPro: IPR003464; Mase.			
DR	Pfam: PF02426; Mase; 1.			
KW	Aromatic hydrocarbons catabolism; Isomerase.			
FT	INIT-MET 0 0			
SQ	SEQUENCE 92 AA; 10780 MW; 9CCE5A17DED4B153 CRC64;			
Query Match	69.2%; Score 36; DB 1; Length 92;			
Best Local Similarity	62.5%; Pred. No. 9.4;			
Matches	5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;			
QY	1 QOSGSWPQT 8			
Db	35 QRSKWPE 42			
RESULT 2				
KV51_MOUSE	STANDARD;			
ID	KV51_MOUSE			
AC	P01642;			
DT	21-JUL-1986 (Rel. 01, Created)			

```
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-V region L7 precursor (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8120975; PubMed=6264318;
RA Pech M., Hochtl J., Schnell H., Zachau H.G.;
RT "Differences between germ-line and rearranged immunoglobulin V kappa
RT coding sequences suggest a localized mutation mechanism.";
RL Nature 291:668-670(1981).
CC -1- MISCELLANEOUS: THERE APPEAR TO BE TWO POSSIBLE SPLICING JUNCTIONS AT
CC THE 3' END OF THE INTRON. THE ALTERNATE WOULD CODE FOR A PROTEIN
CC LACKING RESIDUES 17-19.
DR PIR; A01925; KVM5L7.
DR HSP; P80362; 1WTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 >115 IG KAPPA CHAIN V-V REGION L7.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 69 FRAMEWORK-2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 77 108 FRAMEWORK-3.
FT DOMAIN 109 >115 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12615 MW; C17BEC758C577E00 CRC64;

Query Match 69.2%; Score 36; DB 1; Length 115;
Best Local Similarity 85.7%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSGSWP 7
DB 109 QQSGSWP 115
III III

RESULT 3
RRPO_PVX STANDARD; PRT; 1456 AA.
AC P09395;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE RNA replication protein (165 kDa protein) (ORF 1) [Contains: RNA-
DE directed RNA polymerase (EC 2.7.7.48); Probable helicase].
OS Potato virus X (PVX).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potexvirus.
OX NCBI_TaxID=12183;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89083520; PubMed=3205733;
RA Skryabin K.G., Kraev A.S., Morozov S.Y., Rozanov M.N., Chernov B.K.,
RA Lukashova L.I., Atabekov J.G.;
RT "The nucleotide sequence of potato virus X RNA.";
RL Nucleic Acids Res. 16:10929-10930(1988).
CC -1- FUNCTION: RNA-replication. The central part of this protein
CC possibly functions as an ATP-binding helicase.
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC [RNA](N).
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M31541; AAA47178.1; -
DR EMBL; X55802; CAA39324.1; -
DR PIR; S14005; S14005.
DR InterPro; IPR001788; RNA_dep_RNAPol2.
DR InterPro; IPR000606; Viral_helicase1.
DR Pfam; PF00978; RNA_dep_RNAPol2; 1.
DR Pfam; PF01443; Viral_helicase1; 1.
KW ATP-binding; Helicase; RNA replication; RNA-directed RNA polymerase;
KW Transferase. 735 742 POTENTIAL.
FT NP_BIND 1456 AA; 165301 MW; 489BA57EA070BD2E CRC64;
SQ SEQUENCE 1456 AA; 165406 MW; F09FDF47E298988C CRC64;

Query Match 69.2%; Score 36; DB 1; Length 1456;
Best Local Similarity 62.5%; Pred. No. 1.3e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSGSWPQ 8
DB 1361 ORKGSWE 1368
I: IIII:

RESULT 4
RRPO_PVXCP STANDARD; PRT; 1456 AA.
AC P22591;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE RNA replication protein (165 kDa protein) (ORF 1) [Contains: RNA-
DE directed RNA polymerase (EC 2.7.7.48); Probable helicase].
OS Potato virus X (strain CP) (PVX).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potexvirus.
OX NCBI_TaxID=12184;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90364772; PubMed=2392880;
RA Orman B.E., Celnik R.M., Mandel A.M., Torres H.N., Mentaberry A.N.;
RA "Complete cDNA sequence of a South American isolate of potato virus
RT X.";
RL Virus Res. 16:293-306(1990).
CC -1- FUNCTION: RNA-replication. The central part of this protein
CC possibly functions as an ATP-binding helicase.
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC [RNA](N).
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CC -----
DR EMBL; M31541; AAA47178.1; -
DR EMBL; X55802; CAA39324.1; -
DR PIR; S14005; S14005.
DR InterPro; IPR001788; RNA_dep_RNAPol2.
DR InterPro; IPR000606; Viral_helicase1.
DR Pfam; PF00978; RNA_dep_RNAPol2; 1.
DR Pfam; PF01443; Viral_helicase1; 1.
KW ATP-binding; Helicase; RNA replication; RNA-directed RNA polymerase;
KW Transferase. 735 742 POTENTIAL.
FT NP_BIND 1456 AA; 165301 MW; 489BA57EA070BD2E CRC64;
SQ SEQUENCE 1456 AA; 165406 MW; F09FDF47E298988C CRC64;

Query Match 69.2%; Score 36; DB 1; Length 1456;
Best Local Similarity 62.5%; Pred. No. 1.3e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSGSWPQ 8
DB 1361 ORKGSWE 1368
I: IIII:

RESULT 4
RRPO_PVXCP STANDARD; PRT; 1456 AA.
AC P22591;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE RNA replication protein (165 kDa protein) (ORF 1) [Contains: RNA-
DE directed RNA polymerase (EC 2.7.7.48); Probable helicase].
OS Potato virus X (strain CP) (PVX).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potexvirus.
OX NCBI_TaxID=12184;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90364772; PubMed=2392880;
RA Orman B.E., Celnik R.M., Mandel A.M., Torres H.N., Mentaberry A.N.;
RA "Complete cDNA sequence of a South American isolate of potato virus
RT X.";
RL Virus Res. 16:293-306(1990).
CC -1- FUNCTION: RNA-replication. The central part of this protein
CC possibly functions as an ATP-binding helicase.
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC [RNA](N).
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Db 1361 QKGSWPE 1368
      1: ||||:
      ID RRPO_PVXHB STANDARD; PRT; 1456 AA.
      AC Q07630;
      DT 01-OCT-1996 (Rel. 34, Created)
      DT 01-OCT-1996 (Rel. 34, Last sequence update)
      DT 15-JUN-2002 (Rel. 41, Last annotation update)
      DE RNA replication protein (165 kDa protein) (ORF 1) [Contains: RNA-
      DE directed RNA polymerase (EC 2.7.7.48); Probable helicase].
      OS Potato virus X (strain HB) (PVX).
      OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potexvirus.
      OX NCBI_TaxID=73488;
      RN [1]
      RP SEQUENCE FROM N.A.
      RX MEDLINE=94015010; PubMed=8409947;
      RA Querici M., van der Vliet R., Goldbach R., Salazar L.F.;
      RT "RNA sequence of potato virus X strain HB.";
      RL J. Gen. Virol. 74:2251-2255(1993).
      CC -|- FUNCTION: RNA-replication. The central part of this protein
      CC possibly functions as an ATP-binding helicase.
      CC -|- CATALYTIC ACTIVITY: N nucleoside triphosphate -> N diphosphate +
      CC {RNA}(N).
      CC -----
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      CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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      CC or send an email to license@isb-sib.ch).
      CC -----
      DR EMBL: D00344; BAA00249.1; -
      DR PIR: JAO102; WMMGPV.
      DR InterPro: IPR001788; RNA_dep_RNAPol2.
      DR InterPro: IPR000606; Viral_helicase1.
      DR Pfam: PF00978; RNA_dep_RNAPol2; 1.
      DR Pfam: PF01443; Viral_helicase1; 1.
      KW ATP-binding; Helicase; RNA replication; RNA-directed RNA polymerase;
      KW Transferase.
      FT NP_BIND 735 742 ATP (POTENTIAL).
      SQ SEQUENCE 1456 AA; 165605 MW; E06E3FF2AB48E97B CRC64;
      Query Match 69.2%; Score 36; DB 1; Length 1456;
      Best Local Similarity 62.5%; Pred. No. 1.3e+02;
      Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSGSWPQ 8
      1: ||||:
      Db 1361 QKGSWPE 1368

RESULT 7
VMSA_HPBDC STANDARD; PRT; 365 AA.
AC P30029;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Major surface antigen precursor.
GN S.
OS Duck hepatitis B virus (strain China) (DHBV).
OC Viruses; Retroid viruses; Hepadnaviridae; Avihepadnavirus.
OX NCBI_TaxID=31510;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91045091; PubMed=2235506;
RA Tong S., Mattes F., Teubner K., Blum H.E.;
RT "Complete nucleotide sequence of a Chinese duck hepatitis B virus.";
RL Nucleic Acids Res. 18:6139-6139(1990).
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CC -----
DR EMBL: M21953; AAA45746.1; -
DR PIR: S12842; SAVIWE.
DR InterPro: IPR000349; Hepvir_surfAg.
DR Pfam: PF00695; VMSA; 1.
KW Antigen.
FT PROPEP 1 198
FT CHAIN 199 365 MAJOR SURFACE ANTIGEN.
FT CARBOHYD 297 365 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 365 AA; 40511 MW; 67F3A4174CB7D884 CRC64;
Query Match 67.3%; Score 35; DB 1; Length 365;
Best Local Similarity 71.4%; Pred. No. 51;

Db 1361 QKGSWPE 1368
      1: ||||:
      ID RRPO_PVXX3 STANDARD; PRT; 1456 AA.
      AC P17779;
      DT 01-AUG-1990 (Rel. 15, Created)
      DT 01-AUG-1990 (Rel. 15, Last sequence update)
      DT 15-JUN-2002 (Rel. 41, Last annotation update)
      DE RNA replication protein (165 kDa protein) (ORF 1) [Contains: RNA-
      DE directed RNA polymerase (EC 2.7.7.48); Probable helicase].
      OS Potato virus X (strain X3) (PVX).
      OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potexvirus.
      OX NCBI_TaxID=12185;
      RN [1]
      RP SEQUENCE FROM N.A.
      RX MEDLINE=88299944; PubMed=3404114;
      RA Huisman M.J., Linthorst H.J.M., Bol J.F., Cornelissen B.J.C.;
      RT "The complete nucleotide sequence of potato virus X and its
      RT homologues at the amino acid level with various plus-stranded RNA
      RT viruses.";

```


Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOQSGWP 7
 DB 96 QOQGAWP 102

RESULT 8
 FCGN_RAT STANDARD; PRT; 366 AA.

AC P1359;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE IGG receptor FCN large subunit P51 precursor (FCN) (Neonatal FC
 DE receptor) (IGG FC fragment receptor transporter, alpha chain).
 GN FCGRT OR FCN.

OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC STRAIN-Wistar;
 RX MEDLINE=89097257; PubMed=2911353;
 RA Smolter N.E., Mostov K.E.;
 RT "An Fc receptor structurally related to MHC class I antigens.";
 RL Nature 337:184-187(1989).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Epithelium;
 RX MEDLINE=90315866; PubMed=2534798;
 RA Smolter N.E., Mostov K.E.;
 RT "Cloning and expression of the neonatal rat intestinal Fc receptor, a
 RT major histocompatibility complex class I antigen homolog.";
 RL Cold Spring Harb. Symp. Quant. Biol. 54:571-580(1989).
 RN [3]
 RN X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RX MEDLINE=95059482; PubMed=7969498;
 RA Burmeister W.P., Huber A.H., Bjorkman P.J.;
 RT "Crystal structure of the complex of rat neonatal Fc receptor with
 RT Fc.";
 RL Nature 372:379-383(1994).
 RN [4]
 RN X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RX MEDLINE=98154319; PubMed=9493268;
 RA Vaughn D.E., Bjorkman P.J.;
 RT "Structural basis of pH-dependent antibody binding by the neonatal Fc
 RT receptor.";
 RL Structure 6:63-73(1998).
 CC -1- FUNCTION: BINDS TO THE FC REGION OF MONOMERIC IMMUNOGLOBULINS
 CC GAMMA. MEDIATES THE SELECTIVE UPTAKE OF IGG FROM MILK AND HELPS
 CC NEWBORN ANIMALS TO ACQUIRE PASSIVE IMMUNITY. IGG IN THE MILK IS
 CC BOUND AT THE APICAL SURFACE OF THE INTESTINAL EPITHELIUM. THE
 CC RESULTANT FCN-IGG COMPLEXES ARE TRANSCYTOSED ACROSS THE
 CC INTESTINAL EPITHELIUM AND IGG IS RELEASED FROM FCN INTO BLOOD OR
 CC TISSUE FLUIDS (BY SIMILARITY).
 CC -1- SUBUNIT: FCN COMPLEX CONSIST OF TWO SUBUNITS: P51, AND P14 WHICH
 CC IS EQUIVALENT TO BETA-2-MICROGLOBULIN. IT FORMS AN MCH CLASS I-
 CC LIKE HETERODIMER.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: INTESTINAL EPITHELIUM.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 CC -----
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 CC -----
 CC EMBL; X14323; CAA32503.1; .

DR EMBL; M35495; AAA41611.1; .
 DR PIR; S02117; S02117.
 DR PIR; A37374; A37374.
 DR PDB; 1FRT; 14-FEB-95.
 DR PDB; 3FRU; 10-JUN-98.
 DR InterPro; IPR003006; Iq_MHC.
 DR InterPro; IPR003597; Iq_cl.
 DR InterPro; IPR001039; MHC_I.
 DR Pfam; PF00047; Iq; 1.
 DR Pfam; PF00129; MHC_I; 1.
 DR ProDom; PD000050; MHC_I; 1.
 DR SMART; SM00407; Igcl; 1.
 DR PROSITE; PS00290; IG_MHC; 1.
 DR Igg-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;
 KW Immunoglobulin domain; 3D-structure.
 FT SIGNAL 1 22
 FT CHAIN 23 366 IGG RECEPTOR FCN LARGE SUBUNIT P51.
 FT DOMAIN 23 111 EXTRACELLULAR ALPHA-1.
 FT DOMAIN 112 201 EXTRACELLULAR ALPHA-2.
 FT DOMAIN 202 291 EXTRACELLULAR ALPHA-3.
 FT DOMAIN 292 298 CONNECTING PEPTIDE.
 FT TRANSMEM 299 322 POTENTIAL.
 FT DOMAIN 323 366 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 120 183 BY SIMILARITY.
 FT DISULFID 222 276 BY SIMILARITY.
 FT CARBOHYD 109 109 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 126 126 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 150 150 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 247 247 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 366 AA; 40168 MW; 8ABFF2873A698B5 CRC64;

Query Match 67.3%; Score 35; DB 1; Length 366;
 Best Local Similarity 71.4%; Pred. No. 51;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 SCSWPT 9
 DB 152 SGWPT 158
 ||| |||:
 ||| |||:

RESULT 9
 VMSA_HPBDB STANDARD; PRT; 366 AA.

AC P17194;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 01-MAY-1991 (Rel. 18, Last annotation update)
 DE Major surface antigen precursor.
 GN S.
 OS Duck hepatitis B virus (brown Shanghai duck isolate S5) (DHBV).
 OC Viruses; Retroviruses; Hepadnaviridae; Avihepadnavirus.
 OX NCBI_TaxID=10439;
 RN [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=90085807; PubMed=2596031;
 RA Uchida M., Esumi M., Shikata T.;
 RT "Molecular cloning and sequence analysis of duck hepatitis B virus
 RT genomes of a new variant isolated from Shanghai ducks.";
 RL Virology 173:600-606(1989).
 CC -----
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 CC -----
 CC EMBL; M32990; AAA45755.1; ALT_INIT.
 DR PIR; C33746; SAVLBD.
 DR InterPro; IPR000349; Hepvir_surfa.
 DR Pfam; PF00695; VMSA; 1.
 KW Antigen.

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FT PROPEP      1 199
FT CHAIN       200 366      MAJOR SURFACE ANTIGEN.
FT CARBOHYD    170 170      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD    298 298      N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE    366 AA; 40897 MW; 5872879A182EFF38 CRC64;

Query Match      67.3%; Score 35; DB 1; Length 366;
Best Local Similarity 71.4%; Pred. No. 51;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSGSWP 7
   |||
Db 96 QQQGWAMP 102

RESULT 10
VMSA_HPBWDW
ID VMSA_HPBWDW STANDARD; PRT; 366 AA.
AC P17195;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-MAY-1991 (Rel. 18, Last annotation update)
DE Major surface antigen precursor.
GN S.
OS Duck hepatitis B virus (white Shanghai duck isolate S31) (DHBV).
OC Viruses; Retroviridae; Hepadnaviridae; Avihepadnavirus.
OX NCBI_TaxID=10440;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90085807; PubMed=2596031;
RA Uchida M., Esumi M., Shikata T.;
RT Molecular cloning and sequence analysis of duck hepatitis B virus
RL genomes of a new variant isolated from Shanghai ducks.;
RL Virology 173:600-606(1989).
CC -----
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CC -----
DR EMBL; M32991; AAA45752.1; ALT_INTT.
DR PIR; D33746; SAVLWD.
DR InterPro; IPR000349; Hepvir_surfac.
DR Pfam; PF006095; VMSA; 1.
KW Antigen.
FT PROPEP      1 199
FT CHAIN       200 366      MAJOR SURFACE ANTIGEN.
FT CARBOHYD    170 170      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD    298 298      N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE    366 AA; 40858 MW; CF60E78B7B2FCD52 CRC64;

Query Match      67.3%; Score 35; DB 1; Length 366;
Best Local Similarity 71.4%; Pred. No. 51;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSGSWP 7
   |||
Db 96 QQQGWAMP 102

RESULT 11
IE63_HSVBK
ID IE63_HSVBK STANDARD; PRT; 470 AA.
AC P28939;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-APR-1993 (Rel. 25, Last annotation update)
DE Transcriptional regulator IE63 homolog.
GN S.
OS Equine herpesvirus type 1 (strain Ab4p) (EHV-1).

```

```

OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
OX NCBI_TaxID=31520;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92295566; PubMed=1318606;
RA Telford E.A.R., Watson M.S., McBride K., Davison A.J.;
RT "The DNA sequence of equine herpesvirus-1.";
RL Virology 189:304-316(1992).
CC -!- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL54,
CC HSV-2 UL54, EHV-1 5, VZV 4, EBV BMLF1, HCMV UL69, AND HVS-1 57.
CC -----
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CC -----
DR EMBL; M86664; AAB02440.1; -.
DR PIR; F36795; WZBEA4.
KW Transcription regulation.
SQ SEQUENCE 470 AA; 51320 MW; 99AC5258E9F74B0E CRC64;

Query Match      67.3%; Score 35; DB 1; Length 470;
Best Local Similarity 62.5%; Pred. No. 65;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSGSWPQ 8
   |::|||
Db 127 QSAGSWPK 134

RESULT 12
IE63_HSVBK
ID IE63_HSVBK STANDARD; PRT; 470 AA.
AC Q05906;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Transcriptional regulator IE63 homolog.
GN UL3.
OS Equine herpesvirus type 1 (strain Kentucky A) (EHV-1).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
OX NCBI_TaxID=10329;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92365125; PubMed=1323700;
RA Zhao Y., Holden V.R., Harty R.N., O'Callaghan D.J.;
RT "Identification and transcriptional analyses of the UL3 and UL4 genes
RT of equine herpesvirus 1, homologs of the ICP27 and glycoprotein K
RT genes of herpes simplex virus.";
RL J. Virol. 66:5363-5372(1992).
CC -!- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL54,
CC HSV-2 UL54, EHV-1 5, VZV 4, EBV BMLF1, HCMV UL69, AND HVS-1 57.
CC -----
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CC -----
DR EMBL; M95822; AAA46099.1; -.
DR PIR; B42746; B42746.
KW Transcription regulation.
SQ SEQUENCE 470 AA; 51389 MW; 48DBE440E11363F7 CRC64;

Query Match      67.3%; Score 35; DB 1; Length 470;
Best Local Similarity 62.5%; Pred. No. 65;

```

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOSGSWPQ 8
I :|||||

Db 127 QSAGSWPK 134

RESULT 13
P2X2_HUMAN
ID P2X2_HUMAN STANDARD; PRT; 471 AA.
AC Q9UBL9; Q9Y637; Q9UHD6; Q9UHD7; Q9NR37; Q9NR38;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE P2X purinoceptor 2 (ATP receptor) (P2X2) (Purinergic receptor).
GN P2RX2 OR P2X2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN
RP SEQUENCE FROM N.A. (ISOFORMS A; B; C AND D).
RC TISSUE=Pituitary;
RX MEDLINE=20040550; PubMed=10570044;
RA Lynch K.J., Touma E., Niforatos W., Kage K.L., Burgard E.C.,
van Biesen T., Kowalik E.A., Jarvis M.F.;
RT "Molecular and functional characterization of human P2X(2) receptors.";
RT Mol. Pharmacol. 56:1171-1181(1999).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS A; C; H AND I).
RC TISSUE=Prostate;
RA Chang T.K., Kosaka A.H., Oglesby I.B., Gevers J.R., Lachnit W.G.,
Ford A.P.D.W., Chang D.J.;
RT "Cloning and molecular characterization of human P2X2 and its splice variants.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS A AND B).
RC TISSUE=Placenta;
RA McMahon R.A., Egan T.M., Hurley P.T., Nelson A., Rogers M., Martin F.;
RT "Cloning of the human P2X2 receptor cDNA and multiple splice variants.";
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
CC -I- FUNCTION: BINDING OF THIS LIGAND GATED ION CHANNEL TO ATP MEDIATES SYNAPTIC TRANSMISSION BETWEEN NEURONS AND FROM NEURONS TO SMOOTH MUSCLE.
CC
CC -I- SUBUNIT: HOMO- OR HETEROPOLYMERS.
CC
CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
CC
CC -I- ALTERNATIVE PRODUCTS: 6 ISOFORMS; A (SHOWN HERE), B, C, D, H AND I; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC
CC -I- SIMILARITY: BELONGS TO THE P2X RECEPTOR FAMILY.
CC
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CC
CC
CC EMBL; AF190822; AAF19170.1; -
CC EMBL; AF190823; AAF19171.1; -
CC EMBL; AF190824; AAF19172.1; -
CC EMBL; AF190825; AAF19173.1; -
CC EMBL; AF190826; AAF19174.1; -
CC EMBL; AF260426; AAF74201.1; -
CC EMBL; AF260427; AAF74202.1; -
CC EMBL; AF260428; AAF74203.1; -
CC EMBL; AF260429; AAF74204.1; -
CC EMBL; AF109387; AAD42947.1; -
CC EMBL; AF109388; AAD42948.1; -
CC Genew; HGNC:15459; P2RX2.

MIM; 600844; -
InterPro; IPR001429; P2X_receptor.
DR Pfam; PF00864; P2X_receptor; 1.
DR PRINTS; PR01307; P2XRECEPTOR.
DR TIGRFAMS; TIGR00863; P2X; 1.
DR PROSITE; PS01212; P2X_RECEPTOR; 1.
KW Ionic channel; Transmembrane; Ion transport; Receptor; Glycoprotein;
KW Alternative splicing.
FT DOMAIN 1 42 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 43 63 1 (POTENTIAL).
FT DOMAIN 64 337 EXTRACELLULAR, CYSTEINE-RICH (POTENTIAL).
FT TRANSMEM 338 358 2 (POTENTIAL).
FT DOMAIN 359 471 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 320 333 PORE-FORMING MOTIF (POTENTIAL).
FT CARBOHYD 133 133 N-LINKED (GLCNAC. ...) (POTENTIAL).
FT CARBOHYD 194 194 N-LINKED (GLCNAC. ...) (POTENTIAL).
FT CARBOHYD 310 310 N-LINKED (GLCNAC. ...) (POTENTIAL).
FT VARSPPLIC 36 127 MISSING (IN ISOFORM H).
FT VARSPPLIC 38 152 NRRGLVYRAVQLLLILLVFWYFIVQKSVQSESGPESII
ITKVKYITTSSEHKVWDVEEYKPPGGSVFSLITRVEATHS
QTQGTCPESIRVHNATCLSDADCVAGELDMGN -> IHRA
EKLPGRDGPRELHHHQGGDHHVRAQSVMRGVREAPR
(IN ISOFORM I).
FT VARSPPLIC 104 127 MISSING (IN ISOFORM C).
FT VARSPPLIC 354 354 V -> VVRNPLMGPGCGGSTRPLHTGLCWQ (IN
ISOFORM D).
FT VARSPPLIC 381 447 MISSING (IN ISOFORM B).
FT CONFLICT 1 14 MAAAPKYPAGATA -> MV (IN REF. 3).
SQ SEQUENCE 471 AA; 51754 MW; 84CD61DA136EF420 CRC64;
Query Match 67.3%; Score 35; DB 1; Length 471;
Best Local Similarity 85.7%; Pred. No. 65;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 3 SGSWPOT 9
| | | | | |
Db 388 SGSWPVT 394
RESULT 14
CTCL_ACILW
ID CTCL_ACILW STANDARD; PRT; 96 AA.
AC O33947;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Muconolactone delta-isomerase 1 (EC 5.3.3.4) (Mtiase 1).
GN CATCL.
OS Acinetobacter lwoffii.
OC Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;
OC Acinetobacter.
OX NCBI_TaxID=28090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K24;
RX MEDLINE=97405925; PubMed=9260969;
RA Kim S.I., Leem S.-H., Choi J.-S., Chung Y.H., Kim S., Park Y.-M.,
Park Y.K., Lee Y.N., Ha K.-S.;
RT "Cloning and characterization of two catA genes in Acinetobacter lwoffii K24.";
RT J. Bacteriol. 179:5226-5231(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K24;
RX MEDLINE=98139907; PubMed=9473520;
RA Kim S.I., Leem S.-H., Choi J.-S., Ha K.-S.;
RT "Organization and transcriptional characterization of the catI gene cluster in Acinetobacter lwoffii K24.";
RL Biochem. Biophys. Res. Commun. 243:289-294(1998).
CC -I- CATALYTIC ACTIVITY: 2,5-dihydro-5-oxofuran-2-acetate -> 3,4-dihydro-5-oxofuran-2-acetate.
CC -I- PATHWAY: THIRD STEP IN THE CATABOLISM OF CATECHOL TO SUCCINATE- AND ACETYL-COA IN THE BETA-KETOADIPATE PATHWAY.

```

CC -1- SUBUNIT: HOMODECAMER (BY SIMILARITY).
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CC -----
CC EMBL; U77658; AAC46227.1; -.
CC InterPro: IPR003464; Mfase.
CC Pfam; PF02426; Mfase; 1.
CC Aromatic hydrocarbons catabolism; Isomerase.
KW SEQUENCE 96 AA; 11048 MW; 6955AC14A5DDDEFA CRC64;
SQ -----

Query Match 65.4%; Score 34; DB 1; Length 96;
Best Local Similarity 71.4%; Pred. No. 21;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QSGSWP 7
Db 35 QKSGKWP 41

RESULT 15
YFDK_ECOLI
ID YFDK_ECOLI STANDARD; PRT; 146 AA.
AC P77656;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein yfdk.
GN YFDK OR B2354.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RS SEQUENCE FROM N.A.
RA STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RA "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RS SEQUENCE FROM N.A.
RA STRAIN=K12;
RX MEDLINE=97349980; PubMed=9205837;
RA Yamamoto Y., Alba H., Baba T., Hayashi K., Inada T., Isono K.,
RA Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N.,
RA Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H.,
RA Oshima T., Oyama S., Saito N., Sampei G., Satoh Y., Sivasubram S.,
RA Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C.,
RA Yamagata S., Horinouchi T.;
RT "Construction of a contiguous 874-kb sequence of the Escherichia coli
RT - K12 genome corresponding to 50.0-68.8 min on the linkage map and
RT analysis of its sequence features.";
RL DNA Res. 4:91-113(1997).
CC -1- SIMILARITY: STRONG, TO E.COLI YMFS.
CC -----
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CC -----
CC EMBL; AE000324; AAC75413.1; -.

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DR EMBL; D90866; BAA16221.1; -.
DR EMBL; D90865; BAA16214.1; -.
DR EcoGene; EGI4135; yfdk.
DR InterPro: IPR003458; DUF144.
DR Pfam; PF02413; DUF144; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 146 AA; 16408 MW; 28F3CA711C5E9C79 CRC64;

Query Match 65.4%; Score 34; DB 1; Length 146;
Best Local Similarity 83.3%; Pred. No. 32;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QSGSWP 7
Db 23 QAGSWP 28

Search completed: November 18, 2002, 17:51:39
Job time : 4.85526 secs

```

GenCore version 5.1.3

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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:40:56 : Search time 20.1316 Seconds
(without alignments)
92.115 Million cell updates/sec

Title: US-09-016-061-92

Perfect score: 52

Sequence: 1 QQSGSWPQT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	40	76.9	304	10 Q9FLS6	Q9FLS6 arabidopsis
2	40	76.9	1194	5 Q9VSI2	Q9VSI2 drosophila
3	40	76.9	1346	16 Q98IR5	Q98IR5 rhizobium l
4	38	73.1	986	5 O01443	O01443 caenorhabdi
5	37	71.2	327	12 Q67852	Q67852 duck hepati
6	37	71.2	343	10 Q8W3X5	Q8W3X5 triticum ae
7	37	71.2	350	10 Q49958	Q49958 triticum tu
8	37	71.2	365	10 Q8W3X6	Q8W3X6 triticum ae
9	37	71.2	612	10 Q94LS9	Q94LS9 oryza sativ
10	37	71.2	612	10 Q8RUM5	Q8RUM5 oryza sativ
11	36	69.2	154	12 Q84631	Q84631 paramecium
12	36	69.2	331	2 Q08246	Q08246 streptomyce
13	36	69.2	345	16 Q8ZCH4	Q8ZCH4 yersinia pe
14	36	69.2	371	16 Q9AAL0	Q9AAL0 caulobacter
15	36	69.2	613	5 Q9VHU1	Q9VHU1 drosophila
16	36	69.2	764	10 Q9LRH7	Q9LRH7 pisum sativ

17	36	69.2	800	16 Q8U6H4	Q8U6H4 agrobacteri
18	36	69.2	1456	12 Q85245	Q85245 potato viru
19	36	69.2	1456	12 Q85198	Q85198 potato viru
20	36	69.2	1456	12 Q9JEX8	Q9JEX8 potato viru
21	36	69.2	1456	12 Q9IMP2	Q9IMP2 potato viru
22	36	69.2	1456	12 Q91KX2	Q91KX2 potato viru
23	36	69.2	1456	12 Q8V967	Q8V967 potato viru
24	35	67.3	146	16 Q8Z341	Q8Z341 salmonella
25	35	67.3	153	13 Q9YH52	Q9YH52 gallus gall
26	35	67.3	156	4 Q96HH2	Q96HH2 homo sapien
27	35	67.3	164	2 Q54250	Q54250 streptomyce
28	35	67.3	212	5 Q966H1	Q966H1 caenorhabdi
29	35	67.3	313	16 Q987K4	Q987K4 rhizobium l
30	35	67.3	313	16 Q92WK4	Q92WK4 rhizobium m
31	35	67.3	322	16 Q926E8	Q926E8 rhizobium m
32	35	67.3	329	12 Q91HP5	Q91HP5 duck hepati
33	35	67.3	330	12 Q72885	Q72885 duck hepati
34	35	67.3	330	12 Q66405	Q66405 duck hepati
35	35	67.3	366	12 Q66404	Q66404 duck hepati
36	35	67.3	405	10 Q41516	Q41516 triticum ae
37	35	67.3	405	10 Q9SY0	Q9SY0 triticum ae
38	35	67.3	618	10 Q9LXQ8	Q9LXQ8 arabidopsis
39	35	67.3	633	16 Q8YBA4	Q8YBA4 brucella me
40	35	67.3	714	16 Q98MG6	Q98MG6 rhizobium l
41	35	67.3	789	10 Q42451	Q42451 triticum ae
42	35	67.3	815	10 Q41553	Q41553 triticum ae
43	35	67.3	818	10 Q93XJ8	Q93XJ8 triticum ti
44	35	67.3	830	10 Q03872	Q03872 triticum ae
45	35	67.3	929	5 Q9VR32	Q9VR32 drosophila

ALIGNMENTS

RESULT 1

Q9FLS6 ID Q9FLS6 PRELIMINARY: PRT; 304 AA.

AC Q9FLS6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Carbonyl reductase-like protein.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=98290546; PubMed=9628582;
RA Sato S., Kaneko T., Kotani H., Nakamura Y., Asamizu E., Miyajima N.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. IV.
RT Sequence features of the regions of 1,456,315 bp covered by nineteen
RT physically assigned pl and TAC clones.";
RL DNA Res. 5:41-54(1998).
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
CC EMBL: AB010069; BAB10083.1; -.
DR HSSP: P50162; IAE1.
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short; 1.
DR PRINTS: PR00080; SDRFAMILY.
KW Oxidoreductase.
SQ SEQUENCE 304 AA; 34120 MW; 00D0C6B9880818C5 CRC64;

Query Match 76.9%; Score 40; DB 10; Length 304;
Best Local Similarity 75.0%; Pred. No. 19;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QSGSWPQT 9
: || ||||

Db 211 ESGSWPQT 218

RESULT 2

Q9VSI2 PRELIMINARY; PRT; 1194 AA.

AC Q9VSI2; 2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)

DE CG7112 protein.

GN CG7112

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BERKELEY;

RX MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Ananatiades P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrier S., Fleischmann W.,

RA Esler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Hostin N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Jalali M., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Zhu X., Smith H.O.,

RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RT "The genome sequence of Drosophila melanogaster.";

RL Science 287:2185-2195(2000).

DR EMBL; AE003555; AAF50437.1;

DR FlyBase; FBgn0035879; CG7112.

DR InterPro; IPR000050; PID_domain.

DR Dfam; PF005566; TBC; 1.

DR SMART; SM00462; TBC; 1.

DR SMART; SM00164; TBC; 1.

SQ SEQUENCE 1194 AA; 133393 MW; E0E3DB547B4924E0 CRC64;

Query Match 76.9%; Score 40; DB 5; Length 1194;

Best Local Similarity 77.8%; Pred. No. 81;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QSGSWPQT 9

Db 461 QSSSWPYT 469

RESULT 3

Q98IR5 PRELIMINARY; PRT; 1346 AA.

AC Q98IR5;

DT 01-OCT-2001 (TrEMBLrel. 18, Created)

DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)

DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)

DE Hypothetical protein ml12286.

GN ML12286.

OS Rhizobium loti (Mesorhizobium loti).

OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;

OC Phyllobacteriaceae; Mesorhizobium.

OX NCBI_TaxID=381;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=MAFF303099;

RX MEDLINE=21082930; PubMed=11214968;

RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,

RA Watanabe A., Ideasa K., Ishikawa A., Kawashima K., Kimura T.,

RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,

RA Mochizuki Y., Yamada S., Nakazaki N., Shimpō S., Sugimoto M.,

RA Takeuchi C., Yamada M., Tabata S.;

RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium Mesorhizobium loti.";

RL DNA Res. 7:331-338(2000).

DR EMBL; AP002999; BAB49451.1;

DR InterPro; IPR003975; SHALchannel.

DR PRINTS; PRO1497; SHALCHANNEL.

KW Hypothetical protein; Complete proteome.

SQ SEQUENCE 1346 AA; 148727 MW; 7DL288A3FC36E879 CRC64;

Query Match 76.9%; Score 40; DB 16; Length 1346;

Best Local Similarity 75.0%; Pred. No. 93;

Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QSGSWPQT 9

Db 204 QGSGWPKT 211

RESULT 4

O01443 PRELIMINARY; PRT; 986 AA.

ID O01443; 001444;

AC O01443; 001444;

DT 01-JUL-1997 (TrEMBLrel. 04, Created)

DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE Hypothetical 108.1 kDa protein.

GN C01F4.2.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;

OC Rhabditidae; Peloderinae; Caenorhabditis.

OX NCBI_TaxID=6239;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BRISTOL N2;

RX MEDLINE=99069613; PubMed=9851916;

RA Waterston R.;

RT "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium.";

RL Science 282:2012-2018(1998).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=BRISTOL N2;

RX STRAIN=BRISTOL N2;

RA Wansley P., Geisel C.;

RT "The sequence of C. elegans cosmid C01F4.";

RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=BRISTOL N2;
 RA Waterston R.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U97192; AAB52434.2; -.
 KW Hypothetical protein.
 SQ SEQUENCE 986 AA; 108136 MW; E8076DD8DB6DE7A5 CRC64;

Query Match 73.1%; Score 38; DB 5; Length 986;
 Best Local Similarity 85.1%; Pred. No. 1.5e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQSGSWP 7
 I:|||||
 DB 806 QRSQSWP 812

RESULT 5

Q67852 ID O67852 PRELIMINARY; PRT; 327 AA.
 AC O67852;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Surface protein.
 GN PRES.
 OS Duck hepatitis B virus (DHBV).
 OC Viruses; Retroid viruses; Hepadnaviridae; Avihepadnavirus.
 OX NCBI_TaxID=12639;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Shi H., Cullen J.M., Newbold J.E.;
 RT "A novel isolate of duck hepatitis B virus."
 RL Submitted (DEC-1992) to the EMBL/GenBank/DBJ databases.
 DR EMBL: M95589; AAA5749.1; -.
 DR InterPro: IPR000349; Hepvir_surfa.
 DR Pfam: PF00695; VMSA; 1.
 SQ SEQUENCE 327 AA; 36356 MW; 6875E959746DADBB CRC64;

Query Match 71.2%; Score 37; DB 12; Length 327;
 Best Local Similarity 62.5%; Pred. No. 71;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSGSWP 8
 I:|||||
 DB 60 QQQAWPE 67

RESULT 6

Q8W3X5 ID Q8W3X5 PRELIMINARY; PRT; 343 AA.
 AC Q8W3X5;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Low-molecular-weight glutenin subunit group 2 type I.
 GN LMW-GS.
 OS Triticum aestivum (Wheat).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
 OC Triticeae; Triticum.
 OX NCBI_TaxID=4565;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. NORIN61;
 RA Ikeda T.M., Nagamine T., Fukuoka H., Yano H.;
 RT "Identification of new low molecular weight glutenin subunit genes in wheat."
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB062852; BAB78738.1; -.
 DR InterPro: IPR003612; AAI.
 DR InterPro: IPR001954; Glia_glutenin.
 DR InterPro: IPR001092; HLH_basic.
 DR InterPro: IPR001768; Try/amy1_inhbr.

DR Pfam: PF00234; tryp_alpha_aml1; 1.
 DR PRINTS: PR00208; GLIADGLUTEN.
 DR SMART: SM00499; AAI; 1.
 DR PROSITE: PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
 SQ SEQUENCE 343 AA; 39013 MW; 83B4E974D70D2B1 CRC64;

Query Match 71.2%; Score 37; DB 10; Length 343;
 Best Local Similarity 75.0%; Pred. No. 75;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQSGSWP 8
 I:|||||
 DB 279 QQLGQWPQ 286

RESULT 7

Q49958 ID O49958 PRELIMINARY; PRT; 350 AA.
 AC O49958;
 DT 01-JUN-1998 (TREMBlrel. 06, Created)
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Low molecular weight glutenin subunit precursor (Fragment).
 GN LMW-GS.
 OS Triticum turgidum subsp. durum (durum wheat).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
 OC Triticeae; Triticum.
 OX NCBI_TaxID=4567;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. LANGDON;
 RA D'Ovidio R., Simeone M., Masci S., Porceddu E.;
 RT "Molecular characterization of a LMW-GS gene located on Chromosome 1B and the development of primers specific for the GLU-B3 complex locus in durum wheat."
 RL Theor. Appl. Genet. 95:1119-1126(1997).
 DR EMBL: Y14104; CAA74550.1; -.
 DR InterPro: IPR003612; AAI.
 DR InterPro: IPR001954; Glia_glutenin.
 DR InterPro: IPR001092; HLH_basic.
 DR InterPro: IPR001768; Try/amy1_inhbr.
 DR Pfam: PF00234; tryp_alpha_aml1; 1.
 DR PRINTS: PR00208; GLIADGLUTEN.
 DR SMART: SM00499; AAI; 1.
 DR PROSITE: PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
 KW Signal.
 FT SIGNAL 1 20 POTENTIAL.
 FT CHAIN 21 >350 POTENTIAL.
 FT NON_TER 350 350
 SQ SEQUENCE 350 AA; 39791 MW; 3590FDDFE5545SEC CRC64;

Query Match 71.2%; Score 37; DB 10; Length 350;
 Best Local Similarity 75.0%; Pred. No. 76;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQSGSWP 8
 I:|||||
 DB 286 QQLGQWPQ 293

RESULT 8

Q8W3X6 ID Q8W3X6 PRELIMINARY; PRT; 365 AA.
 AC Q8W3X6;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Low-molecular-weight glutenin subunit group 1 type I.
 GN LMW-GS.
 OS Triticum aestivum (Wheat).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;

[4] RP SEQUENCE FROM N.A.
RA Van Etten J.L.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
[5] RP SEQUENCE FROM N.A.
RA Van Etten J.L.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
[6] RP SEQUENCE FROM N.A.
RA Van Etten J.L.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
[7] RP SEQUENCE FROM N.A.
RA Graves M.V., Van Etten J.L.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
[8] RP SEQUENCE FROM N.A.
RA Graves M.V., Van Etten J.L.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
[9] RP SEQUENCE FROM N.A.
RA Gurnon J.R., Graves M.V., Van Etten J.L.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: U42580; AAC96685.1; -.
SQ SEQUENCE 154 AA; 18564 MW; 7B45E2E7F518E15 CRC64;

Query Match 69.2%; Score 36; DB 12; Length 154;
Best Local Similarity 85.7%; Pred. No. 48;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QSGSWP 7
I I I I I I

DB 33 QTSQSWP 39

RESULT 12
O08246

ID O08246 PRELIMINARY; PRT; 331 AA.
AC O08246;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE TDP-D-glucose-4,6,-dehydratase.
GN MTME.
OS Streptomyces argillaceus.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=41951;

[1] RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 12956;
RX MEDLINE=97294479; PubMed=9150235;
RA Lombo F., Siems K., Brana A.F., Mendez C., Bindsail K., Salas J.A.;
RT "Cloning and insertional inactivation of Streptomyces argillaceus genes involved in the earliest steps of biosynthesis of the sugar moieties of the antitumor polyketide mithramycin.";
RL J. Bacteriol. 179:3354-3357(1997).
[2] RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 12956;
RA Salas J.A.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
[3] RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 12956;
RX MEDLINE=96257259; PubMed=8654997;
RA Lombo F., Blanco G., Fernandez E., Mendez C., Salas J.A.;
RT "Characterization of Streptomyces argillaceus genes encoding a polyketide synthase involved in the biosynthesis of the antitumor mithramycin.";
RL Gene 172:87-91(1996).
DR EMBL: Y10907; CAA71847.1; -.
OX

DR EMBL: AJ007932; CAA07755.1; -.
DR HSSP; P27830; 1BXX.
DR InterPro: IPR002198; ADH_short.
DR InterPro: IPR001509; Epimerase_Dh.
DR Pfam: PF01370; Epimerase; 1.
DR TIGRFAMS: TIGR01181; dTDP_gluc_dehyt; 1.
DR PROSITE: PS0061; ADH_SHORT; UNKNOWN_1.
SQ SEQUENCE 331 AA; 36352 MW; D6F8E881928837AB CRC64;

Query Match 69.2%; Score 36; DB 2; Length 331;
Best Local Similarity 71.4%; Pred. No. 11e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 SSGSWPOT 9

DB 137 AGSWPET 143

RESULT 13

O082CH4 PRELIMINARY; PRT; 345 AA.
ID O082CH4

AC O082CH4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Thiosulfate-binding protein.

GN CYP OR YPO3015.
OS Yersinia pestis.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Yersinia.
OX NCBI_TaxID=632;

RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=CO-92 / BIOVAR ORIENTALIS;
RX MEDLINE=21470413; PubMed=11586360;
RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
RA Prentice M.B., Sebahia M., James K.D., Churcher C., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdono-Tarraga A.M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
RT "Genome sequence of Yersinia pestis, the causative agent of plague.";
RL Nature 413:523-527(2001).

DR EMBL: AJ414154; CAC92258.1; -.
DR InterPro: IPR000957; Sulphate bind.

DR Pfam: PF01100; Sulphate_bind; 1.

DR ProDom: PD008688; Sulphate_bind; 1.

KW Complete proteome.

SQ SEQUENCE 345 AA; 38505 MW; B446DD90A21146DD CRC64;

Query Match 69.2%; Score 36; DB 16; Length 345;
Best Local Similarity 85.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QSGSWPQ 8

DB 318 QFGSWPQ 324

RESULT 14

O09AAL0 PRELIMINARY; PRT; 371 AA.
ID O09AAL0

AC O09AAL0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Pentapeptide repeat family protein.

GN CC0587

OS Caulobacter crescentus.

OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;

OC Caulobacter.

OX NCBI_TaxID=155892;

```

RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=APCC 19089 / CB15;
RX  MEDLINE=21173698; PubMed=11259647;
RA  Nierman W.C., Feldblum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA  Etsen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA  Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA  DeBoy R.F., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA  Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
RA  Uitterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
RA  Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RT  "Complete genome sequence of Caulobacter crescentus.";
RL  Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
DR  EMBL: AE005733; AAK22573.1; -.
DR  TIGR: CC0587; -.
DR  InterPro: IPR001646; 5peptide_repeat.
DR  Pfam: PF00805; Pentapeptide; 6.
KW  Complete proteome.
SQ  SEQUENCE 371 AA; 33345 MW; 8978C36E0A19B302 CRC64;

.Query Match 69.2%; Score 36; DB 16; Length 371;
Best Local Similarity 62.5%; Pred. NO. 1.2e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOQSGSWPQ 8
DB 355 KRSGNWFPQ 362

RESULT 15
Q9VHU1
ID Q9VHU1 PRELIMINARY; PRT; 613 AA.
AC Q9VHU1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE CG9630 protein (GH16590P).
GN CG9630.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananatiades P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballwey R.M., Basu A., Baxendale J., Bayraktaroglu L., Beaslev E.M.,
RA Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Fertiera S., Fleischmann W.,
RA Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

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RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nuncio J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE "DEAD" BOX FAMILY HELICASE.
DR EMBL: AE003678; AAF54208.1; -.
DR EMBL: AY051513; AAK92937.1; -.
DR HSSP: Q58083; 1HV8.
DR Flybase: FBgn0037561; CG9630.
DR InterPro: IPR001410; DEAD.
DR InterPro: IPR000629; DEAD_box.
DR InterPro: IPR001650; Helicase_C.
DR Pfam: PF00270; DEAD; 1.
DR Pfam: PF00271; Helicase_C; 1.
DR SMART: SM00487; DEXdc; 1.
DR SMART: SM00490; HELICC; 1.
DR PROSITE: PS00039; DEAD_ATP_HELICASE; 1.
KW ATP-binding; Helicase; RNA-binding.
SQ SEQUENCE 613 AA; 69083 MW; C779803336A02879 CRC64;

.Query Match 69.2%; Score 36; DB 5; Length 613;
Best Local Similarity 71.4%; Pred. NO. 2.1e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOQSGSWP 7
DB 513 EOTGSWP 519

```

Search completed: November 18, 2002, 17:54:38

Job time : 22.1316 secs

Result No.	Score	Query Match %	Length	DB	ID	Description
1	52	100.0	9	19	AAW76036	LM609 grafted anti
2	52	100.0	9	22	AAB61394	Mutant VL CDR3 pep
3	47	90.4	9	19	AAW76013	LM609 grafted anti
4	47	90.4	9	22	AAB61371	LM609 VL CDR3 pep
5	47	90.4	107	19	AAW76006	LM609 grafted anti
6	47	90.4	107	19	AAW76002	Vitaxin antibody 1
7	47	90.4	107	19	AAW76004	LM609 antibody lig
8	47	90.4	107	22	AAG63588	A light chain vari
9	47	90.4	107	22	AAG63590	A light chain vari
10	47	90.4	107	22	AAB61360	Vitaxin light chai

XX Humanised antibody. Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
PS Claim 62; Page 44; 129pp; English.
XX
XX AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
CC antibodies contain non-murine framework regions so are suitable for use
CC in humans. Enhanced types of LM609 have affinity more than 90 times
CC greater than that of parent the parent antibody.
XX
SQ Sequence 9 AA;
Query Match 100.0%; Score 52; DB 19; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 QQSGSWPQT 9
Db 1 QQSGSWPQT 9
|||||
RESULT 2
AAB61394
ID AAB61394 standard; peptide; 9 AA.
XX
AC AAB61394;
XX
XX 03-APR-2001 (first entry)
XX
XX Mutant VL CDR3 peptide #4.
XX
XX LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
KW inflammatory; cancer; retina; restenosis; osteoporosis.
KW
XX Unidentified.
OS
XX WO200078815-A1.
PN
XX 28-DEC-2000.
PD
XX 23-JUN-2000; 2000WO-US17454.
PF
XX 24-JUN-1999; 99US-0339922.
PR
XX (MOLE-) APPLIED MOLECULAR EVOLUTION.
PA
XX Huse WD, Wu H;
PI
XX WPI; 2001-050110/06.
DR
XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
XX to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
PT osteoporosis -
XX
XX Disclosure; Page 41; 132pp; English.
PS
XX The present invention relates to enhanced LM609 grafted antibodies
CC exhibiting selective binding affinity to alphavbeta_3 integrin or
CC their functional fragments. The antibodies or their functional
CC fragments can be used in the diagnosis and treatment of
CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory

CC diseases (such as psoriasis and chronic articular rheumatism),
CC disorders associated with inappropriate or inopportune invasion of
CC vessels (such as diabetic retinopathy, neovascular glaucoma and
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
CC diseases (such as macular degeneration), restenosis and
CC osteoporosis.
XX
SQ Sequence 9 AA;
Query Match 100.0%; Score 52; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 QQSGSWPQT 9
Db 1 QQSGSWPQT 9
|||||
RESULT 3
AAW76013
ID AAW76013 standard; Protein; 9 AA.
XX
XX AAW76013;
AC
XX 02-NOV-1998 (first entry)
DT
XX LM609 grafted antibody V-L region CDR3 protein fragment #1.
DE
XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-L region; CDR;
KW complementarity determining region.
XX
OS Mus sp.
XX
XX WO9833919-A2.
PN
XX 06-AUG-1998.
PD
XX 30-JAN-1998; 98WO-US01826.
PF
XX 30-JAN-1997; 97US-0791391.
PR
XX (IXSY-) IXSYS INC.
PA
XX Glaser SM, Huse WD;
PI
XX WPI; 1998-437472/37.
DR
XX N-PSDB; AAV49850.
DR
XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
XX integrin - and related grafted antibodies based on murine monoclonal
XX LM609, also related nucleic acid, used to treat, prevent or diagnose
XX angiogenesis or restenosis
XX
XX Disclosure; Page 40; 129pp; English.
PS
XX AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
XX LM609 heavy and light chain variable region. LM609 and the antibody
XX vitaxin bind selectively to integrin alphavbeta3 and can be used to
XX inhibit binding of alphavbeta3 to a ligand and thus block
XX integrin-mediated signal transduction. This is useful in the treatment,
XX prevention and diagnosis of alphavbeta3-mediated disease, specifically
XX angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
XX diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
XX rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
XX antibodies contain non-murine framework regions so are suitable for use
XX in humans. Enhanced types of LM609 have affinity more than 90 times
XX greater than that of parent the parent antibody.
XX
SQ Sequence 9 AA;

Query Match 90.4%; Score 47; DB 19; Length 9;
 Best Local Similarity 88.9%; Pred. No. 7.8e+05;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSGSWPQT 9
 I I I I I I I
 Db 1 QQSGSWPHT 9

RESULT 4
 AAB61371
 ID AAB61371 standard; peptide; 9 AA.

XX AAB61371;
 AC AAB61371;
 DT 03-APR-2001 (first entry)

XX LM609 VL CDR3 peptide.

XX LM609; grafted antibody; alphaVbeta3 integrin; angiogenesis;
 KW Inflammatory; cancer; retina; restenosis; osteoporosis.

XX Unidentified.

XX WO200078815-A1.

XX 28-DEC-2000.

XX 23-JUN-2000; 2000WO-US17454.

XX 24-JUN-1999; 99US-0339922.

XX (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX Huse WD, Wu H;

XX WPI: 2001-050110/06.

XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -

PS Disclosure; Page 39; 132pp; English.

XX The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphaVbeta3 integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphaVbeta3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.

XX Sequence 9 AA;

Query Match 90.4%; Score 47; DB 22; Length 9;
 Best Local Similarity 88.9%; Pred. No. 7.8e+05;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSGSWPQT 9
 I I I I I I I
 Db 1 QQSGSWPHT 9

RESULT 5
 AAW76006
 ID AAW76006 standard; Protein; 107 AA.
 XX

AC AAW76006;
 XX
 DT 02-NOV-1998 (first entry)
 XX
 DE LM609 grafted antibody light chain variable region protein fragment.
 XX
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 49
 FT /label= Arg, Met
 XX
 PN WO9833919-A2.
 XX
 PD 06-AUG-1998.
 XX
 PF 30-JAN-1998; 98WO-US01826.
 XX
 PR 30-JAN-1997; 97US-0791391.
 XX
 PA (IXSY-) IXSYS INC.
 XX
 PI Glaser SM, Huse WD;
 XX
 DR WPI: 1998-437472/37.
 DR N-PSDB; AAV49843.
 XX
 PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 PS Claim 19; Fig 7; 129pp; English.
 XX
 CC This sequence represents a LM609 grafted antibody variable light chain
 CC region. LM609 and the antibody vitaxin bind selectively to integrin
 CC alphaVbeta3 and can be used to inhibit binding of alphaVbeta3 to a ligand
 CC and thus block integrin-mediated signal transduction. This is useful in
 CC the treatment, prevention and diagnosis of alphaVbeta3-mediated disease,
 CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
 CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
 CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
 CC etc.). The antibodies contain non-murine framework regions so are
 CC suitable for use in humans. Enhanced types of LM609 have affinity more
 CC than 90 times greater than that of parent the parent antibody.
 XX
 SQ Sequence 107 AA;
 Query Match 90.4%; Score 47; DB 19; Length 107;
 Best Local Similarity 88.9%; Pred. No. 0.81;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QQSGSWPQT 9
 I I I I I I I
 Db 89 QQSGSWPHT 97
 XX
 RESULT 6
 AAW76002
 ID AAW76002 standard; Protein; 107 AA.
 XX
 AC AAW76002;
 XX
 DT 02-NOV-1998 (first entry)
 XX
 DE Vitaxin antibody light chain variable region protein fragment.
 XX

KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.

XX OS Mus sp.

XX PN WO9833919-A2.

XX PD 06-AUG-1998.

XX PF 30-JAN-1998; 98WO-US01826.

XX PR 30-JAN-1997; 97US-0791391.

XX PA (IXSY-) IXSYS INC.

XX PI Glaser SM, Huse WD;

XX DR WPI; 1998-437472/37.

XX DR N-PSDB; AAV49821.

XX PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

XX PS Claim 1; Fig 1b; 129pp; English.

XX CC This sequence represents the vitaxin antibody variable light chain
 CC region. Vitaxin and the antibody LM609 bind selectively to integrin
 CC alphavbeta3 and can be used to inhibit binding of alphavbeta3 to a
 CC ligand and thus block integrin-mediated signal transduction. This is
 CC useful in the treatment, prevention and diagnosis of alphavbeta3-mediated
 CC disease, specifically angiogenesis and restenosis (but also e.g.
 CC (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,
 CC cancer, psoriasis, rheumatoid arthritis, macular degeneration,
 CC osteoporosis etc.). The antibodies contain non-murine framework regions
 CC so are suitable for use in humans. Enhanced types of LM609 have affinity
 CC more than 90 times greater than that of parent the parent antibody.

XX SQ Sequence 107 AA;

Query Match 90.4%; Score 47; DB 19; Length 107;

Best Local Similarity 88.9%; Pred. No. 0.81;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSGSWPQT 9

|||||||

DB 89 QQSGSWPHT 97

RESULT 7

AAW76004

ID AAW76004 standard; Protein; 107 AA.

XX AC AAW76004;

XX DT 02-NOV-1998 (first entry)

XX DE LM609 antibody light chain variable region protein fragment.

XX KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.

XX OS Mus sp.

XX PN WO9833919-A2.

XX

PD 06-AUG-1998.

PF 30-JAN-1998; 98WO-US01826.

PR 30-JAN-1997; 97US-0791391.

XX PA (IXSY-) IXSYS INC.

XX PI Glaser SM, Huse WD;

XX DR WPI; 1998-437472/37.

XX DR N-PSDB; AAW76004.

XX PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

XX PS Claim 46; Fig 2b; 129pp; English.

XX CC This sequence represents the LM609 antibody variable light chain region.
 CC LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3
 CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus
 CC block integrin-mediated signal transduction. This is useful in the
 CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,
 CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
 CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
 CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
 CC etc.). The antibodies contain non-murine framework regions so are
 CC suitable for use in humans. Enhanced types of LM609 have affinity more
 CC than 90 times greater than that of parent the parent antibody.

XX SQ Sequence 107 AA;

Query Match 90.4%; Score 47; DB 19; Length 107;

Best Local Similarity 88.9%; Pred. No. 0.81;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSGSWPQT 9

|||||||

DB 89 QQSGSWPHT 97

RESULT 8

AAAG63588

ID AAG63588 standard; Protein; 107 AA.

XX AC AAG63588;

XX DT 15-OCT-2001 (first entry)

XX DE A light chain variable region of LM609 grafted antibody.

XX KW Grafted antibody; LM609; integrin; alphavbeta3; inflammatory disorder;
 KW chronic articular rheumatism; psoriasis; diabetic retinopathy;
 KW neovascular glaucoma; capillary proliferation; atherosclerotic plaque;
 KW cancer.

XX OS Synthetic.

XX OS Mus sp.

XX FH Key Location/Qualifiers

XX FT Misc-difference 49 /note= "unspecified residue encoded by MKK"

XX US2001011125-A1.

XX PD 02-AUG-2001.

XX PF 30-JAN-1997; 97US-0790540.

XX PR 30-JAN-1997; 97US-0790540.

XX

PA (HUSE/) HUSE W D.
 XX Huse WD;
 PI WPI: 2001-496171/54.
 XX N-PSDB; AAH74624.
 XX New LM609 grafted antibody exhibiting selective binding affinity to
 PT alphavbeta3, comprising at least one LM609 grafted heavy and light
 PT chain polypeptide, useful for diagnosing and treating e.g. inflammatory
 PT disorders or cancer -
 XX Disclosure; Fig 1B; 25pp; English.
 PS Claim 1; Fig 1B; 25pp; English.
 XX The present sequence represents the light chain variable region of the
 CC grafted monoclonal antibody LM609. LM609 is a murine antibody which
 CC specifically recognises the integrin alphavbeta3, and inhibits its
 CC functional activity. The LM609 grafted antibody has the
 CC complementarity determining regions (CDRs) substituted into a non-murine
 CC framework. Nucleic acids encoding LM609 grafted heavy and light chain
 CC polypeptides and fragments are useful in diagnostic and therapeutic
 CC purposes, such as in the production of LM609 grafted antibodies and
 CC fragments having binding specificity and inhibitory activity against
 CC the integrin alphavbeta3. The antibody can be used for the diagnosis
 CC or treatment of alphavbeta3-mediated diseases (e.g. inflammatory
 CC disorders, chronic articular rheumatism, psoriasis, disorders
 CC associated with inappropriate or inopportune invasion of vessels such
 CC as diabetic retinopathy, neovascular glaucoma and capillary
 CC proliferation in atherosclerotic plaques, or cancers), and to inhibit
 CC binding activity of alphavbeta3 that are necessary for progression of
 CC an alphavbeta3-mediated disease.
 XX SQ Sequence 107 AA;
 Query Match 90.4%; Score 47; DB 22; Length 107;
 Best Local Similarity 88.9%; Pred. No. 0.81;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSGSWPQT 9
 DB 89 QQSGSWPHT 97

RESULT 9
 AAG63590
 ID AAG63590 standard; Protein; 107 AA.
 XX AAG63590;
 AC A light chain variable region of LM609 antibody.
 XX 15-OCT-2001 (first entry)
 DT A light chain variable region of LM609 antibody.
 DE Grafted antibody; LM609; Integrin; alphavbeta3; inflammatory disorder;
 XX chronic articular rheumatism; psoriasis; diabetic retinopathy;
 KW neovascular glaucoma; capillary proliferation; atherosclerotic plaque;
 KW cancer.
 XX Mus sp.
 OS US200101125-A1.
 XX 02-AUG-2001.
 PD 30-JAN-1997; 97US-0790540.
 XX 30-JAN-1997; 97US-0790540.
 PR (HUSE/) HUSE W D.
 PA Huse WD;
 PI WPI: 2001-496171/54.
 XX

DR N-PSDB; AAH74626.
 XX New LM609 grafted antibody exhibiting selective binding affinity to
 PT alphavbeta3, comprising at least one LM609 grafted heavy and light
 PT chain polypeptide, useful for diagnosing and treating e.g. inflammatory
 PT disorders or cancer -
 XX Disclosure; Fig 2B; 25pp; English.
 PS The present sequence represents the light chain variable region of the
 XX monoclonal antibody LM609. LM609 is a murine antibody which specifically
 CC recognises the integrin alphavbeta3, and inhibits its functional activity.
 CC The specification describes a LM609 grafted antibody which has the
 CC complementarity determining regions (CDRs) substituted into a non-murine
 CC framework. Nucleic acids encoding LM609 grafted heavy and light chain
 CC polypeptides and fragments are useful in diagnostic and therapeutic
 CC purposes, such as in the production of LM609 grafted antibodies and
 CC fragments having binding specificity and inhibitory activity against
 CC the integrin alphavbeta3. The antibody can be used for the diagnosis
 CC or treatment of alphavbeta3-mediated diseases (e.g. inflammatory
 CC disorders, chronic articular rheumatism, psoriasis, disorders
 CC associated with inappropriate or inopportune invasion of vessels such
 CC as diabetic retinopathy, neovascular glaucoma and capillary
 CC proliferation in atherosclerotic plaques, or cancers), and to inhibit
 CC binding activity of alphavbeta3 that are necessary for progression of
 CC an alphavbeta3-mediated disease.
 XX SQ Sequence 107 AA;
 Query Match 90.4%; Score 47; DB 22; Length 107;
 Best Local Similarity 88.9%; Pred. No. 0.81;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSGSWPQT 9
 DB 89 QQSGSWPHT 97

RESULT 10
 AAB61360
 ID AAB61360 standard; protein; 107 AA.
 XX AAB61360;
 AC 03-APR-2001 (first entry)
 DT Vitaxin light chain variable region protein.
 DE LM609; grafted antibody; alphavbeta3 integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis.
 XX Unidentified.
 OS WO200078815-A1.
 XX 28-DEC-2000.
 PD 23-JUN-2000; 2000WO-US17454.
 XX 24-JUN-1999; 99US-0339922.
 PR (MOLE-) APPLIED MOLECULAR EVOLUTION.
 XX Huse WD, Wu H;
 PI WPI: 2001-050110/06.
 XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -
 XX Disclosure; Fig 1; 132pp; English.

XX The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphavbeta_3 integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.
 XX
 SQ Sequence 107 AA;

Query Match 90.4%; Score 47; DB 22; Length 107;
 Best Local Similarity 88.9%; Pred. No. 0.81;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSGSWPQT 9
 | | | | | | | |
 Db 89 QQSGSWPHT 97

RESULT 11

AAB61362
 ID AAB61362 standard; protein; 107 AA.

XX
 AC AAB61362;

XX
 DT 03-APR-2001 (first entry)

XX
 DE Antibody LM609 light chain variable region protein.

XX LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis.
 XX

OS Unidentified.

XX WO200078815-A1.

PN
 XX 28-DEC-2000.

XX
 PF 23-JUN-2000; 2000WO-US17454.

XX
 PR 24-JUN-1999; 99US-0339922.

XX (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX
 PI Huse WD, Wu H;

XX
 DR WPI; 2001-050110/06.

XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -

XX
 PS Disclosure; Fig 2; 132pp; English.

XX The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphavbeta_3 integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.

XX
 SQ Sequence 107 AA;

Query Match 90.4%; Score 47; DB 22; Length 107;
 Best Local Similarity 88.9%; Pred. No. 0.81;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSGSWPQT 9
 | | | | | | | |
 Db 89 QQSGSWPHT 97

RESULT 12

AAB61364
 ID AAB61364 standard; protein; 107 AA.

XX
 AC AAB61364;

XX
 DT 03-APR-2001 (first entry)

XX
 DE Light chain variable region of LM609.

XX LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis.
 XX

OS Unidentified.

XX WO200078815-A1.

PN
 XX 28-DEC-2000.

XX
 PF 23-JUN-2000; 2000WO-US17454.

XX
 PR 24-JUN-1999; 99US-0339922.

XX (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX
 PI Huse WD, Wu H;

XX
 DR WPI; 2001-050110/06.

XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -

XX
 PS Disclosure; Fig 7; 132pp; English.

XX The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphavbeta_3 integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.

XX
 SQ Sequence 107 AA;

Query Match 90.4%; Score 47; DB 22; Length 107;
 Best Local Similarity 88.9%; Pred. No. 0.81;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSGSWPQT 9
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 Db 89 QQSGSWPHT 97

RESULT 13

AAW76035
 ID AAW76035 standard; Protein; 9 AA.

XX


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XX (IXSY-) IXSYS INC.
PA
XX Glaser SM, Huse WD;
PI
XX WPI; 1998-437472/37.
DR N-PSDB; AAV49870.
DR
XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
XX Claim 62; Page 41; 129pp; English.
PS
XX AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
CC antibodies contain non-murine framework regions so are suitable for use
CC in humans. Enhanced types of LM609 have affinity more than 90 times
CC greater than that of parent the parent antibody.
XX
SQ Sequence 9 AA;

Query Match 78.8%; Score 41; DB 19; Length 9;
Best Local Similarity 77.8%; Pred. No. 7.8e+05;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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   III III I
Db 1 QQSNWPHPT 9

Search completed: November 18, 2002, 17:50:49
Job time : 26.4079 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 18:45:22 ; Search time 4.14474 Seconds
(without alignments)
32.704 Million cell updates/sec

Title: US-09-016-061-92

Perfect score: 52

Sequence: 1 QQSGSWPQT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 97044 seqs, 15060890 residues

Total number of hits satisfying chosen parameters: 97044

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA:*

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14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	47	90.4	107	8	US-08-790-540A-4
2	47	90.4	107	8	US-08-790-540A-8
3	47	90.4	107	8	US-08-791-391A-4
4	47	90.4	107	8	US-08-791-391A-8
5	47	90.4	107	8	US-08-791-391A-32
6	40	76.9	33	9	US-09-956-206A-12
7	39	75.0	128	12	US-10-006-773-6
8	36	69.2	107	10	US-09-756-301A-3
9	36	69.2	107	10	US-09-927-703-3
10	36	69.2	107	10	US-09-766-535A-3
11	36	69.2	107	10	US-09-756-161A-3
12	36	69.2	107	12	US-10-010-229-3
13	36	69.2	107	12	US-10-043-450-3
14	36	69.2	107	12	US-10-044-534-3
15	34	65.4	52	10	US-09-864-761-48217
16	34	65.4	100	10	US-09-899-896-2
17	34	65.4	166	12	US-10-142-373-4
18	34	65.4	244	10	US-09-764-864-1075
19	34	65.4	251	10	US-09-764-853-686
20	47	90.4	107	8	Sequence 4, Appli
21	47	90.4	107	8	Sequence 8, Appli
22	47	90.4	107	8	Sequence 4, Appli
23	47	90.4	107	8	Sequence 8, Appli
24	47	90.4	107	8	Sequence 32, Appl
25	40	76.9	33	9	Sequence 12, Appl
26	39	75.0	128	12	Sequence 6, Appli
27	36	69.2	107	10	Sequence 3, Appli
28	36	69.2	107	10	Sequence 3, Appli
29	36	69.2	107	10	Sequence 3, Appli
30	36	69.2	107	10	Sequence 3, Appli
31	36	69.2	107	10	Sequence 3, Appli
32	36	69.2	107	10	Sequence 3, Appli
33	36	69.2	107	10	Sequence 3, Appli
34	36	69.2	107	10	Sequence 3, Appli
35	34	65.4	52	10	Sequence 48217, A
36	34	65.4	100	10	Sequence 2, Appli
37	34	65.4	166	12	Sequence 4, Appli
38	34	65.4	244	10	Sequence 1075, Ap
39	34	65.4	251	10	Sequence 686, App

20	33	63.5	100	10	US-09-899-896-4	Sequence 4, Appli
21	33	63.5	516	10	US-09-822-863-2	Sequence 2, Appli
22	33	63.5	1148	9	US-10-108-605-67	Sequence 67, Appl
23	33	63.5	1148	9	US-10-108-605-173	Sequence 173, App
24	33	63.5	1148	9	US-10-108-605-275	Sequence 275, App
25	32	61.5	33	8	US-08-424-550B-411	Sequence 411, App
26	32	61.5	39	10	US-09-925-299-1108	Sequence 1108, Ap
27	32	61.5	49	10	US-09-864-761-36011	Sequence 36011, A
28	32	61.5	66	10	US-09-864-761-46439	Sequence 46439, A
29	32	61.5	72	10	US-09-764-869-744	Sequence 744, App
30	32	61.5	244	10	US-09-940-391-1	Sequence 1, Appli
31	32	61.5	578	10	US-09-740-041-4	Sequence 4, Appli
32	32	61.5	582	10	US-09-915-181A-4	Sequence 4, Appli
33	31	59.6	97	10	US-09-795-926-18	Sequence 18, Appl
34	31	59.6	117	10	US-09-893-737-208	Sequence 208, App
35	31	59.6	134	10	US-09-864-761-47478	Sequence 47478, A
36	31	59.6	148	10	US-09-795-926-8	Sequence 8, Appli
37	31	59.6	151	10	US-09-764-864-1009	Sequence 1009, Ap
38	31	59.6	157	10	US-09-925-302-446	Sequence 446, App
39	31	59.6	186	10	US-09-795-926-12	Sequence 12, Appl
40	31	59.6	235	12	US-10-020-139-3	Sequence 3, Appli
41	31	59.6	288	10	US-09-755-016-6	Sequence 6, Appli
42	31	59.6	326	9	US-10-084-700-29	Sequence 29, Appl
43	31	59.6	328	9	US-10-084-700-2	Sequence 2, Appli
44	31	59.6	328	10	US-09-095-881-4	Sequence 4, Appli
45	31	59.6	330	9	US-10-084-700-27	Sequence 27, Appl

ALIGNMENTS

RESULT 1
US-08-790-540A-4
; Sequence 4, Application US/08790540A
; Patent No. US2001001125A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,540A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-790-540A-4
Query Match 90.4%; Score 47; DB 8; Length 107;
Best Local Similarity 88.9%; Pred. No. 0.21;

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Matches      8;  Conservative      0;  Mismatches      1;  Indels      0;  Gaps      0;

QY      1  QOQSGSWPQT 9
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Db      89  QOQSGSWPHT 97

RESULT 2
US-08-790-540A-8
; Sequence 8, Application US/08790540A
; Patent No. US20010011125A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; NUCLEIC ACIDS ENCODING SAME AND METHODS OF USE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,540A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-790-540A-8

Query Match      90.4%;  Score 47;  DB 8;  Length 107;
Best Local Similarity 88.9%;  Pred. No. 0.21;
Matches      8;  Conservative      0;  Mismatches      1;  Indels      0;  Gaps      0;

QY      1  QOQSGSWPQT 9
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Db      89  QOQSGSWPHT 97

RESULT 3
US-08-791-391A-4
; Sequence 4, Application US/08791391A
; Patent No. US20010016645A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; NUCLEIC ACIDS ENCODING SAME AND METHODS OF USE
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,391A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-391A-4

Query Match      90.4%;  Score 47;  DB 8;  Length 107;
Best Local Similarity 88.9%;  Pred. No. 0.21;
Matches      8;  Conservative      0;  Mismatches      1;  Indels      0;  Gaps      0;

QY      1  QOQSGSWPQT 9
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Db      89  QOQSGSWPHT 97

RESULT 4
US-08-791-391A-8
; Sequence 8, Application US/08791391A
; Patent No. US20010016645A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; NUCLEIC ACIDS ENCODING SAME AND METHODS OF USE
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,391A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-391A-8

Query Match      90.4%;  Score 47;  DB 8;  Length 107;
Best Local Similarity 88.9%;  Pred. No. 0.21;
Matches      8;  Conservative      0;  Mismatches      1;  Indels      0;  Gaps      0;

QY      1  QOQSGSWPQT 9
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Db      89  QOQSGSWPHT 97

RESULT 5
US-08-791-391A-4
; Sequence 4, Application US/08791391A
; Patent No. US20010016645A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; NUCLEIC ACIDS ENCODING SAME AND METHODS OF USE
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,540A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-790-540A-8

Query Match      90.4%;  Score 47;  DB 8;  Length 107;
Best Local Similarity 88.9%;  Pred. No. 0.21;
Matches      8;  Conservative      0;  Mismatches      1;  Indels      0;  Gaps      0;

QY      1  QOQSGSWPQT 9
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Db      89  QOQSGSWPHT 97
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/791,391A
FILING DATE: 30-JAN-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX 1482
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-791-391A-4

Query Match      90.4%;  Score 47;  DB 8;  Length 107;
Best Local Similarity 88.9%;  Pred. No. 0.21;
Matches      8;  Conservative      0;  Mismatches      1;  Indels      0;  Gaps      0;

QY      1  QOQSGSWPQT 9
      111111111
Db      89  QOQSGSWPHT 97

RESULT 4
US-08-791-391A-8
; Sequence 8, Application US/08791391A
; Patent No. US20010016645A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; NUCLEIC ACIDS ENCODING SAME AND METHODS OF USE
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,391A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-391A-8
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Query Match          90.4%  Score 47;  DB 8;  Length 107;
Best Local Similarity 88.9%  Pred. No. 0.21;
Matches 8;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

QY 1 QQSGSWPQT 9
Db 89 QQSGSWPQT 97

RESULT 5
US-08-791-391A-32
; Sequence 32, Application US/08791391A
; Patent No. US20010016645A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791.391A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-391A-32

Query Match          90.4%  Score 47;  DB 8;  Length 107;
Best Local Similarity 88.9%  Pred. No. 0.21;
Matches 8;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

QY 1 QQSGSWPQT 9
Db 89 QQSGSWPQT 97

RESULT 6
US-09-956-206A-12
; Sequence 12, Application US/09956206A
; Patent No. US20020164339A1
; GENERAL INFORMATION:
; APPLICANT: DO COUTO, FERNANDO J.R.
; APPLICANT: CERIANI, ROBERTO L.
; APPLICANT: PETERSON, JERRY A.
; TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
; MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND
; METHODS OF HUMANIZING ANTIBODY PEPTIDES
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:

Query Match          90.4%  Score 39;  DB 12;  Length 128;
Best Local Similarity 77.8%  Pred. No. 5.1;
Matches 7;  Conservative 0;  Mismatches 2;  Indels 0;  Gaps 0;
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ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/956,206A
; FILING DATE: 19-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/525,539
; FILING DATE: 14-SEP-1995
; APPLICATION NUMBER: PCT/US95/11683
; FILING DATE: 14-SEP-1995
; APPLICATION NUMBER: 08/487,598
; FILING DATE: 7-JUNE-1995
; APPLICATION NUMBER: 08/307,868
; FILING DATE: 16-SEPT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: WITT, ERIC
; REGISTRATION NUMBER: 44,408
; REFERENCE/DOCKET NUMBER: 276332000101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-956-206A-12

Query Match          76.9%  Score 40;  DB 9;  Length 33;
Best Local Similarity 77.8%  Pred. No. 1;
Matches 7;  Conservative 0;  Mismatches 2;  Indels 0;  Gaps 0;

QY 1 QQSGSWPQT 9
Db 21 QQSNWSPYT 29

RESULT 7
US-10-006-773-6
; Sequence 6, Application US/10006773
; Patent No. US20020132983A1
; GENERAL INFORMATION:
; APPLICANT: Junghans, Richard P.
; TITLE OF INVENTION: Antibodies as Chimeric Effector Cell Receptors Against Tumor A
; FILE REFERENCE: 003
; CURRENT APPLICATION NUMBER: US/10/006,773
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: 60/250,089
; PRIOR FILING DATE: 2000-11-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-006-773-6

Query Match          75.0%  Score 39;  DB 12;  Length 128;
Best Local Similarity 77.8%  Pred. No. 5.1;
Matches 7;  Conservative 0;  Mismatches 2;  Indels 0;  Gaps 0;
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QY 1 QOQSGWPOT 9
||| ||| |
Db 109 QOQSNWPLT 117

RESULT 8
US-09-756-301A-3
; Sequence 3, Application US/09756301A
; Patent No. US20010027249A1
; GENERAL INFORMATION:
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Grayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
; TITLE OF INVENTION: Human Tumor Necrosis Factor
; FILE REFERENCE: 0975.1005-008
; CURRENT APPLICATION NUMBER: US/09756.301A
; CURRENT FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: U.S. 09/133,119
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1994-10-18
; PRIOR APPLICATION NUMBER: U.S. 08/192,102
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,861
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/010,406
; PRIOR FILING DATE: 1993-01-29
; PRIOR APPLICATION NUMBER: U.S. 08/013,413
; PRIOR FILING DATE: 1993-02-02
; PRIOR APPLICATION NUMBER: U.S. 07/943,852
; PRIOR FILING DATE: 1992-09-11
; PRIOR APPLICATION NUMBER: U.S. 07/853,606
; PRIOR FILING DATE: 1992-03-18
; PRIOR APPLICATION NUMBER: U.S. 07/670,827
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus Balb/c
US-09-756-301A-3

Query Match 69.2%; Score 36; DB 10; Length 107;
Best Local Similarity 77.8%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOQSGWPOT 9
||| ||| |
Db 89 QOQSHWPFT 97

RESULT 9
US-09-756-703-3
; Sequence 3, Application US/09927703
; Patent No. US20020022720A1
; GENERAL INFORMATION:
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Grayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of

; TITLE OF INVENTION: Human Tumor Necrosis Factor
; FILE REFERENCE: 0975.1005-013
; CURRENT APPLICATION NUMBER: US/09/927,703
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: U.S. 09/756,398
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: U.S. 09/133,119
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1994-10-18
; PRIOR APPLICATION NUMBER: U.S. 08/192,102
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,861
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,093
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/010,406
; PRIOR FILING DATE: 1993-01-29
; PRIOR APPLICATION NUMBER: U.S. 08/013,413
; PRIOR FILING DATE: 1993-02-02
; PRIOR APPLICATION NUMBER: U.S. 07/943,852
; PRIOR FILING DATE: 1992-09-11
; PRIOR APPLICATION NUMBER: U.S. 07/853,606
; PRIOR FILING DATE: 1992-03-18
; PRIOR APPLICATION NUMBER: U.S. 07/670,827
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus Balb/c
US-09-927-703-3

Query Match 69.2%; Score 36; DB 10; Length 107;
Best Local Similarity 77.8%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOQSGWPOT 9
||| ||| |
Db 89 QOQSHWPFT 97

RESULT 10
US-09-766-535A-3
; Sequence 3, Application US/09766535A
; Patent No. US20020106372A1
; GENERAL INFORMATION:
; APPLICANT: Le, Junming
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Grayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
; TITLE OF INVENTION: Human Tumor Necrosis Factor
; FILE REFERENCE: 0975.1005-010
; CURRENT APPLICATION NUMBER: US/09/766,535A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: U.S. 09/133,119
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1994-10-18
; PRIOR APPLICATION NUMBER: U.S. 08/192,102
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,861
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,093
; PRIOR FILING DATE: 1994-02-04

Query Match 69.2%; Score 36; DB 10; Length 107;
Best Local Similarity 77.8%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQSGSWPQT 9
DB 89 QQSHSWPFT 97

RESULT 11
US-10-010-229-3
; Sequence 3, Application US/10010229
; Patent No. US20020114805A1
; GENERAL INFORMATION:
; APPLICANT: Le, Junming
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Grayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
; FILE REFERENCE: 0975.1005-013
; CURRENT APPLICATION NUMBER: US/10/010,229
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US/09/927,703
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus Balb/c
US-09-756-161A-3

Query Match 69.2%; Score 36; DB 10; Length 107;
Best Local Similarity 77.8%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQSGSWPQT 9
DB 89 QQSHSWPFT 97

RESULT 11
US-09-756-161A-3
; Sequence 3, Application US/09756161A
; Patent No. US20020132307A1
; GENERAL INFORMATION:
; APPLICANT: Le, Junming
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Grayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
; FILE REFERENCE: 0975.1005-007
; CURRENT APPLICATION NUMBER: US/09/756,161A
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: U.S. 09/133,119
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1994-10-18
; PRIOR APPLICATION NUMBER: U.S. 08/192,102
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,861
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,093
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/010,406
; PRIOR FILING DATE: 1993-01-29
; PRIOR APPLICATION NUMBER: U.S. 08/013,413
; PRIOR FILING DATE: 1993-02-02
; PRIOR APPLICATION NUMBER: U.S. 07/943,852
; PRIOR FILING DATE: 1992-09-11
; PRIOR APPLICATION NUMBER: U.S. 07/853,606
; PRIOR FILING DATE: 1992-03-18
; PRIOR APPLICATION NUMBER: U.S. 07/670,827
; PRIOR FILING DATE: 1991-03-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus Balb/c
US-09-756-161A-3

Query Match 69.2%; Score 36; DB 10; Length 107;
Best Local Similarity 77.8%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQSGSWPQT 9
DB 89 QQSHSWPFT 97

RESULT 12
US-10-010-229-3
; Sequence 3, Application US/10010229
; Patent No. US20020114805A1
; GENERAL INFORMATION:
; APPLICANT: Le, Junming
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Grayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
; FILE REFERENCE: 0975.1005-013
; CURRENT APPLICATION NUMBER: US/10/010,229
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US/09/927,703
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus Balb/c
US-10-010-229-3

Query Match 69.2%; Score 36; DB 12; Length 107;
Best Local Similarity 77.8%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQSGSWPQT 9
DB 89 QQSHSWPFT 97

RESULT 13
US-10-043-450-3
; Sequence 3, Application US/10043450
; Patent No. US20020141996A1
; GENERAL INFORMATION:
; APPLICANT: Le, Junming
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Grayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
; FILE REFERENCE: 0975.1005-013
; CURRENT APPLICATION NUMBER: US/10/043,450
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: 09/927,703
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: U.S. 09/756,398
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: U.S. 09/133,119
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1994-10-18
; PRIOR APPLICATION NUMBER: U.S. 08/192,102
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,861

; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,093
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/010,406
; PRIOR FILING DATE: 1993-01-29
; PRIOR APPLICATION NUMBER: U.S. 08/013,413
; PRIOR FILING DATE: 1993-02-02
; PRIOR APPLICATION NUMBER: U.S. 07/943,852
; PRIOR FILING DATE: 1992-09-11
; PRIOR APPLICATION NUMBER: U.S. 07/853,606
; PRIOR FILING DATE: 1992-03-18
; PRIOR APPLICATION NUMBER: U.S. 07/670,827
; PRIOR FILING DATE: 1991-03-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus Balb/c
US-10-043-450-3

Query Match 69.2%; Score 36; DB 12; Length 107;
Best Local Similarity 77.8%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 0; Indels 2; Gaps 0;

QY 1 QQSGSWPQT 9
||| ||| |
DB 89 QQSHSWPFT 97

RESULT 14
US-10-044-534-3
; Sequence 3, Application US/10044534
; Patent No. US20020146419A1
; GENERAL INFORMATION:
; APPLICANT: Le, Junming
; APPLICANT: Vliceck, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Grayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and peptides of
; FILE REFERENCE: 0975.1005-013
; CURRENT APPLICATION NUMBER: US/10/044,534
; CURRENT FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: 09/927,703
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: U.S. 09/756,398
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: U.S. 09/133,119
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1994-10-18
; PRIOR APPLICATION NUMBER: U.S. 08/192,102
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,861
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,093
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/010,406
; PRIOR FILING DATE: 1993-01-29
; PRIOR APPLICATION NUMBER: U.S. 08/013,413
; PRIOR FILING DATE: 1993-02-02
; PRIOR APPLICATION NUMBER: U.S. 07/943,852
; PRIOR FILING DATE: 1992-09-11
; PRIOR APPLICATION NUMBER: U.S. 07/853,606
; PRIOR FILING DATE: 1992-03-18
; PRIOR APPLICATION NUMBER: U.S. 07/670,827
; PRIOR FILING DATE: 1991-03-18
; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus Balb/c
US-10-044-534-3

Query Match 69.2%; Score 36; DB 12; Length 107;
Best Local Similarity 77.8%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQSGSWPQT 9
||| ||| |
DB 89 QQSHSWPFT 97

RESULT 15
US-09-864-761-48217
; Sequence 48217, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; FILE REFERENCE: Aecomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 48217
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:

; OTHER INFORMATION: MAP TO AC006151.3
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.48
; OTHER INFORMATION: EST_HUMAN HIT: A1631520.1, EVALUE 3.00e-24
; OTHER INFORMATION: SWISSPROT HIT: P22272, EVALUE 3.60e+00
US-09-864-761-48217

Query Match 65.4%; Score 34; DB 10; Length 52;
Best Local Similarity 83.3%; Pred. No. 15;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SGSWPQ 8
:|||||
Db 19 TGSWPQ 24

Search completed: November 18, 2002, 19:04:22
Job time : 4.14474 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:43:42 ; Search time 8.52632 Seconds
(without alignments)
31.058 Million cell updates/sec

Title: US-09-016-061-92

Perfect score: 52

Sequence: 1 QQSGSWPQT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/1aa/5A-COMB.pep.*
- 2: /cgn2_6/ptodata/1/1aa/5B-COMB.pep.*
- 3: /cgn2_6/ptodata/1/1aa/6A-COMB.pep.*
- 4: /cgn2_6/ptodata/1/1aa/6B-COMB.pep.*
- 5: /cgn2_6/ptodata/1/1aa/PCTUS-COMB.pep.*
- 6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	78.8	100	1	US-08-436-463-19
2	41	78.8	107	1	US-07-634-278-62
3	41	78.8	107	1	US-07-634-278-63
4	41	78.8	107	1	US-07-634-278-87
5	41	78.8	107	1	US-08-477-728-62
6	41	78.8	107	1	US-08-477-728-63
7	41	78.8	107	1	US-08-477-728-87
8	41	78.8	107	1	US-08-474-040-62
9	41	78.8	107	1	US-08-474-040-63
10	41	78.8	107	1	US-08-474-040-87
11	41	78.8	107	1	US-08-487-200-62
12	41	78.8	107	1	US-08-487-200-63
13	41	78.8	107	1	US-08-487-200-87
14	41	78.8	107	4	US-08-484-537-62
15	41	78.8	107	4	US-08-484-537-63
16	41	78.8	107	4	US-08-484-537-87
17	41	78.8	127	1	US-07-634-278-83
18	41	78.8	127	1	US-08-477-728-83
19	41	78.8	127	1	US-08-474-040-83
20	41	78.8	127	1	US-08-487-200-83
21	41	78.8	127	1	US-08-436-463-4
22	41	78.8	127	4	US-08-484-537-83
23	40	76.9	33	4	US-08-525-539A-12
24	40	76.9	107	1	US-08-436-463-20
25	40	76.9	107	1	US-08-107-669D-1
26	40	76.9	107	1	US-08-472-788A-1
27	40	76.9	107	2	US-08-477-531B-1

28	40	76.9	107	2	US-08-082-842A-1	Sequence 1, Appli
29	40	76.9	109	1	US-07-942-243-4	Sequence 4, Appli
30	40	76.9	143	2	US-08-653-402B-8	Sequence 8, Appli
31	39	75.0	9	2	US-08-232-081B-6	Sequence 6, Appli
32	39	75.0	9	2	US-08-476-176B-55	Sequence 55, Appli
33	39	75.0	9	3	US-08-127-721A-55	Sequence 55, Appli
34	39	75.0	9	3	US-08-485-246A-55	Sequence 55, Appli
35	39	75.0	103	1	US-08-436-463-21	Sequence 21, Appli
36	39	75.0	106	2	US-08-800-198-4	Sequence 4, Appli
37	39	75.0	106	3	US-09-296-595-4	Sequence 4, Appli
38	39	75.0	107	2	US-08-232-081B-9	Sequence 9, Appli
39	39	75.0	107	2	US-08-232-081B-40	Sequence 40, Appli
40	39	75.0	107	2	US-08-476-176B-4	Sequence 4, Appli
41	39	75.0	107	3	US-08-127-721A-4	Sequence 4, Appli
42	39	75.0	107	3	US-08-485-246A-4	Sequence 4, Appli
43	39	75.0	127	1	US-08-436-463-18	Sequence 18, Appli
44	39	75.0	127	2	US-08-476-176B-6	Sequence 6, Appli
45	39	75.0	127	2	US-08-476-176B-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-08-436-463-19
; Sequence 19, Application US/08436463
; Patent No. 5760185
; GENERAL INFORMATION:
; APPLICANT: KIMACHI, Kazuhiko
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: NISHIYAMA, Kiyoto
; APPLICANT: TOKIYOSHI, Sachio
; TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT
; TITLE OF INVENTION: ANTIBODY AND GENE FRAGMENT CODING FOR SAID ANTIBODY
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,463
FILING DATE: 26-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 341255/1992
FILING DATE: 28-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: KIMACHI-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 100 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-436-463-19

Query Match 78.8%; Score 41; DB 1; Length 100;
Best Local Similarity 77.8%; Pred. No. 3.8;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	1	QOQSGSWPQT 9	III III I
Db	89	QOQNSWPHT 97	
RESULT 2			
US-07-634-278-62			
; Sequence 62, Application US/07634278			
; Patent No. 5530101			
; GENERAL INFORMATION:			
; APPLICANT: QUEEN, Cary L.			
; APPLICANT: CO, Man Sung			
; APPLICANT: SCHNEIDER, William P.			
; APPLICANT: LANDOLFI, Nicholas F.			
; APPLICANT: COELINGH, Kathleen L.			
; APPLICANT: SELICK, Harold E.			
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS			
; NUMBER OF SEQUENCES: 113			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Townsend and Townsend Kourie and Crew			
; STREET: 379 Lytton Avenue			
; CITY: Palo Alto			
; STATE: California			
; COUNTRY: US			
; ZIP: 94301			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: PatentIn Release #1.0, Version #1.25			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/07/634, 278			
; FILING DATE: 19-DEC-1990			
; CLASSIFICATION: 424			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US 07/590, 274			
; FILING DATE: 28-SEP-1990			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US 07/310, 252			
; FILING DATE: 13-FEB-1989			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US 07/290, 975			
; FILING DATE: 28-DEC-1988			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Smith, William M			
; REGISTRATION NUMBER: 30,223			
; REFERENCE/DOCKET NUMBER: 11823-002600			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: (415) 326-2400			
; TELEFAX: (415) 326-2422			
; INFORMATION FOR SEQ ID NO: 62:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 107 amino acids			
; TYPE: amino acid			
; STRANDEDNESS: single			
; TOPOLOGY: linear			
; MOLECULE TYPE: peptide			
US-07-634-278-62			
Query Match 78.8%; Score 41; DB 1; Length 107;			
Best Local Similarity 77.8%; Pred. No. 4.1;			
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;			
QY	1	QOQSGSWPQT 9	III III I
Db	89	QOQNSWPHT 97	
RESULT 3			
US-07-634-278-63			
; Sequence 63, Application US/07634278			
; Patent No. 5530101			
; GENERAL INFORMATION:			
; APPLICANT: QUEEN, Cary L.			
; APPLICANT: CO, Man Sung			
; APPLICANT: SCHNEIDER, William P.			
; APPLICANT: LANDOLFI, Nicholas F.			
; APPLICANT: COELINGH, Kathleen L.			
; APPLICANT: SELICK, Harold E.			
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS			
; NUMBER OF SEQUENCES: 113			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Townsend and Townsend Kourie and Crew			
; STREET: 379 Lytton Avenue			
; CITY: Palo Alto			
; STATE: California			
; COUNTRY: US			
; ZIP: 94301			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: PatentIn Release #1.0, Version #1.25			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/07/634, 278			
; FILING DATE: 19-DEC-1990			
; CLASSIFICATION: 424			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US 07/590, 274			
; FILING DATE: 28-SEP-1990			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US 07/310, 252			
; FILING DATE: 13-FEB-1989			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US 07/290, 975			
; FILING DATE: 28-DEC-1988			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Smith, William M			
; REGISTRATION NUMBER: 30,223			
; REFERENCE/DOCKET NUMBER: 11823-002600			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: (415) 326-2400			
; TELEFAX: (415) 326-2422			
; INFORMATION FOR SEQ ID NO: 62:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 107 amino acids			
; TYPE: amino acid			
; STRANDEDNESS: single			
; TOPOLOGY: linear			
; MOLECULE TYPE: peptide			
US-07-634-278-62			
Query Match 78.8%; Score 41; DB 1; Length 107;			
Best Local Similarity 77.8%; Pred. No. 4.1;			
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;			
QY	1	QOQSGSWPQT 9	III III I
Db	89	QOQNSWPHT 97	
RESULT 4			
US-07-634-278-87			
; Sequence 87, Application US/07634278			
; Patent No. 5530101			
; GENERAL INFORMATION:			
; APPLICANT: QUEEN, Cary L.			
; APPLICANT: CO, Man Sung			
; APPLICANT: SCHNEIDER, William P.			
; APPLICANT: LANDOLFI, Nicholas F.			
; APPLICANT: COELINGH, Kathleen L.			
; APPLICANT: SELICK, Harold E.			
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS			
; NUMBER OF SEQUENCES: 113			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Townsend and Townsend Kourie and Crew			
; STREET: 379 Lytton Avenue			
; CITY: Palo Alto			
; STATE: California			
; COUNTRY: US			
; ZIP: 94301			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: PatentIn Release #1.0, Version #1.25			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/07/634, 278			
; FILING DATE: 19-DEC-1990			
; CLASSIFICATION: 424			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US 07/590, 274			
; FILING DATE: 28-SEP-1990			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US 07/310, 252			
; FILING DATE: 13-FEB-1989			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US 07/290, 975			
; FILING DATE: 28-DEC-1988			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Smith, William M			
; REGISTRATION NUMBER: 30,223			
; REFERENCE/DOCKET NUMBER: 11823-002600			
; TELECOMMUNICATION INFORMATION:</			

ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/590,274
FILING DATE: 28-SEP-1990
APPLICATION NUMBER: US/07/310,252
FILING DATE: 13-FEB-1989
APPLICATION NUMBER: US/07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 87:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-634-278-87

Query Match 78.8%; Score 41; DB 1; Length 107;
Best Local Similarity 77.8%; Pred. No. 4.1;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQSGSWPQT 9
||| ||| |
Db 89 QQSNSWPHT 97

RESULT 5
US-08-477-728-62
Sequence 62, Application US/08477728
Patent No. 5585089
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,728

FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-477-728-62

Query Match 78.8%; Score 41; DB 1; Length 107;
Best Local Similarity 77.8%; Pred. No. 4.1;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQSGSWPQT 9
||| ||| |
Db 89 QQSNSWPHT 97

RESULT 6
US-08-477-728-63
Sequence 63, Application US/08477728
Patent No. 5585089
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,728
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/310,252

; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-477-728-63

Query Match 78.8%; Score 41; DB 1; Length 107;
Best Local Similarity 77.8%; Pred. No. 4.1;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQSGSWPQT 9
Db 89 QQSNWPHT 97

RESULT 7

US-08-477-728-87
; Sequence 87, Application US/08477728
; Patent No. 5585089
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,728
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400

; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 87:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-477-728-87

Query Match 78.8%; Score 41; DB 1; Length 107;
Best Local Similarity 77.8%; Pred. No. 4.1;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQSGSWPQT 9
Db 89 QQSNWPHT 97

RESULT 8

US-08-474-040-62
; Sequence 62, Application US/08474040
; Patent No. 5693761
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELING, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,040
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-474-040-62

Query Match 78.8%; Score 41; DB 1; Length 107;
Best Local Similarity 77.8%; Pred. No. 4.1;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQSGSWPQT 9
111 111 1
Db 89 QQSNWPHT 97

RESULT 9

US-08-474-040-63
; Sequence 63, Application US/08474040
; Patent No. 5693761
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELING, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,040
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 63:

SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-474-040-63

Query Match 78.8%; Score 41; DB 1; Length 107;
Best Local Similarity 77.8%; Pred. No. 4.1;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQSGSWPQT 9
111 111 1

Db 89 QQSNWPHT 97

RESULT 10

US-08-474-040-87
; Sequence 87, Application US/08474040
; Patent No. 5693761
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELING, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,040
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 87:

SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-474-040-87

Query Match 78.8%; Score 41; DB 1; Length 107;
Best Local Similarity 77.8%; Pred. No. 4.1;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQSGSWPQT 9
111 111 1
Db 89 QQSNWPHT 97

RESULT 11

US-08-487-200-62
; Sequence 62, Application US/08487200
; Patent No. 5693762
; GENERAL INFORMATION:

APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,200
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/487,200
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002610
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-487-200-62

Query Match 78.8%; Score 41; DB 1; Length 107;
Best Local Similarity 77.8%; Pred. No. 4.1;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOQSGSWPQT 9
Db 89 QQSNWPHT 97

RESULT 12
US-08-487-200-63
Sequence 63, Application US/08487200
Patent No. 5693762
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS

NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,200
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002610
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-487-200-63
Query Match 78.8%; Score 41; DB 1; Length 107;
Best Local Similarity 77.8%; Pred. No. 4.1;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 QOQSGSWPQT 9
Db 89 QQSNWPHT 97
RESULT 13
US-08-487-200-87
Sequence 87, Application US/08487200
Patent No. 5693762
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US

ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,200
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002610
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 87:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-487-200-87

Query Match 78.8%; Score 41; DB 1; Length 107;
Best Local Similarity 77.8%; Pred. No. 4.1;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOQSGSWPQT 9
Db 89 QOQSNWPHT 97

RESULT 14
US-08-484-537-62
Sequence 62, Application US/08484537
Patent No. 6180370
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/484,537
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-484-537-62

Query Match 78.8%; Score 41; DB 4; Length 107;
Best Local Similarity 77.8%; Pred. No. 4.1;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOQSGSWPQT 9
Db 89 QOQSNWPHT 97

RESULT 15
US-08-484-537-63
Sequence 63, Application US/08484537
Patent No. 6180370
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,537
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990


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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-484-537-63

```

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Query Match          78.8%  Score 41;  DB 4;  Length 107;
Best Local Similarity 77.8%  Pred. No. 4.1;
Matches 7;  Conservative 0;  Mismatches 2;  Indels 0;  Gaps 0;

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QY 1 QQSGSWPQT 9
Db 89 QQNSWPHT 97

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Search completed: November 18, 2002, 17:55:52
Job time : 8.52632 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:47:14 ; Search time 10.6579 Seconds
(without alignments)
90.200 Million cell updates/sec

Title: US-09-016-061-94

Perfect score: 55

Sequence: 1 ARNHGSPAS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_73.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	69.1	136	2	H64968
2	38	69.1	208	2	AC2830
3	38	69.1	219	1	QOECA5
4	38	69.1	219	2	C9038
5	38	69.1	219	2	G85786
6	38	69.1	225	2	H97607
7	37	67.3	731	1	JC2464
8	36	65.5	322	1	A29928
9	36	65.5	360	2	S48566
10	36	65.5	470	2	H71657
11	36	65.5	473	2	D70405
12	35	63.6	233	2	H82163
13	35	63.6	272	2	S27819
14	35	63.6	272	2	S27820
15	35	63.6	446	2	T19625
16	35	63.6	448	1	A60003
17	35	63.6	538	2	T28874
18	35	63.6	628	1	A56707
19	35	63.6	722	2	S64492
20	35	63.6	1291	2	T13389
21	34	61.8	89	2	S38688
22	34	61.8	89	2	S38683
23	34	61.8	89	2	S38684
24	34	61.8	127	2	D54759
25	34	61.8	170	2	D75554
26	34	61.8	207	2	B97320
27	34	61.8	225	2	I47095
28	34	61.8	236	2	S16389
29	34	61.8	270	2	AG0036

30	34	61.8	284	2	S62931
31	34	61.8	335	2	AC2686
32	34	61.8	338	2	H97467
33	34	61.8	379	1	F64633
34	34	61.8	381	2	A71882
35	34	61.8	415	2	C84829
36	34	61.8	463	2	D88104
37	34	61.8	491	2	AF1104
38	34	61.8	491	2	AF1466
39	34	61.8	1446	1	A45344
40	34	61.8	1460	1	EDBEIF
41	33	60.0	222	2	G81124
42	33	60.0	242	2	H82061
43	33	60.0	243	2	B81896
44	33	60.0	259	2	D72425
45	33	60.0	266	2	D82979

ALIGNMENTS

RESULT 1

H64968

acetyl CoA acetyltransferase - Escherichia coli (strain K-12)

C:Species: Escherichia coli

C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002

C:Accession: H64968; I69646; I69656

R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;

A.: Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A:Title: The complete genome sequence of Escherichia coli K-12.

A:Reference number: A64720; MUID:97426617; PMID:9278503

A:Accession: H64968

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-196 <BLAT>

A:Cross-references: GB:AE000294; GB:U000096; NID:91788338; PIDN:AACT5094.1; PID:gl7883

A:Experimental source: strain K-12, substrain MG1655

R:Yao, Z.; Valvano, M.A.

J. Bacteriol. 176, 4133-4143, 1994

A:Title: Genetic analysis of the O-specific lipopolysaccharide biosynthesis region (r

erotypes Y and 4a.

A:Reference number: I55053; MUID:94292434; PMID:7517390

A:Accession: I69646

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-167,'LFRKYCHC',177-186,'TMR',190-196 <RES>

A:Cross-references: EMBL:U03041; NID:g501028; PIDN:AACT31635.1; PID:g510256

R:Stevenson, G.; Neal, B.; Liu, D.; Hobbs, M.; Packer, N.H.; Batley, M.; Redmond, J.W

J. Bacteriol. 176, 4144-4156, 1994

A:Title: Structure of the O antigen of Escherichia coli K-12 and the sequence of its

A:Reference number: I55054; MUID:94292435; PMID:7517391

A:Accession: I69656

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-167,'LFRKYCHC',177-186,'TMR',190-196 <RE2>

A:Cross-references: EMBL:U09876; NID:g508236; PID:g508245

C:Genetics:

A:Gene: yefH

A:Map position: 45 min

C:Superfamily: galactoside acetyltransferase

Query Match 69.1%; Score 38; DB 2; Length 196;

Best Local Similarity 100.0%; Pred.No.9.8;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNHGSF 8

Db 105 HNHGSF 110

RESULT 2

AC2830

pyrazinamidase/nicotinamidase [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
 C:Species: Agrobacterium tumefaciens
 C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 03-Jun-2002
 C:Accession: AC2830
 R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.; Erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellan; Karp, P.; Romero, P.; Zhang, S.
 A:Title: Structure and expression in Escherichia coli K-12 of the L-asparaginase I-encoding gene 78, 37-46, 1989
 A:Reference number: JU0047; MUID:89357501; PMID:2670682
 A:Accession: JU0048
 A:Molecule type: DNA
 A:Residues: 7-219 <JER>
 A:Cross-references: GB:M26934; NID:g145278; PIDN:AAA23447.1; PID:g145280
 C:Genetics:
 A:Gene: ydjb
 A:Map position: 39 min
 C:Superfamily: Escherichia coli hypothetical 23.4K protein (ansa 3' region)
 Query Match 69.1%; Score 38; DB 1; Length 219;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 NHGSFAS 10
 Db 63 NHGSFAS 69
 RESULT 4
 QBCAS5
 hypothetical 23.4K protein (ansa 3' region) - Escherichia coli (strain K-12)
 C:Species: Escherichia coli
 C:Date: 31-Dec-1990 #sequence_revision 17-Oct-1997 #text_change 01-Mar-2002
 C:Accession: H64936; JU0048
 R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cohen; Rose, D.J.; Mau, B.; Shao, Y.
 A:Title: The complete genome sequence of Escherichia coli K-12.
 A:Reference number: A64720; MUID:97426617; PMID:9278503
 A:Accession: H64936
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-219 <BLAT>
 A:Cross-references: GB:AE000271; GB:U00096; NID:g1788058; PIDN:AAC74838.1; PID:g1788066;
 A:Experimental source: strain K-12, substrain MG1655
 R:Jerlstroem, P.G.; Bezjak, D.A.; Jennings, M.P.; Beacham, I.R.
 A:Title: Structure and expression in Escherichia coli K-12 of the L-asparaginase I-encoding gene 78, 37-46, 1989
 A:Reference number: JU0047; MUID:89357501; PMID:2670682
 A:Accession: JU0048
 A:Molecule type: DNA
 A:Residues: 7-219 <JER>
 A:Cross-references: GB:M26934; NID:g145278; PIDN:AAA23447.1; PID:g145280
 C:Genetics:
 A:Gene: ydjb
 A:Map position: 39 min
 C:Superfamily: Escherichia coli hypothetical 23.4K protein (ansa 3' region)
 Query Match 69.1%; Score 38; DB 1; Length 219;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 NHGSFAS 10
 Db 63 NHGSFAS 69
 RESULT 4
 C90938

hypothetical protein ECS2475 [imported] - Escherichia coli (strain O157:H7, substrain C)
 C:Species: Escherichia coli
 C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
 C:Accession: C90938
 R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.; Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
 A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genome analysis
 A:Reference number: A99629; MUID:21156231; PMID:11258796
 A:Accession: C90938
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-219 <HAY>
 A:Cross-references: GB:BA000007; PIDN:BA035898.1; PID:g13361942; GSPDB:GN00154
 A:Experimental source: strain O157:H7, substrain RIMD 050952
 C:Genetics:
 A:Gene: ECS2475
 C:Superfamily: Escherichia coli hypothetical 23.4K protein (ansa 3' region)
 Query Match 69.1%; Score 38; DB 2; Length 219;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 NHGSFAS 10
 Db 63 NHGSFAS 69
 RESULT 5
 G85786
 hypothetical protein ydjb [imported] - Escherichia coli (strain O157:H7, substrain ED)
 C:Species: Escherichia coli
 C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
 C:Accession: G85786
 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May; Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda; Nature 409, 529-533, 2001
 A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A:Reference number: A85480; MUID:21074935; PMID:11206551
 A:Accession: G85786
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-219 <STO>
 A:Cross-references: GB:AE005174; NID:g12515794; PIDN:AAG56755.1; GSPDB:GN00145; UWGP:
 A:Experimental source: strain O157:H7, substrain EDL933
 C:Genetics:
 A:Gene: ydjb
 C:Superfamily: Escherichia coli hypothetical 23.4K protein (ansa 3' region)
 Query Match 69.1%; Score 38; DB 2; Length 219;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 NHGSFAS 10
 Db 63 NHGSFAS 69
 RESULT 6
 H97607
 hypothetical protein AGR_C_3739 [imported] - Agrobacterium tumefaciens (strain C58, C)
 C:Species: Agrobacterium tumefaciens
 C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
 C:Accession: H97607
 R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldm; A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, Science 294, 2323-2328, 2001
 A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium
 A:Reference number: A97359; PMID:11743194
 A:Accession: H97607
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-225 <KUR>

A:Cross-references: GB:AE007869; PIDN:AAK87817.1; PID:g15157195; GSPDB:GN00169
 C:Genetics:
 A:Gene: AGR_C_3739
 A:Map position: circular chromosome
 C:Superfamily: Escherichia coli hypothetical 23.4K protein (ansa 3' region)

Query Match 69.1%; Score 38; DB 2; Length 225;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NHGSPAS 10
 DB 70 NHGSPAS 76

RESULT 7
 JC2464
 probable copper-transporting ATPase (EC 3.6.1.-) HRA-1 - Enterobacteriaceae spp.
 C:Species: Enterobacteriaceae spp.
 C:Date: 16-Oct-1998 #sequence_revision 16-Oct-1998 #text_change 18-Jun-1999
 R:Trener III., C.; Lin, W.; Andrews, N.C.
 Biochem. Biophys. Res. Commun. 205, 1644-1650, 1994
 A:Title: Novel bacterial P-type ATPases with histidine-rich heavy-metal-associated sequence
 A:Reference number: JC2464; MUID:95110304; PMID:7811248
 A:Accession: JC2464
 A:Molecule type: mRNA
 A:Residues: 1-731 <ACT>
 A:Cross-references: GB:U16658; NID:g643612; PIDN:AAA62113.1; PID:g643613
 A:Experimental source: human small intestine cDNA library
 A:Note: the source species is uncertain; the cloned sequence did not hybridize with human
 C:Superfamily: Enterococcus copper-transporting ATPase copB; ATPase nucleotide-binding d
 C:Keywords: ATP; copper transport; hydrolase; ion transport; phosphoprotein; transmembr
 F:7-92/Region: His-rich
 F:135-477/Domain: ATPase transduction domain homology <ATP>
 F:544-685/Domain: ATPase nucleotide-binding domain homology <ATN>
 F:287/Active site: Glu #status predicted
 F:431/Active site: Asp (aspartylphosphate intermediate) #status predicted

Query Match 67.3%; Score 37; DB 1; Length 731;
 Best Local Similarity 75.0%; Pred. No. 55;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARNHGSPF 8
 DB 88 ARHHGSPF 95

RESULT 8
 A29928
 membrane-associated 40K protein precursor - Vibrio anguillarum plasmid pJM1
 C:Species: Vibrio anguillarum
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 18-Aug-2000
 C:Accession: A29928; C41671
 R:Actis, L.A.; Tolmasey, M.E.; Farrell, D.H.; Croso, J.H.
 J. Biol. Chem. 263, 2853-2860, 1988
 A:Title: Genetic and molecular characterization of essential components of the Vibrio an
 A:Reference number: A92707; MUID:88139336; PMID:2830268
 A:Accession: A29928
 A:Molecule type: DNA
 A:Residues: 1-322 <ACT>
 A:Cross-references: GB:J03529; NID:g150755; PIDN:AAA91580.1; PID:g150756
 R:Koester, W.L.; Actis, L.A.; Waldbeser, L.S.; Tolmasey, M.E.; Croso, J.H.
 J. Biol. Chem. 266, 23829-23833, 1991
 A:Title: Molecular characterization of the iron transport system mediated by the pJM1 pl
 A:Reference number: A41671; MUID:92084677; PMID:1748657
 A:Accession: C41671
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-154 <KOE>
 A:Cross-references: GB:M74068
 C:Superfamily: Iron(III) dicitrate transport protein
 C:Keywords: membrane protein

F:1-22/Domain: signal sequence #status predicted <SIG>
 F:23-322/Product: membrane-associated 40K protein #status predicted <MAT>

Query Match 65.5%; Score 36; DB 1; Length 322;
 Best Local Similarity 75.0%; Pred. No. 37;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 HHNGSPAS 10
 DB 203 HHNGSPAS 210

RESULT 9
 S48566
 hypothetical protein YLR215c - yeast (Saccharomyces cerevisiae)
 N:Alternate names: hypothetical protein L8167.23
 C:Species: Saccharomyces cerevisiae
 C:Date: 02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change 19-Apr-2002
 C:Accession: S48566
 R:Pauley, A.
 submitted to the EMBL Data Library, September 1994
 A:Description: The sequence of S. cerevisiae cosmid 8167.
 A:Reference number: S48545
 A:Accession: S48566
 A:Molecule type: DNA
 A:Residues: 1-360 <PAU>
 A:Cross-references: EMBL:U14913; NID:g544497; PIDN:AA67444.1; PID:g544519; GSPDB:GN0

Query Match 65.5%; Score 36; DB 2; Length 360;
 Best Local Similarity 77.8%; Pred. No. 42;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNGSPAS 10
 DB 304 RHNGSPAS 312

RESULT 10
 H71667
 glutamate-tRNA ligase (EC 6.1.1.17) (gltX2) RP623 - Rickettsia prowazekii
 C:Species: Rickettsia prowazekii
 C:Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 03-Jun-2002
 C:Accession: H71667
 R:Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark
 Nature 396, 133-140, 1998
 A:Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.
 A:Reference number: A71630; MUID:99039499; PMID:9823893

Query Match 65.5%; Score 36; DB 2; Length 470;
 Best Local Similarity 75.0%; Pred. No. 54;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARNHGSPF 8
 DB 31 ARHHNGKF 38

RESULT 11

D70405
glutamate-tRNA ligase (EC 6.1.1.17) - Aquifex aeolicus
C:Species: Aquifex aeolicus
C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 03-Jun-2002
C:Accession: D70405
R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O'V.
Nature 392, 353-358, 1998
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A:Reference number: A70300; MUID:98196666; PMID:9537320
A:Accession: D70405
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-473 <AQF>
A:Cross-references: GB:AE000729; NID:g2983659; PIDN:AAC07230.1; PID:g2983664; GB:AE00065
A:Experimental source: strain VF5
C:Genetics:

A:Gene: gltX
C:Superfamily: glutamate-tRNA ligase; glutamine-tRNA ligase homology
C:Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis
F:4-276/Domain: glutamine-tRNA ligase homology <EGL>

Query Match 65.5%; Score 36; DB 2; Length 473;
Best Local Similarity 75.0%; Pred. No. 55;
Matches 6; Conservative 1; Mismatches 0; Indels 1; Gaps 0;

QY 1 ARNHGGSF 8
|||||
DB 31 ARHNGGKF 38

RESULT 12

H82163
arginyl-tRNA-protein transferase-related protein VC1736 [imported] - Vibrio cholerae (st
C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C:Accession: H82163
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, B
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000

A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833; PMID:10952301

A:Accession: H82163
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-233 <HEI>
A:Cross-references: GB:AE004251; GB:AE003852; NID:g9656248; PIDN:AAF94886.1; GSPDB:GN001
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC1736
A:Map position: 1

Query Match 63.6%; Score 35; DB 2; Length 233;
Best Local Similarity 85.7%; Pred. No. 42;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARNHGGS 7
||| |||
DB 117 ARHRHGS 123

RESULT 13

S27819
vitelline B1 precursor - liver fluke
N:Alternate names: eggshell protein B1
C:Species: Fasciola hepatica (liver fluke)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 04-Feb-2000
C:Accession: A48436; A48437; A59161; S27819
R:Rice-Ficht, A.C.; Dusek, K.A.; Kochevar, G.J.; Waite, J.H.
Mol. Biochem. Parasitol. 54, 129-141, 1992
A:Title: Eggshell precursor proteins of Fasciola hepatica, I. Structure and expression o

?

A:Reference number: A48436; MUID:93063029; PMID:1435854

A:Accession: A48436
A:Molecule type: mRNA; protein
A:Residues: 1-272 <RIC>
A:Cross-references: EMBL:M93024; NID:g159065; PIDN:AAA29143.1; PID:g159066
A:Note: sequence extracted from NCBI backbone (NCBIN:117208, NCBIP:117210)
R:Waite, J.H.; Rice-Ficht, A.C.
Mol. Biochem. Parasitol. 54, 143-151, 1992
A:Title: Eggshell precursor proteins of Fasciola hepatica, II. Microheterogeneity in
A:Reference number: A48437; MUID:93063030; PMID:1435855

A:Accession: A48437
A:Status: preliminary
A:Molecule type: protein
A:Residues: 20-47 <WAI>

A:Cross-references: PID:g259030; PIDN:AAB23982.1
A:Note: sequence extracted from NCBI backbone (NCBIP:117211)

A:Accession: B48437
A:Status: preliminary
A:Molecule type: protein
A:Residues: 172-193 <WAZ>

A:Cross-references: PID:g259031; PIDN:AAB23983.1
A:Note: sequence extracted from NCBI backbone (NCBIP:117213)
R:Waite, J.H.

Anal. Biochem. 192, 429-433, 1991
A:Title: Detection of peptidyl-3,4-dihydroxyphenylalanine by amino acid analysis and
A:Reference number: A59161; MUID:91241559; PMID:1903612

A:Accession: A59161
A:Molecule type: protein
A:Residues: 62-70 <WAZ>
A:Experimental source: egg shell

C:Keywords: egg shell
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-272/Product: vitelline B1 #status predicted <MAT>
F:63/Modified site: 3',4'-dihydroxyphenylalanine (Tyr) #status experimental

Query Match 63.6%; Score 35; DB 2; Length 272;
Best Local Similarity 75.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARNHGGSF 8
||| |||
DB 19 ARHPHGKF 26

RESULT 14

S27820
vitelline B2 precursor - liver fluke
N:Alternate names: eggshell protein B2
C:Species: Fasciola hepatica (liver fluke)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 04-Feb-2000
C:Accession: S27820
R:Rice-Ficht, A.C.; Dusek, K.A.; Kochevar, G.J.; Waite, J.H.
submitted to the EMBL Data Library, May 1992

A:Description: Eggshell precursor proteins of Fasciola hepatica: I. structure and exp
A:Reference number: S27819
A:Accession: S27820

A:Molecule type: mRNA
A:Residues: 1-272 <RIC>
A:Cross-references: EMBL:M93025; NID:g159067; PIDN:AAA29144.1; PID:g159068
C:Keywords: egg shell

F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-272/Product: vitelline B2 #status predicted <MAT>

Query Match 63.6%; Score 35; DB 2; Length 272;
Best Local Similarity 75.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARNHGGSF 8
||| |||
DB 19 ARHPHGKF 26

RESULT 15

Search completed: November 18, 2002, 17:57:22
Job time : 11.6579 secs


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RA Saito N., Sampei G., Seki Y., Sivasundaram S., Tagami H.,
RA Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.;
RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome
RL corresponding to the 40.1-50.0 min region on the linkage map.";
RL DNA Res. 3:379-392(1996).
CC -1- FUNCTION: PUTATIVE O-ACETYLTRANSFERASE THAT TRANSFERS AN O-ACETYL
CC ON THE O ANTIGEN.
CC -1- PATHWAY: Lipopolysaccharide biosynthesis.
CC -1- SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NDL FAMILY OF
CC ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
CC -----
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CC -----
DR EMBL; U03041; AAC31635.1; -
DR EMBL; U09876; AAB88406.1; -
DR EMBL; AE000294; AAC75094.1; -
DR EMBL; D90841; BAA15875.1; -
DR EMBL; D90842; BAA15887.1; -
DR EcoGene; EG11984; wbbJ.
DR InterPro; IPR001451; Hexapep_transf.
DR Pfam; PF00132; hexapep; 4.
DR PROSITE; PS00101; HEXAPEP_TRANSFERRASES; FALSE_NEG.
KW Lipopolysaccharide biosynthesis; Transferrase; Acyltransferase; Repeat;
KW Complete proteome.
FT CONFLICT 168 176 SIPENTVIA -> LFRKYCHC (IN REF. 1).
FT CONFLICT 187 189 NHE -> IMR (IN REF. 1).
SQ SEQUENCE 196 AA; 21675 MW; DIC2FA7D3B29A1B1 CRC64;

Query Match 69.1%; Score 38; DB 1; Length 196;
Best Local Similarity 100.0%; Pred. No. 2.1; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;

QY 3 NHGGSF 8
Db 105 NHGGSF 110
|||||

RESULT 2
PNCA_ECOLI STANDARD; PRT; 213 AA.
ID PNCA_ECOLI
AC P21369; P76229; P76910;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Pyrazinamidase/nicotinamidase [Includes: Pyrazinamidase (EC 3.5.1.-)
DE (pZaase); Nicotinamidase (EC 3.5.1.19) (Nicotine deamidase)].
GN PNCA OR NAM OR B1768.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=89357501; PubMed=2670682;
RA Jerlstrom P.G., Bezjak D.A., Jennings M.P., Beacham I.R.;
RT "Structure and expression in Escherichia coli K-12 of the
RT L-asparaginase I-encoding ansA gene and its flanking regions.";
RL Gene 78:37-46(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96338362; PubMed=8726014;
RA Frothingham R., Meeker-O'Connell W.A., Talbot E.A., George J.W.,
RA Krexner K.N.;
RT "Identification, cloning, and expression of the Escherichia coli
RT pyrazinamidase and nicotinamidase gene, pncA.";
RL Antimicrob. Agents Chemother. 40:1426-1431(1996).

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RN SEQUENCE FROM N.A.
RP STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97251357; PubMed=9097039;
RA Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,
RA Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N.,
RA Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J.,
RA Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;
RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome
RL corresponding to the 28.0-40.1 min region on the linkage map.";
RL DNA Res. 3:363-377(1996).
CC -1- CATALYTIC ACTIVITY: Nicotinamide + H(2)O = nicotinate + NH(3).
CC -1- PATHWAY: NAD biosynthesis; nicotinamide to NAMN; first step.
CC -1- SIMILARITY: TO YEAST YGL037C.
CC -----
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CC -----
DR EMBL; M26934; AAA23447.1; -
DR EMBL; AE000271; AAC74838.1; ALT_INIT.
DR EMBL; D90820; BAA15559.1; -
DR EMBL; D90821; BAA15566.1; -
DR PIR; JU0048; QOECAS.
DR EcoGene; EG11135; pncA.
DR InterPro; IPR000868; Isochorismatase.
DR Pfam; PF00857; Isochorismatase; 1.
DR KW Pyridine nucleotide biosynthesis; Hydrolase; Complete proteome.
SQ SEQUENCE 213 AA; 23362 MW; B9F8D946FA18433F CRC64;

Query Match 69.1%; Score 38; DB 1; Length 213;
Best Local Similarity 100.0%; Pred. No. 2.3; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

QY 4 NHGGSFAS 10
Db 57 NHGGSFAS 63
|||||

RESULT 3
Y4VH_RHISN STANDARD; PRT; 218 AA.
ID Y4VH_RHISN
AC Q53216;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Hypothetical 24.6 kDa protein Y4VH.
GN Y4VH.
OS Rhizobium sp. (strain NGR234).
OG Plasmid sym pNGR234a.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=394;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97305956; PubMed=9163424;
RA Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,

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RA Perret X.;
RT "Molecular basis of symbiosis between Rhizobium and legumes.";
RL Nature 387:394-401(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96389014; PubMed=8796346;
RA Freiberg C., Perret X., Broughton W.J., Rosenthal A.;
RT "Sequencing the 500-kb GC-rich symbiotic replicon of Rhizobium sp.
RN NGR234 using dye terminators and a thermostable 'sequenase': a
RT beginning.";
RL Genome Res. 6:590-600(1996).
CC -1- SIMILARITY: NONE OBVIOUS.
CC -----
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CC -----
DR EMBL: 268203; CAAG2423.1; -.
DR EMBL: AF000101; AAB91896.1; -.
KW Hypothetical protein; Plasmid.
SQ SEQUENCE 218 AA; 24594 MW; 501C6CB38A09A2E5 CRC64;

Query Match 65.5%; Score 36; DB 1; Length 218;
Best Local Similarity 66.7%; Pred. No. 5.9;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARNHGSFA 9
DB 68 ARDNHGSYS 76

RESULT 4
FATB_VIBAN
ID FATB_VIBAN STANDARD; PRT; 322 AA.
AC P11460;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ferric anguibactin-binding protein precursor.
FATB.
OS Vibrio anguillarum (Listonella anguillarum).
OG Plasmid pJMI.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Listonella.
OX NCBI_TaxID=55601;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=775;
RX MEDLINE=88139336; PubMed=2830268;
RA Actis L.A., Tolmasky M.E., Farrell D.H., Crosa J.H.;
RT "Genetic and molecular characterization of essential components of
RT the Vibrio anguillarum plasmid-mediated iron-transport system.";
RL J. Biol. Chem. 263:2853-2860(1988).
RN [2]
RP SEQUENCE OF 1-154 FROM N.A.
RC STRAIN=775;
RX MEDLINE=92084677; PubMed=1748657;
RA Koester W.L., Actis L.A., Waldbeser L.S., Tolmasky M.E., Crosa J.H.;
RT "Molecular characterization of the iron transport system mediated by
RT the pJMI plasmid in Vibrio anguillarum 775.";
RL J. Biol. Chem. 266:23829-23833(1991).
CC -1- FUNCTION: BINDS FERRIC ANGUIBACTIN; PART OF THE BINDING-PROTEIN-
CC DEPENDENT TRANSPORT SYSTEM FOR UPTAKE OF FERRIC ANGUIBACTIN.
CC -1- SUBCELLULAR LOCATION: Attached to the inner membrane by a lipid
CC anchor (potential).
CC -1- SIMILARITY: BELONGS TO THE BACTERIAL EXTRACELLULAR SOLUTE-BINDING
CC PROTEIN FAMILY 8.
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CC -----
DR EMBL: J03529; AAA91580.1; -.
DR EMBL: M74068; AA225643.1; ALT_INIT.
PIR: A29928; A29928.
DR InterPro: IPR002491; Peripla_BP.
DR Pfam: PF01497; Peripla_BP_2; 1.
DR PROSITE: PS00113; PROKAR_LIPOPROTEIN; 1.
KW Transport; Iron transport; Signal; Inner membrane; Lipoprotein;
KW Plasmid.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 322 FERRIC ANGUIBACTIN-BINDING PROTEIN.
FT LIPID 23 23 N-ACYL DIGLYCERIDE (POTENTIAL).
SQ SEQUENCE 322 AA; 35635 MW; FB6674ED5CF73F7 CRC64;

Query Match 65.5%; Score 36; DB 1; Length 322;
Best Local Similarity 75.0%; Pred. No. 8.9;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNHGSFAS 10
DB 203 HNHGSFSS 210

RESULT 5
CCSA_LOTJA
ID CCSA_LOTJA STANDARD; PRT; 323 AA.
AC Q9BBP4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cytochrome c biogenesis protein ccsa.
GN CCSA.
OS Lotus japonicus.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Lotaeae; Lotus.
OX NCBI_TaxID=34305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Accession MG-20;
RX MEDLINE=21082929; PubMed=11214967;
RA Kato T., Kaneko T., Sato S., Nakamura Y., Tabata S.;
RT "Complete structure of the chloroplast genome of a legume, Lotus
RT japonicus.";
RL DNA Res. 7:323-330(2000).
CC -1- FUNCTION: REQUIRED DURING CYTOCHROME BIOGENESIS AT THE STEP OF
CC HEME ATTACHMENT (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CCMF/CYCK/CCL/NRFE/CCSA FAMILY.
CC -----
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CC -----
DR EMBL: AP002983; BAB33244.1; -.
DR InterPro: IPR002541; CytC_asm.
DR Pfam: PF01578; CytC_asm; 1.
KW Cytochrome c-type biogenesis; Chloroplast.
SQ SEQUENCE 323 AA; 37185 MW; 5A034E3E2829FE35 CRC64;

Query Match 65.5%; Score 36; DB 1; Length 323;
Best Local Similarity 75.0%; Pred. No. 8.9;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

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QY      3 HHNGSFAS 10
DB      315 HHNGSFAS 322

RESULT 6
SYE2_RICPR
ID SYE2_RICPR STANDARD; PRT; 470 AA.
AC Q9ZCT8;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Glutamyl-tRNA synthetase 2 (EC 6.1.1.17) (Glutamate--trna ligase 2)
DE (GluRS 2).
GN GLTX2 OR PG623.
OS Rickettsia prowazekii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=782;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Madrid E;
RX MEDLINE=99039499; PubMed=9823893;
RA Andersson S.G.E., Zomorodipour A., Andersson J.O., Naeslund A.K.,
RA Sticheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Kurland C.G.;
RT "The genome sequence of Rickettsia prowazekii and the origin of
RT mitochondria.";
RL Nature 396:133-140(1998).
CC -I- CATALYTIC ACTIVITY: ATP + L-glutamate + tRNA(Glu) = AMP +
CC diphosphate + L-glutamyl-tRNA(Glu).
CC -I- SUBUNIT: MONOMER (BY SIMILARITY).
CC -I- SUBCELLULAR LOCATION: Cytoplasmic.
CC -I- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
CC -----
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CC -----
DR EMBL; AJ235272; CAA15066.1; -.
DR HSSP; P27000; 1GLN.
DR InterPro; IPR004527; Gltx_bact.
DR InterPro; IPR000924; Glu_trna-synt_lc.
DR InterPro; IPR001412; trna-synt_I.
DR Pfam; PF00749; trna-synt_lc; 1.
DR PRINTS; PR00987; TRNASYNTHGLU.
DR TIGRFAMS; TIGR00464; gltx_bact; 1.
DR PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
KW Complete proteome.
FT SITE 10 20 "HIGH" REGION.
FT SITE 239 243 "KMSKS" REGION.
FT BINDING 242 242 ATP (BY SIMILARITY).
SQ SEQUENCE 470 AA; 53696 MW; DFCE50A20B8A9FD CRC64;

Query Match 65.5%; Score 36; DB 1; Length 470;
Best Local Similarity 75.0%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARNHGFSF 8
DB 31 ARHNGGKF 38
||||:|

RESULT 7
SYE_AQUAE
ID SYE_AQUAE STANDARD; PRT; 473 AA.
AC O67271;
DT 30-MAY-2000 (Rel. 39, Created)

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DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Glutamyl-tRNA synthetase (EC 6.1.1.17) (Glutamate--trna ligase)
DE (GluRS).
GN GLTX OR AQ_1221.
OS Aquifex aeolicus.
OC Bacteria; Aquificae; Aquificae (class); Aquificales; Aquificaceae;
OC Aquifex.
OX NCBI_TaxID=63363;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VF5;
RX MEDLINE=98196666; PubMed=9537320;
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Sneed M.A., Keller M., Aufay M., Huber R.,
RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus.";
RL Nature 392:353-358(1998).
CC -I- CATALYTIC ACTIVITY: ATP + L-glutamate + tRNA(Glu) = AMP +
CC diphosphate + L-glutamyl-tRNA(Glu).
CC -I- SUBUNIT: MONOMER (BY SIMILARITY).
CC -I- SUBCELLULAR LOCATION: Cytoplasmic.
CC -I- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
CC -----
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CC -----
DR EMBL; AE000729; AAC07230.1; -.
DR HSSP; P27000; 1GLN.
DR InterPro; IPR004527; Gltx_bact.
DR InterPro; IPR000924; Glu_trna-synt_lc.
DR InterPro; IPR001412; trna-synt_I.
DR Pfam; PF00749; trna-synt_lc; 1.
DR PRINTS; PR00987; TRNASYNTHGLU.
DR TIGRFAMS; TIGR00464; gltx_bact; 1.
DR PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
KW Complete proteome.
FT SITE 10 20 "HIGH" REGION.
FT SITE 242 246 "KMSKS" REGION.
FT BINDING 245 245 ATP (BY SIMILARITY).
SQ SEQUENCE 473 AA; 55121 MW; 5CB4D1590973E07A CRC64;

Query Match 65.5%; Score 36; DB 1; Length 473;
Best Local Similarity 75.0%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARNHGFSF 8
DB 31 ARHNGGKF 38
||||:|

RESULT 8
EGGS_FASHE
ID EGGS_FASHE STANDARD; PRT; 197 AA.
AC P07915;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Putative eggshell protein precursor.
OS Fasciola hepatica (Liver fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
OC Echinostomida; Echinostomata; Fascioloidae; Fasciolidae; Fasciola.
OX NCBI_TaxID=6192;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87175670; PubMed=3470798;

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RA Zurita M., Bieher D., Ringold G., Mansour T.E.;
RT "Cloning and characterization of a female genital complex cDNA from
RL the liver fluke Fasciola hepatica.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:2340-2344 (1987).
CC -----
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CC -----
DR EMBL: M15871; AAA29138.1; -.
KW Eggshell; Signal.
FT SIGNAL 1
FT CHAIN 18 197 PUTATIVE EGGSHELL PROTEIN.
SQ SEQUENCE 197 AA; 22470 MW; 72033ED203FC1A3E CRC64;

Query Match 63.68; Score 35; DB 1; Length 197;
Best Local Similarity 75.0%; Pred. No. 8.2;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARNHGSF 8
DB 17 ARHPHGKF 24

RESULT 9
NCAP_CVHOC STANDARD; PRT; 448 AA.
AC P33469;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE Nucleocapsid protein.
GN N.
OS Human coronavirus (strain OC43).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=31631;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89243809; PubMed=2541577;
RA Kamahora T., Soe L.H., Lai M.M.C.;
RT "Sequence analysis of nucleocapsid gene and leader RNA of human
RT coronavirus OC43.";
RL Virus Res. 12:1-9(1989).
DR PIR; A60003; A60003.
DR InterPro; IPR001218; Corona_nucleocap.
DR Pfam; PF00937; Corona_nucleoca; 1.
KW Nucleocapsid.
SQ SEQUENCE 448 AA; 49316 MW; 5193AB1AE0D75626 CRC64;

Query Match 63.68; Score 35; DB 1; Length 448;
Best Local Similarity 85.7%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNHGSF 8
DB 103 RHNRGSF 109

RESULT 10
CC45_XENLA STANDARD; PRT; 567 AA.
AC Q9YH26;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CDC45-related protein.
GN CDC45.
OS Xenopus laevis (African clawed frog).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8335;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98429493; PubMed=9755170;
RA Mimura S., Takisawa H.;
RT "Xenopus Cdc45-dependent loading of DNA polymerase alpha onto
RT chromatin under the control of S-phase Cdk.";
RL EMBO J. 17:5699-5707(1998).
CC -!- FUNCTION: REQUIRED FOR INITIATION OF CHROMOSOMAL DNA REPLICATION.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: BELONGS TO THE CDC45 FAMILY.
CC -----
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CC -----
DR EMBL: AF062494; AAC67520.1; -.
DR InterPro; IPR003874; CDC45_like.
DR Pfam; PF02724; CDC45; 1.
KW DNA replication; Cell cycle; Nuclear protein.
SQ SEQUENCE 567 AA; 65444 MW; 9A32FB20097F7C86 CRC64;

Query Match 63.68; Score 35; DB 1; Length 567;
Best Local Similarity 71.4%; Pred. No. 25;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARNHGGS 7
DB 251 SRNHGHN 257

RESULT 11
KSYK_RAT STANDARD; PRT; 629 AA.
ID KSYK_RAT
AC Q64725;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tyrosine-protein kinase SYK (EC 2.7.1.112) (Spleen tyrosine kinase).
GN SYK.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95279402; PubMed=7759516;
RA Rowley R.B., Bolen J.B., Fargnoli J.;
RT "Molecular cloning of rodent p72Syk. Evidence of alternative mRNA
RT splicing.";
RL J. Biol. Chem. 270:12659-12664(1995).
CC -!- FUNCTION: MAY PARTICIPATE IN SIGNALING PATHWAYS. PLAYS A ROLE IN
CC LYMPHOCYTE ACTIVATION.
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; SYKA AND SYKB (SHOWN HERE);
CC ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -!- PTM: AUTOPHOSPHORYLATED (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SYK/ZAP-
CC 70 SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 2 SH2 DOMAINS.
CC -----
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CC EMBL: U21684; AAA75167.1; -;
 CC EMBL: U21683; AAA75166.1; -;
 CC HSPSP; P43405; IAB1.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam: PF00017; SH2; 2.
 DR Pfam: PF00069; pkinase; 1.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR ProDom: PD000001; Euk_pkinase; 1.
 DR ProDom: PD000093; SH2; 2.
 DR SMART; SM00252; SH2; 2.
 DR SMART; SM00219; TyKc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00001; SH2; 2.
 DR Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
 KW SH2 domain; Repeat; Alternative splicing.
 FT DOMAIN 14 106
 FT DOMAIN 167 258
 FT DOMAIN 365 625
 FT NP_BIND 371 379 ATP (BY SIMILARITY).
 FT BINDING 396 396 ATP (BY SIMILARITY).
 FT ACT_SITE 488 488 BY SIMILARITY.
 FT MOD_RES 519 519 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT VARSPLOC 277 299 MISSING (IN ISOFORM SYKA).
 SQ SEQUENCE 629 AA; 71528 MW; 81169A643EC6A6FE CRC64;

Query Match 63.6%; Score 35; DB 1; Length 629;
 Best Local Similarity 77.8%; Pred. No. 28;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARNHGSFA 9
 ||| |
 DB 195 ARDNGSFA 203

RESULT 12

PBPI_YEAST
 ID PBPI_YEAST STANDARD; PRT; 722 AA.
 AC P53297;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE PAB1-binding protein 1.
 GN PBPI OR MRS16 OR YGR178C.
 OS Saccharomyces cerevisiae (Baker's yeast).
 CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hebling U., Hofmann B., Delli H.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DY747;
 RA Mecklenbrauker I.;
 RT "Sequencing and characterization of a suppressor of the pet- phenotype
 RT in a Saccharomyces cerevisiae strain without mitochondrial group II
 RT introns.";
 RL Thesis (1996), Vienna Biocentre, Austria.
 [3]
 RP CHARACTERIZATION.
 RX MEDLINE=99038243; PubMed=9819425;
 RA Mangus D.A., Amrani N., Jacobson A.;
 RT "Pb1p, a factor interacting with Saccharomyces cerevisiae poly(A)-
 RT binding protein, regulates polyadenylation.";

RL Mol. Cell. Biol. 18:7383-7396(1998).
 CC -!- FUNCTION: APPEARS TO PROMOTE PROPER POLYADENYLATION. IN THE
 CC ABSENCE OF PB1P, THE 3'TERMINI OF PRE-MRNAS ARE PROPERLY CLEAVED
 CC BUT LACK FULL-LENGTH POLY(A) TAILS. MAY ACT TO REPRESS THE ABILITY
 CC OF PAB1 TO NEGATIVELY REGULATE POLYADENYLATION.
 CC -!- SUBUNIT: INTERACTS WITH PAB1.
 CC -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
 CC
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DR EMBL: 272963; CAA97204.1; -;
 DR EMBL: U46931; AB94294.1; -;
 DR SGD; S0003410; PBPI.
 KW Nuclear protein.
 SQ SEQUENCE 722 AA; 78781 MW; 92005F3A2346193E CRC64;

Query Match 63.6%; Score 35; DB 1; Length 722;
 Best Local Similarity 85.7%; Pred. No. 33;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNHGSF 8
 | | | | |
 DB 474 RHNHGSF 480

RESULT 13

YNB9_YEAST
 ID YNB9_YEAST STANDARD; PRT; 284 AA.
 AC P53975;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Hypothetical 31.3 kDa protein in HDAL-PUB1 intergenic region
 DE precursor.
 GN YNL019C OR N2827.
 OS Saccharomyces cerevisiae (Baker's yeast).
 CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Andre B., Iraqui Houssaini I., Urrestarazu L.A., Vissers S.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: TO YEAST YNL033W.

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DR EMBL: 271295; CAA95881.1; -;
 DR SGD; S0004964; YNL019C.
 KW Hypothetical protein; Signal.
 FT SIGNAL 1 24 POTENTIAL.
 FT CHAIN 25 284 HYPOTHETICAL PROTEIN YNL019C.
 FT CARBOHYD 270 270 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 284 AA; 31326 MW; 0AD5E3495B2B284 CRC64;

Query Match 61.8%; Score 34; DB 1; Length 284;
 Best Local Similarity 55.6%; Pred. No. 19;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARNHGSFA 9
 | | | | |

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Db 194 SHNHGSGS 202

RESULT 14
YND3_YEAST
ID YND3_YEAST STANDARD; PRT; 284 AA.
AC P33964;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Hypothetical 31.4 kDa protein in NCE3-HHT2 intergenic region
DE precursor.
GN YNL033W OR N2743.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Dueterhoeft A., Floeth M., Fritz C., Heuss-Neitzel D.,
RA Hilbert H., Moestl D.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO YEAST YNL019C.
CC -----
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CC -----
CC EMBL; Z71309; CAA95896.1; -.
DR SGD; S0004978; YNL033W.
KW Hypothetical protein; Signal.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 284 HYPOTHETICAL PROTEIN YNL033W.
FT CARBOHYD 270 270 N-LINKED (GLCNAC...)(POTENTIAL).
SQ SEQUENCE 284 AA; 31386 MW; 18C45E3495B2A395 CRC64;

Query Match 61.8%; Score 34; DB 1; Length 284;
Best Local Similarity 55.6%; Pred. No. 19;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARNHGSPA 9
: ||||| :
Db 194 SHNHGSGS 202

RESULT 15
SYE_LISIN
ID SYE_LISIN STANDARD; PRT; 491 AA.
AC Q92F38;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Glutamyl-tRNA synthetase (EC 6.1.1.17) (Glutamate--tRNA ligase)
DE (Glurs).
GN GLTX OR LIN0269.
OS Listeria innocue.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1642;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CLIP 11262 / Serovar 6a;
RX MEDLINE=21537279; PubMed=11679669;
RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetoui F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkai G.,
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RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordsiek G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
CC -!- CATALYTIC ACTIVITY: ATP + L-glutamate + tRNA(Glu) = AMP +
CC diphosphate + L-glutamyl-tRNA(Glu).
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO CLASS-I AMINOCYL-TRNA SYNTHETASE FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AL596164; CAC95502.1; -.
DR ListList; LIN00269; -.
DR InterPro; IPR004527; GLTX_bact.
DR InterPro; IPR000924; Glu.tRNA-synt_1c.
DR InterPro; IPR001412; tRNA-synt_1.
DR Pfam; PF00749; tRNA-synt_1c; 1.
DR TIGRFAMs; TIGR00464; gltx_bact; 1.
DR PROSITE; PS00178; AA.tRNA_LIGASE-I; 1.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
KW Complete proteome.
FT SITE 13 23 "HIGH" REGION.
FT SITE 254 258 "KMSKS" REGION.
FT BINDING 257 257 ATP (BY SIMILARITY).
SQ SEQUENCE 491 AA; 56003 MW; B94060A6A7AC9760 CRC64;

Query Match 61.8%; Score 34; DB 1; Length 491;
Best Local Similarity 75.0%; Pred. No. 34;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARNHGSGF 8
: ||||| :
Db 34 ARHNDGDF 41

Search completed: November 18, 2002, 17:51:40
Job time : 6.39474 secs
```

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:40:56 ; Search time 22.3684 Seconds
(without alignments)
92.115 Million cell updates/sec

Title: US-09-016-061-94
Perfect score: 55
Sequence: 1 ARNHGSFAS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. Is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	39	70.9	593	5 Q8T5L2	Q8T5L2 anopheles g
2	38	69.1	219	16 Q8XDW3	Q8XDW3 escherichia
3	38	69.1	225	16 Q8UDQ5	Q8UDQ5 agrobacteri
4	38	69.1	839	10 Q9LIE5	Q9LIE5 arabidopsis
5	38	69.1	1108	10 Q9FNQ7	Q9FNQ7 arabidopsis
6	37	67.3	227	5 Q9VNI9	Q9VNI9 drosophila
7	37	67.3	326	16 Q9RJG3	Q9RJG3 streptomyce
8	37	67.3	710	2 Q8VPE6	Q8VPE6 enterococcu
9	37	67.3	731	2 Q93699	Q93699 escherichia
10	37	67.3	2075	13 Q90WA4	Q90WA4 fugu rubrip
11	36	65.5	85	7 Q95HR7	Q95HR7 peromyscus
12	36	65.5	89	7 Q19495	Q19495 gallus gall
13	36	65.5	360	3 Q05791	Q05791 saccharomyc
14	36	65.5	444	2 Q9AKB5	Q9AKB5 rickettsia
15	35	63.6	134	10 Q8S4F4	Q8S4F4 areca catec
16	35	63.6	161	5 Q9VZ39	Q9VZ39 drosophila

17	35	63.6	233	16 Q9KRA6	Q9KRA6 vibrio chol
18	35	63.6	272	5 Q24950	Q24950 fasciola he
19	35	63.6	272	5 Q24951	Q24951 fasciola he
20	35	63.6	276	7 Q9GJN0	Q9GJN0 calman croc
21	35	63.6	305	10 Q8RUD9	Q8RUD9 glycine max
22	35	63.6	446	5 Q62086	Q62086 caenorhabdi
23	35	63.6	615	11 Q63614	Q63614 rattus norv
24	35	63.6	762	5 Q9GYL2	Q9GYL2 caenorhabdi
25	35	63.6	782	5 Q8T029	Q8T029 drosophila
26	35	63.6	825	5 Q8T3U6	Q8T3U6 drosophila
27	35	63.6	1291	5 Q77261	Q77261 drosophila
28	35	63.6	1300	5 Q9W5E0	Q9W5E0 drosophila
29	34	61.8	39	7 P79474	P79474 cervus elap
30	34	61.8	39	7 P79477	P79477 cervus elap
31	34	61.8	39	7 P79478	P79478 cervus elap
32	34	61.8	39	7 P79479	P79479 cervus elap
33	34	61.8	67	7 Q8SP02	Q8SP02 hapalemur g
34	34	61.8	76	7 Q9TPC2	Q9TPC2 macaca mula
35	34	61.8	82	7 Q19287	Q19287 macaca mula
36	34	61.8	82	7 Q19288	Q19288 macaca mula
37	34	61.8	82	7 Q9MXN1	Q9MXN1 macaca mula
38	34	61.8	82	7 Q9TPC9	Q9TPC9 callicebus
39	34	61.8	82	7 Q30606	Q30606 macaca mula
40	34	61.8	82	7 Q30608	Q30608 macaca mula
41	34	61.8	82	7 Q30637	Q30637 macaca mula
42	34	61.8	82	7 Q30638	Q30638 macaca mula
43	34	61.8	82	7 Q30658	Q30658 macaca mula
44	34	61.8	82	7 Q30659	Q30659 macaca mula
45	34	61.8	82	7 Q30666	Q30666 macaca mula

ALIGNMENTS

RESULT 1

Q8T5L2 ID Q8T5L2 PRELIMINARY; PRT; 593 AA.
AC Q8T5L2;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative transcription factor.
GN 4F11.4.
OS Anopheles gambiae (African malaria mosquito).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
OC Anopheles.
OX NCBI_TaxID=7165;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Thomasova D., Ton L.O., Collins F.H., Kafatos F.C.;
RT "Sequencing and analysis of Pen1 region from Anopheles gambiae
chromosome 2R.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ438610; CAD27476.1; -
SQ SEQUENCE 593 AA; 63339 MW; 65CFED4BC35B148F CRC64;

Query Match 70.9%; Score 39; DB 5; Length 593;
Best Local Similarity 60.0%; Pred. No. 37;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARNHGSFAS 10

Db 573 ARNHGSFAS 582
| | | | | | | | | |

RESULT 2

Q8XDW3 ID Q8XDW3 PRELIMINARY; PRT; 219 AA.
AC Q8XDW3;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Oxf, hypothetical protein.
GN YDJB OR Z2802 OR ECS2475.
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OX Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfal G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamoukis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7";
RL Nature 409:529-533(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
O157:H7 and genomic comparison with a laboratory strain K-12";
RL DNA Res. 8:11-22(2001).
DR EMBL; AE005399; AGS56755.1; -;
DR EMBL; AP002558; BAB35898.1; -;
DR InterPro; IPR000868; Isochorismatase.
DR Pfam; PF00857; Isochorismatase; 1.
KW Complete proteome.
SQ SEQUENCE 219 AA; 24013 MW; 8FE31AD452414A3B CRC64;
Query Match 69.1%; Score 38; DB 16; Length 219;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 NHGSFAS 10
DB 63 NHGSFAS 69
RESULT 3
ID Q8UDQ5 PRELIMINARY; PRT; 225 AA.
AC Q8UDQ5;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Pyrazinamidase/nicotinamidase.
GN PNCB OR ATU2066 OR AGR_C.3739.
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=176299;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608550; PubMed=11743193;
RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
RA Chen Y., Paulsen I.F., Elsen J.A., Karp P.D., Bovee D. Str.,
RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
RA Kutayavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA Humphrey F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA Nester E.W.;
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens

C58."; RT
Science 294:2317-2323(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608551; PubMed=11743194;
RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
RA Ourlo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
RA Houmlel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
RA Wollan C., Allinger M., Dougherty D., Scott C., Lappas C., Markelz B.,
RA Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
RA Cielo C., Slater S.;
RT "Genome sequence of the plant pathogen and biotechnology agent
Agrobacterium tumefaciens C58.";
RL Science 294:2323-2328(2001).
DR EMBL; AE009157; AAL43057.1; ALT_INIT.
DR EMBL; AE008123; AAK87817.1; -;
KW Complete proteome.
SQ SEQUENCE 225 AA; 24555 MW; 663C29F0A32C32CD CRC64;
Query Match 69.1%; Score 38; DB 16; Length 225;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 NHGSFAS 10
DB 70 NHGSFAS 76
RESULT 4
ID Q9LIE5 PRELIMINARY; PRT; 839 AA.
AC Q9LIE5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Far-red impaired response protein, mutator-like transposase-like
DE protein, phytochrome A signaling protein-like.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=COLUMBIA;
RX MEDLINE=20363099; PubMed=10907853;
RA Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.
Sequence features of the regions of 4,251,695 bp covered by ninety pl,
TAC and BAC clones";
RL DNA Res. 7:217-221(2000).
DR EMBL; AP001306; BAB03065.1; -;
DR InterPro; IPR004330; FARL.
DR InterPro; IPR001000; Glyco_hydro_10.
DR Pfam; PF03101; FARL; 1.
DR PROSITE; PS00591; GLYCOSYL_HYDROL_F10; UNKNOWN_1.
SQ SEQUENCE 839 AA; 95996 MW; CBBF60DF8B6797F8 CRC64;
Query Match 69.1%; Score 38; DB 10; Length 839;
Best Local Similarity 75.0%; Pred. No. 82;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 ARNHGGSF 8
DB 274 SRHNYGSP 281
RESULT 5

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Q9FN07
ID Q9FN07 PRELIMINARY; PRT; 1108 AA.
AC Q9FN07;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Similarity to histone deacetylase.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=98069011; PubMed=9405937;
RA Kotani H., Nakamura Y., Sato S., Kaneko T., Asamizu E., Miyajima N.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. II.
RT Sequence features of the regions of 1,044,062 bp covered by thirteen
RT physically assigned pl clones.";
RL DNA Res. 4:291-300(1997).
DR EMBL; AB006696; BAB10370.1;
DR InterPro; IPR000286; His.deacetylase.
DR Pfam; PF00850; Hist.deacetyl; 2.
DR PRINTS; PR01270; HDASUPER.
SQ SEQUENCE 1108 AA; 123609 MW; 9BCF5A2BCD90A1E2 CRC64;

Query Match 69.1%; Score 38; DB 10; Length 1108;
Best Local Similarity 85.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHNGSF 8
Db 255 RHDSGF 261

RESULT 6
Q9VNI9
ID Q9VNI9 PRELIMINARY; PRT; 227 AA.
AC Q9VNI9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE CG2023 protein.
GN CG2023.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abriel J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballwey R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Bouchan M.R., Bouck J., Brockstein P., Brotter P.,
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,

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RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL; AE003601; AAF51945.1;
DR FlyBase; FBgn0037383; CG2023.
SQ SEQUENCE 227 AA; 25695 MW; 768718C22AE7C60E CRC64;

Query Match 67.3%; Score 37; DB 5; Length 227;
Best Local Similarity 70.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARNHGSFAS 10
Db 126 ARHNGSLVS 135

RESULT 7
Q9RJG3
ID Q9RJG3 PRELIMINARY; PRT; 326 AA.
AC Q9RJG3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative araC family transcriptional regulator.
GN SC00471 OR SCF76.11.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Murphy L., Harris D.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=97000351; PubMed=8843436;
RA Redenbach M., Kieser H.M., Denapaita D., Eichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL Mol. Microbiol. 21:77-96(1996).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,

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RA Rabbinitzsch E., Rajandream M.A., Rutherford K., Rutter S.,
 RA Seger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete Streptomyces
 RT coelicolor A3(2).";
 RL Nature 417:141-147(2002).
 CC -1- SIMILARITY: BELONGS TO THE ARAC/XLXS FAMILY OF TRANSCRIPTIONAL
 CC REGULATORS.
 DR EMBL: AL2121600; CAB56731.1; -.
 DR InterPro: IPR000005; HTHAcAc.
 DR Pfam: PF00165; HTH_Arac; 2.
 DR SMART: SM00342; HTH_ARAC; 1.
 DR PROSITE: PS01124; HTH_ARAC_FAMILY_2; 1.
 KW DNA-binding; Transcription regulation.
 SQ SEQUENCE 326 AA; 34425 MW; 2FEF5346ACAC80D6 CRC64;
 Query Match 67.3%; Score 37; DB 16; Length 326;
 Best Local Similarity 85.7%; Pred. No. 48;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 RHNGHSF 8
 Db 85 RHNGHSF 91
 ID Q8VPE6 PRELIMINARY; PRT; 710 AA.
 AC Q8VPE6;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Transferable copper resistance protein TcrB.
 GN TCRB.
 OS Enterococcus faecium (Streptococcus faecium).
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
 OC Enterococcaceae; Enterococcus.
 OC NCBI_TaxID=1352;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AL7SV1;
 RA Hasman H., Aarestrup F.M.;
 RT "A novel gene conferring transferable copper resistance from
 RT Enterococcus faecium: occurrence, transferability and linkage to
 RT macrolide and glycopeptide resistance.";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY048044; AAL05407.1; -.
 DR InterPro: IPR001757; ATPase_E1-E2.
 DR InterPro: IPR001454; Hlgnase/hydrilase.
 DR Pfam: PF00122; E1-E2_ATPase; 1.
 DR Pfam: PF00702; Hydrilase; 1.
 DR PRINTS: PR00119; CATATPASE.
 DR PROSITE: PS00154; ATPASE_E1_E2; UNKNOWN_1.
 DR SEQUENCE 710 AA; 76237 MW; 14AC9CC5080FAD7A CRC64;
 Query Match 67.3%; Score 37; DB 2; Length 710;
 Best Local Similarity 75.0%; Pred. No. 11e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ARNHGSF 8
 Db 67 ARNHGSF 74
 ID Q59369 PRELIMINARY; PRT; 731 AA.
 AC Q59369;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Histidine rich p type ATPase.

GN HRA-1.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95110304; PubMed=7811248;
 RA Trenor C.C., Lin W., Andrews N.C.;
 RT "Novel bacterial p-type ATPases with histidine-rich heavy-metal-
 RT associated sequences.";
 RL Biochem. Biophys. Res. Commun. 205:1644-1650(1994).
 DR EMBL: U16658; AAA62113.1; -.
 DR InterPro: IPR001757; ATPase_E1-E2.
 DR InterPro: IPR001454; Hlgnase/hydrilase.
 DR Pfam: PF00122; E1-E2_ATPase; 1.
 DR Pfam: PF00702; Hydrilase; 1.
 DR PROSITE: PS00154; ATPASE_E1_E2; UNKNOWN_1.
 KW Hydrolyase; Transmembrane; Phosphorylation; ATP-binding.
 FT MOD_RES 431 431 PHOSPHORYLATION (PROBABLE).
 SQ SEQUENCE 731 AA; 78453 MW; 06237F155E151F0D CRC64;
 Query Match 67.3%; Score 37; DB 2; Length 731;
 Best Local Similarity 75.0%; Pred. No. 11e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ARNHGSF 8
 Db 88 ARNHGSF 95
 ID Q90WA4 PRELIMINARY; PRT; 2075 AA.
 AC Q90WA4;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Pericentriolar material 1 protein.
 GN PCMI.
 OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontidae; Takifugu.
 OX NCBI_TaxID=31033;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=OVARY;
 RA Bolland D.J., van Geel M., Carim Todd L., Beck A.F., Grewal P.K.,
 RA van der Maarel S., Frants R.R., de Jong P.J., Hewitt J.E.;
 RT "Comparative sequence analysis of an evolutionary chromosomal
 RT breakpoint in human, mouse and Fugu rubripes.";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF389403; AAK69357.1; -.
 SQ SEQUENCE 2075 AA; 229612 MW; 88A27A058F15045B CRC64;
 Query Match 67.3%; Score 37; DB 13; Length 2075;
 Best Local Similarity 77.8%; Pred. No. 3.2e+02;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 RHNGHSF 10
 Db 941 RHNGSLAS 949
 ID Q95HR7 PRELIMINARY; PRT; 85 AA.
 AC Q95HR7;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)

```

DE MHC class II antigen beta chain (Fragment).
GN PEWA-EB.
OS Peromyscus maniculatus (Deer mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Peromyscus.
OX NCBI_TaxID=10042;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SQPM17C;
RA Richman A.D., Herrera L.G., Nash D.;
RT "MHC Class II Beta Sequence Diversity in the Deermouse (Peromyscus
maniculatus): Implications for Models of Balancing Selection.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF312758; AAK98038.1; -.
DR InterPro; IPR000353; MHC_II_beta.
DR Pfam; PF00969; MHC_II_beta; 1.
DR ProDom; PD000328; MHC_II_beta; 1.
DR Glycoprotein; MHC; MHC II; Transmembrane.
FT NON_TER 1
FT NON_TER 85
SQ SEQUENCE 85 AA; 10332 MW; 2A9DC62670E938B3 CRC64;

Query Match 65.5%; Score 36; DB 7; Length 85;
Best Local Similarity 66.7%; Pred. No. 18;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RHNGSFAS 10
Db 71 KHHGVFDS 79

RESULT 12
O19495 PRELIMINARY; PRT; 89 AA.
ID O19495
AC O19495;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II beta 1 domain (Fragment).
GN B-LBI.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=15.151-5; TISSUE=BURSA;
RX MEDLINE=98179131; PubMed=9510552;
RA Pharr G.T., Dodgson J.B., Hunt H.D., Bacon L.D.;
RT "Class II MHC cDNAs in 1515 B-congenic chickens.";
RL Immunogenetics 47:350-354(1998).
DR EMBL; U91532; AAC15813.1; -.
DR InterPro; IPR000353; MHC_II_beta.
DR Pfam; PF00969; MHC_II_beta; 1.
DR ProDom; PD000328; MHC_II_beta; 1.
DR Glycoprotein; MHC II; Transmembrane.
FT NON_TER 1
FT NON_TER 89
SQ SEQUENCE 89 AA; 10724 MW; BC7D558B6AEB1379 CRC64;

Query Match 65.5%; Score 36; DB 7; Length 89;
Best Local Similarity 66.7%; Pred. No. 19;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RHNGSFAS 10
Db 75 RHNYGDFES 83

RESULT 13
Q05791 PRELIMINARY; PRT; 360 AA.
ID Q05791;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Chromosome XII COSMID 8167.
GN CDC123 OR L8167.23 OR YLR215C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=97313267; PubMed=9169871;
RA Johnston M., Hillier L., Riles L., Dubois E., Dusterhoft A.,
RA Benes V., Bruckner M., Delius H., Dubois E., Dusterhoft A.,
RA Entian K.D., Floeth M., Goffeau A., Hebling U., Heumann K.,
RA Heuss-Neitzel D., Hilbert H., Hilger F., Kiehn K., Kotter P.,
RA Louis E.J., Messenguy F., Mewes H.W., Miosga T., Mostl D.,
RA Muller-Auer S., Nentwich U., Obermaier B., Piravandi E., Pohl T.M.,
RA Portetelle D., Putnelle B., Reckmann S., Rieger M., Rinke M., Rose M.,
RA Scharfe M., Scherens B., Scholler P., Schwager C., Schwarz S.,
RA Underwood A.P., Urrestarazu L.A., Vandenbol M., Verhasselt P.,
RA Vierendeels F., Voet M., Voickaert G., Voss H., Wambutt R., Weoler E.,
RA Wedler H., Zimmermann F.K., Zollner A., Hani J., Hoheisel J.D.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XII.";
RL Nature 387:0-0(0).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RA Pauley A.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RA Waterston R.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RA Cherry J.M.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14913; AAB67444.1; -.
DR SGD; S0004205; CDC123
SQ SEQUENCE 360 AA; 41852 MW; 61CCC9DCEAF1197 CRC64;

Query Match 65.5%; Score 36; DB 3; Length 360;
Best Local Similarity 77.8%; Pred. No. 81;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RHNGSFAS 10
Db 304 RHNTGRFAS 312

RESULT 14
Q9AKB5 PRELIMINARY; PRT; 444 AA.
ID Q9AKB5;
AC Q9AKB5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Glutamyl-tRNA synthetase (Fragment).
GN GLTX2.
OS Rickettsia typhi.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=785;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WILMINGTON;
RX MEDLINE=21219194; PubMed=11319266;

```

RA Andersson J.O., Andersson S.G.E.;
 RT "Pseudogenes, junk DNA and the dynamics of Rickettsia genomes.";
 RL Mol. Biol. Evol. 18:829-839(2001).
 DR EMBL; AJ293325; CAC33753.1; -.
 DR HSSP; P27000; IGLN.
 DR InterPro; IPR004527; GltX_bact.
 DR InterPro; IPR000924; Glu_trna-synt_lc.
 DR Pfam; PF00749; tRNA-synt_lc; 1.
 DR PRINTS; PR00987; TRNASYNTHGLU.
 DR TIGRFAMS; TIGR00464; gltX_bact; 1.
 KW Aminoacyl-tRNA synthetase.
 FT NON_TER 1
 SQ SEQUENCE 444 AA; 50791 MW; FF00E12E10FD6FCB CRC64;

Query Match 65.5%; Score 36; DB 2; Length 444;
 Best Local Similarity 75.0%; Pred. NO. 1e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNHGSF 8
 ||||:|
 Db 6 ARHNNGKF 13

RESULT 15

Q8S4F4
 ID Q8S4F4 PRELIMINARY; PRT; 134 AA.
 AC Q8S4F4;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Malate synthase (EC 4.1.3.2) (Fragment).
 OS Areca catechu.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Arecaceae; Arecoideae;
 OC Arecaeae; Arecinae; Areca.
 OX NCBI_TaxID=184783;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lewis C.E., Doyle J.J.;
 RT "A phylogenetic analysis of palm tribe Areceae using two low-copy
 RT nuclear genes.";
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF455572; AAL99506.1; -.
 KW Lyase.
 FT NON_TER 1
 FT NON_TER 134
 SQ SEQUENCE 134 AA; 15539 MW; 3B866EC83B288E54 CRC64;

Query Match 63.6%; Score 35; DB 10; Length 134;
 Best Local Similarity 83.3%; Pred. NO. 45;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNHGSF 8
 ||||:|
 Db 45 HNHGTF 50

Search completed: November 18, 2002, 17:54:38
 Job time : 22.3684 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:31:45 ; Search time 29.3421 Seconds
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Title: US-09-016-061-94

Perfect score: 55

Sequence: 1 ARNHGSEFAS 10

Scoring table: BLOSUM62

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Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	55	100.0	10	19	AAW76037
2	55	100.0	10	22	AAW76037
3	51	92.7	10	19	AAW76020
4	51	92.7	10	22	AAW76038
5	49	89.1	10	19	AAW76037
6	49	89.1	10	19	AAW76024
7	49	89.1	10	22	AAW76038
8	49	89.1	10	22	AAW76038
9	46	83.6	10	19	AAW76025
10	46	83.6	10	19	AAW76030

11	46	83.6	10	22	AAW76037	Mutant VH CDR3 pep
12	46	83.6	10	22	AAW76037	Mutant VH CDR3 pep
13	45	81.8	10	19	AAW76026	LM609 grafted anti
14	45	81.8	10	19	AAW76027	LM609 grafted anti
15	45	81.8	10	19	AAW76028	LM609 grafted anti
16	45	81.8	10	19	AAW76029	LM609 grafted anti
17	45	81.8	10	19	AAW76010	LM609 grafted anti
18	45	81.8	10	22	AAW76038	LM609 VH CDR3 pep
19	45	81.8	10	22	AAW76038	Mutant VH CDR3 pep
20	45	81.8	10	22	AAW76038	Mutant VH CDR3 pep
21	45	81.8	10	22	AAW76038	Mutant VH CDR3 pep
22	45	81.8	10	22	AAW76038	Mutant VH CDR3 pep
23	45	81.8	117	19	AAW76001	Vitaxin antibody h
24	45	81.8	117	19	AAW76003	LM609 antibody hea
25	45	81.8	117	20	AAW76038	Murine monoclonal
26	45	81.8	117	20	AAW76038	Humanised LM609 an
27	45	81.8	117	22	AAW76038	A heavy chain vari
28	45	81.8	117	22	AAW76038	A heavy chain vari
29	45	81.8	117	22	AAW76038	Vitaxin heavy chai
30	45	81.8	117	22	AAW76038	Antibody LM609 hea
31	45	81.8	118	20	AAW76038	Humanised LM609 an
32	45	81.8	118	20	AAW76038	Humanised LM609 an
33	45	81.8	118	20	AAW76038	Humanised LM609 an
34	45	81.8	118	20	AAW76038	Humanised LM609 an
35	45	81.8	130	20	AAW76038	Murine monoclonal
36	43	78.2	10	19	AAW76040	LM609 grafted anti
37	43	78.2	10	22	AAW76038	Multiple mutant VH
38	42	76.4	10	19	AAW76021	LM609 grafted anti
39	42	76.4	10	22	AAW76038	Mutant VH CDR3 pep
40	41	74.5	10	19	AAW76039	LM609 grafted anti
41	41	74.5	10	19	AAW76022	LM609 grafted anti
42	41	74.5	10	19	AAW76023	LM609 grafted anti
43	41	74.5	10	22	AAW76038	Mutant VH CDR3 pep
44	41	74.5	10	22	AAW76038	Mutant VH CDR3 pep
45	41	74.5	10	22	AAW76038	Multiple mutant VH

ALIGNMENTS

RESULT 1

AAW76037
ID AAW76037 standard; Protein; 10 AA.

XX AC AAW76037;

XX DT 02-NOV-1998 (first entry)

XX DE LM609 grafted antibody V-H region CDR3 protein fragment #13.

XX KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
XX KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
XX KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
XX KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
XX KW macular degeneration; osteoporosis; primer; V-H region; CDR;
XX KW complementarity determining region.

XX OS Mus SP.

XX PN WO9833919-A2.

XX PD 06-AUG-1998.

XX PF 30-JAN-1998; 98WO-US01826.

XX PR 30-JAN-1997; 97US-0791391.

XX PA (IXSY-) IXSYS INC.

XX PI Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

DR N-PSDB; AAW49874.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT Integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
XX
XX Claim 62; Page 43; 129pp; English.
XX
XX AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
CC antibodies contain non-murine framework regions so are suitable for use
CC in humans. Enhanced types of LM609 have affinity more than 90 times
CC greater than that of parent the parent antibody.
XX
XX Sequence 10 AA;
SQ
Query Match 100.0%; Score 55; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00076;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ARHNHGSFAS 10
DB 1 ARHNHGSFAS 10
|||||
RESULT 2
AAB61395
ID AAB61395 standard; peptide; 10 AA.
XX
XX AAB61395;
XX
XX 03-APR-2001 (first entry)
XX
XX Multiple mutant VH CDR3 #1.
XX
XX LM609; grafted antibody; alphavbeta3 integrin; angiogenesis;
KW inflammatory; cancer; retina; restenosis; osteoporosis.
XX
XX Unidentified.
XX
XX WO200078815-A1.
XX
XX 28-DEC-2000.
XX
XX 23-JUN-2000; 2000WO-US17454.
XX
XX 24-JUN-1999; 99US-0339922.
XX
XX (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX
XX Huse WD, Wu H;
XX
XX WPI; 2001-050110/06.
XX
XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
PT osteoporosis -
XX
XX Disclosure; Page 42; 132pp; English.
XX
XX The present invention relates to enhanced LM609 grafted antibodies
CC exhibiting selective binding affinity to alphavbeta3 integrin or
CC their functional fragments. The antibodies or their functional
CC fragments can be used in the diagnosis and treatment of
CC alphavbeta3-mediated diseases such as angiogenesis, inflammatory

CC diseases (such as psoriasis and chronic articular rheumatism),
CC disorders associated with inappropriate or inopportune invasion of
CC vessels (such as diabetic retinopathy, neovascular glaucoma and
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
CC diseases (such as macular degeneration), restenosis and
CC osteoporosis.
XX
XX Sequence 10 AA;
SQ
Query Match 100.0%; Score 55; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00076;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ARHNHGSFAS 10
DB 1 ARHNHGSFAS 10
|||||
RESULT 3
AAW76020
ID AAW76020 standard; Protein; 10 AA.
XX
XX AAW76020;
XX
XX 02-NOV-1998 (first entry)
XX
XX LM609 grafted antibody V-H region CDR3 protein fragment #2.
XX
XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
XX
XX Mus sp.
XX
XX WO9833919-A2.
XX
XX 06-AUG-1998.
XX
XX 30-JAN-1998; 98WO-US01826.
XX
XX 30-JAN-1997; 97US-0791391.
XX
XX (IXSY-) IXSYS INC.
XX
XX Glaser SM, Huse WD;
XX
XX WPI; 1998-437472/37.
XX
XX N-PSDB; AAV49857.
XX
XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
XX Claim 62; Page 41; 129pp; English.
XX
XX AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
CC antibodies contain non-murine framework regions so are suitable for use
CC in humans. Enhanced types of LM609 have affinity more than 90 times
CC greater than that of parent the parent antibody.
XX
XX Sequence 10 AA;
SQ

Query Match 92.7%; Score 51; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0041;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARNHGSA 9
 DB 1 ARNHGSA 9

RESULT 4
 AAB61378
 ID AAB61378 standard; peptide; 10 AA.

XX AAB61378;

XX 03-APR-2001 (first entry)

XX Mutant VH CDR3 peptide #1.

XX LM609; grafted antibody; alphaVbeta3 integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis.

XX Unidentified.

XX WO200078815-A1.

XX 28-DEC-2000.

XX 23-JUN-2000; 2000WO-US17454.

XX 24-JUN-1999; 99US-0339922.

XX (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX Huse WD, Wu H;

XX WPI; 2001-050110/06.

XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -

XX Disclosure; Page 41; 132pp; English.

XX The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphaVbeta3 integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphaVbeta3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.

XX Sequence 10 AA;

Query Match 92.7%; Score 51; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0041;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARNHGSA 9
 DB 1 ARNHGSA 9

RESULT 5
 AAW76038
 ID AAW76038 standard; Protein; 10 AA.

AC AAW76038;
 DT 02-NOV-1998 (first entry)
 DE LM609 grafted antibody V-H region CDR3 protein fragment #14.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.

XX Mus sp.

XX WO9833919-A2.

XX 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

XX Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

XX N-PSDB; AAV49875.

XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

XX Claim 62; Page 43; 129pp; English.

XX AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphaVbeta3 and can be used to
 CC inhibit binding of alphaVbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphaVbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
 CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
 CC antibodies contain non-murine framework regions so are suitable for use
 CC in humans. Enhanced types of LM609 have affinity more than 90 times
 CC greater than that of parent the parent antibody.

XX Sequence 10 AA;

Query Match 89.1%; Score 49; DB 19; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.0097;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARNHGSA 10

DB 1 ARNHGSA 10

RESULT 6

AAW76024

XX AAW76024 standard; Protein; 10 AA.

XX AAW76024;

XX 02-NOV-1998 (first entry)

XX LM609 grafted antibody V-H region CDR3 protein fragment #6.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;

KW LM609; inhibitor; integrin-mediated signal transduction; treatment;

KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.

XX Mus sp.

XX W09833919-A2.

XX 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

XX Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

XX N-PSDB; AAV49861.

XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

XX Claim 62; Page 41; 129pp; English.

XX AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
 CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
 CC antibodies contain non-murine framework regions so are suitable for use
 CC in humans. Enhanced types of LM609 have affinity more than 90 times
 CC greater than that of parent the parent antibody.

XX Sequence 10 AA;

Query Match 89.1%; Score 49; DB 19; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.0097;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNHGSFAS 10

Db 1 ARHNHGSFAS 10

||||:|||||

RESULT 7

AAB61382

ID AAB61382 standard; peptide: 10 AA.

XX AAB61382;

XX 03-APR-2001 (first entry)

XX Mutant VH CDR3 peptide #5.

KW LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
 KW Inflammatory; cancer; retina; restenosis; osteoporosis.

XX Unidentified.

XX W0200078815-A1.

XX 28-DEC-2000.

XX 23-JUN-2000; 2000WO-US17454.

XX 24-JUN-1999; 99US-0339922.
 XX (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX Huse WD, Wu H;

XX WPI; 2001-050110/06.

XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -

XX Disclosure; Page 41; 132pp; English.

XX The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphavbeta_3 integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.

XX Sequence 10 AA;

Query Match 89.1%; Score 49; DB 22; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.0097;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNHGSFAS 10

Db 1 ARHNHGSFAS 10

||||:|||||

RESULT 8

AAB61396

ID AAB61396 standard; peptide: 10 AA.

XX AAB61396;

XX 03-APR-2001 (first entry)

XX Multiple mutant VH CDR3 #2.

KW LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
 KW Inflammatory; cancer; retina; restenosis; osteoporosis.

XX Unidentified.

XX W0200078815-A1.

XX 28-DEC-2000.

XX 23-JUN-2000; 2000WO-US17454.

XX 24-JUN-1999; 99US-0339922.

XX (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX Huse WD, Wu H;

XX WPI; 2001-050110/06.

XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -


```
Query Match      83.6%; Score 46; DB 19; Length 10;
Best Local Similarity 80.0%; Pred. No. 0.035; 0; Indels 0; Gaps 0;
Matches 8; Conservative 2; Mismatches 0;

QY 1 ARNHGSPAS 10
    ||||:||||:
DB 1 ARHNYGSFAA 10

RESULT 11
AAB61383
ID AAB61383 standard; peptide; 10 AA.
XX
AC AAB61383;
XX
XX 03-APR-2001 (first entry)
XX
DE Mutant VH CDR3 peptide #6.
XX
XX LM609; grafted antibody; alphaVbeta_3 integrin; angiogenesis;
KW inflammatory; cancer; retina; restenosis; osteoporosis.
XX
OS Unidentified.
XX
PN WO200078815-A1.
XX
PD 28-DEC-2000.
XX
PF 23-JUN-2000; 2000WO-US17454.
XX
PR 24-JUN-1999; 99US-0339922.
XX
PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX
PI Huse WD, Wu H;
XX
DR WPI; 2001-050110/06.
XX
XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
PT osteoporosis -
XX
PS Disclosure; Page 41; 132pp; English.
XX
XX The present invention relates to enhanced LM609 grafted antibodies
CC exhibiting selective binding affinity to alphaVbeta_3 integrin or
CC their functional fragments. The antibodies or their functional
CC fragments can be used in the diagnosis and treatment of
CC alphaVbeta_3-mediated diseases such as angiogenesis, inflammatory
CC diseases (such as psoriasis and chronic articular rheumatism),
CC disorders associated with inappropriate or inopportune invasion of
CC vessels (such as diabetic retinopathy, neovascular glaucoma and
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
CC diseases (such as macular degeneration), restenosis and
XX osteoporosis.
XX
PS Sequence 10 AA;
XX
XX Query Match      83.6%; Score 46; DB 22; Length 10;
XX Best Local Similarity 80.0%; Pred. No. 0.035; 0; Indels 0; Gaps 0;
XX Matches 8; Conservative 2; Mismatches 0;

QY 1 ARNHGSPAS 10
    ||||:||||:
DB 1 ARHNYGSFAT 10

RESULT 12
AAB61388
ID AAB61388 standard; peptide; 10 AA.
XX
AC AAB61388;
XX
XX Query Match      83.6%; Score 46; DB 22; Length 10;
XX Best Local Similarity 80.0%; Pred. No. 0.035; 0; Indels 0; Gaps 0;
XX Matches 8; Conservative 2; Mismatches 0;

QY 1 ARNHGSPAS 10
    ||||:||||:
DB 1 ARHNYGSFAT 10

RESULT 13
AAW76026
ID AAW76026 standard; Protein; 10 AA.
XX
AC AAW76026;
XX
XX 02-NOV-1998 (first entry)
XX
XX LM609 grafted antibody V-H region CDR3 protein fragment #8.
XX
XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
XX
OS Mus sp.
XX
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```
XX
DT 03-APR-2001 (first entry)
XX
DE Mutant VH CDR3 peptide #11.
XX
XX LM609; grafted antibody; alphaVbeta_3 integrin; angiogenesis;
KW inflammatory; cancer; retina; restenosis; osteoporosis.
XX
XX Unidentified.
XX
PN WO200078815-A1.
XX
PD 28-DEC-2000.
XX
PF 23-JUN-2000; 2000WO-US17454.
XX
PR 24-JUN-1999; 99US-0339922.
XX
PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX
PI Huse WD, Wu H;
XX
DR WPI; 2001-050110/06.
XX
XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
PT osteoporosis -
XX
PS Disclosure; Page 41; 132pp; English.
XX
XX The present invention relates to enhanced LM609 grafted antibodies
CC exhibiting selective binding affinity to alphaVbeta_3 integrin or
CC their functional fragments. The antibodies or their functional
CC fragments can be used in the diagnosis and treatment of
CC alphaVbeta_3-mediated diseases such as angiogenesis, inflammatory
CC diseases (such as psoriasis and chronic articular rheumatism),
CC disorders associated with inappropriate or inopportune invasion of
CC vessels (such as diabetic retinopathy, neovascular glaucoma and
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
CC diseases (such as macular degeneration), restenosis and
XX osteoporosis.
XX
PS Sequence 10 AA;
XX
XX Query Match      83.6%; Score 46; DB 22; Length 10;
XX Best Local Similarity 80.0%; Pred. No. 0.035; 0; Indels 0; Gaps 0;
XX Matches 8; Conservative 2; Mismatches 0;

QY 1 ARNHGSPAS 10
    ||||:||||:
DB 1 ARHNYGSFAA 10

RESULT 13
AAW76026
ID AAW76026 standard; Protein; 10 AA.
XX
AC AAW76026;
XX
XX 02-NOV-1998 (first entry)
XX
XX LM609 grafted antibody V-H region CDR3 protein fragment #8.
XX
XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
XX
OS Mus sp.
XX
```

PA WO9833919-A2.
 XX 06-AUG-1998.
 PI 30-JAN-1998; 98WO-US01826.
 XX 30-JAN-1997; 97US-0791391.
 XX (IXSY-) IXSYS INC.
 XX Glaser SM, Huse WD;
 PI WPI: 1998-437472/37.
 DR N-PSDB; AAV49863.
 XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX Claim 62; Page 41; 129pp; English.
 PS AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
 XX LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
 CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
 CC antibodies contain non-murine framework regions so are suitable for use
 CC in humans. Enhanced types of LM609 have affinity more than 90 times
 CC greater than that of parent the antibody.
 XX Sequence 10 AA;
 SQ Query Match 81.8%; Score 45; DB 19; Length 10;
 Best Local Similarity 88.9%; Pred. No. 0.053;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ARNHGSA 9
 DB 1 ARHNGSFA 9
 IIII:IIII
 RESULT 14
 AAW76027 standard; Protein; 10 AA.
 XX AAW76027;
 AC 02-NOV-1998 (first entry)
 XX LM609 grafted antibody V-H region CDR3 protein fragment #9.
 DE Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 XX LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 XX Mus sp.
 OS WO9833919-A2.
 XX 06-AUG-1998.
 PD 30-JAN-1998; 98WO-US01826.
 XX 30-JAN-1997; 97US-0791391.
 XX (IXSY-) IXSYS INC.
 PA Glaser SM, Huse WD;
 PI WPI: 1998-437472/37.
 DR N-PSDB; AAV49865.
 XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3

PA (IXSY-) IXSYS INC.
 XX Glaser SM, Huse WD;
 PI WPI: 1998-437472/37.
 DR N-PSDB; AAV49864.
 XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX Claim 62; Page 41; 129pp; English.
 PS AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
 XX LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
 CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
 CC antibodies contain non-murine framework regions so are suitable for use
 CC in humans. Enhanced types of LM609 have affinity more than 90 times
 CC greater than that of parent the antibody.
 XX Sequence 10 AA;
 SQ Query Match 81.8%; Score 45; DB 19; Length 10;
 Best Local Similarity 88.9%; Pred. No. 0.053;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ARNHGSA 9
 DB 1 ARHNGSFA 9
 IIII:IIII
 RESULT 15
 AAW76028 standard; Protein; 10 AA.
 XX AAW76028;
 AC 02-NOV-1998 (first entry)
 XX LM609 grafted antibody V-H region CDR3 protein fragment #10.
 DE Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 XX LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 XX Mus sp.
 OS WO9833919-A2.
 XX 06-AUG-1998.
 PD 30-JAN-1998; 98WO-US01826.
 XX 30-JAN-1997; 97US-0791391.
 XX (IXSY-) IXSYS INC.
 PA Glaser SM, Huse WD;
 PI WPI: 1998-437472/37.
 DR N-PSDB; AAV49865.
 XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3

PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT anglogenesis or restenosis
XX
XX Claim 62: Page 41; 129pp; English.
XX
XX AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
CC antibodies contain non-murine framework regions so are suitable for use
CC in humans. Enhanced types of LM609 have affinity more than 90 times
CC greater than that of parent the parent antibody.
XX
SQ Sequence 10 AA;

Query Match 81.8%; Score 45; DB 19; Length 10;
Best Local Similarity 88.9%; Pred. No. 0.053;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNHGSFA 9
| | | | |
Db 1 ARHNYGSFA 9

Search completed: November 18, 2002, 17:50:49
Job time : 29.3421 secs

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OM protein - protein search, using sw model

Run on: November 18, 2002, 18:45:22 ; Search time 4.60526 Seconds
(without alignments)
32.704 Million cell updates/sec

Title: US-09-016-061-94
Perfect score: 55
Sequence: 1 ARNHGSFAS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 97044 seqs, 15060890 residues

Total number of hits satisfying chosen parameters: 97044

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match %	Score	Length	ID	Description
1	45	81.8	117	8	US-08-790-540A-2
2	45	81.8	117	8	US-08-790-540A-6
3	45	81.8	117	8	US-08-791-391A-2
4	45	81.8	117	8	US-08-791-391A-6
5	38	69.1	196	10	US-09-741-669-368
6	38	69.1	196	10	US-09-912-020-376
7	38	69.1	554	10	US-09-981-649A-30
8	34	61.8	59	10	US-09-864-761-35802
9	34	61.8	482	10	US-09-815-242-4953
10	34	61.8	482	10	US-09-815-242-10940
11	33	60.0	181	10	US-09-734-017A-46
12	33	60.0	309	10	US-09-886-055-21
13	33	60.0	480	10	US-09-815-242-10999
14	32	58.2	29	10	US-09-864-761-34610
15	32	58.2	51	10	US-09-864-761-49074
16	32	58.2	59	10	US-09-864-761-48682
17	32	58.2	100	10	US-09-864-761-35983
18	32	58.2	189	9	US-09-992-738-1
19	32	58.2	299	9	US-09-992-598-213

Query Match 81.8%; Score 45; DB 8; Length 117;
Best Local Similarity 88.9%; Pred. No. 0.13;

ALIGNMENTS

RESULT 1
US-08-790-540A-2
; Sequence 2, Application US/08790540A
; Patent No. US2001001125A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; ; Sequence 2, Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,540A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-790-540A-2

20	58.2	299	10	US-09-989-723-213	Sequence 213, App
32	58.2	299	10	US-09-989-723-213	Sequence 213, App
21	58.2	299	10	US-09-989-723-213	Sequence 213, App
22	58.2	299	10	US-09-989-723-213	Sequence 213, App
23	58.2	299	10	US-09-989-723-213	Sequence 213, App
24	58.2	299	10	US-09-989-723-213	Sequence 213, App
25	58.2	299	10	US-09-989-723-213	Sequence 213, App
26	58.2	299	10	US-09-989-723-213	Sequence 213, App
27	58.2	299	10	US-09-989-723-213	Sequence 213, App
28	58.2	299	10	US-09-989-723-213	Sequence 213, App
29	58.2	299	10	US-09-989-723-213	Sequence 213, App
30	58.2	299	10	US-09-989-723-213	Sequence 213, App
31	58.2	299	10	US-09-989-723-213	Sequence 213, App
32	58.2	299	10	US-09-989-723-213	Sequence 213, App
33	58.2	299	10	US-09-989-723-213	Sequence 213, App
34	58.2	299	10	US-09-989-723-213	Sequence 213, App
35	58.2	299	10	US-09-989-723-213	Sequence 213, App
36	58.2	299	10	US-09-989-723-213	Sequence 213, App
37	58.2	299	10	US-09-989-723-213	Sequence 213, App
38	58.2	299	10	US-09-989-723-213	Sequence 213, App
39	58.2	299	10	US-09-989-723-213	Sequence 213, App
40	58.2	299	10	US-09-989-723-213	Sequence 213, App
41	58.2	299	10	US-09-989-723-213	Sequence 213, App
42	58.2	299	10	US-09-989-723-213	Sequence 213, App
43	58.2	299	10	US-09-989-723-213	Sequence 213, App
44	58.2	299	10	US-09-989-723-213	Sequence 213, App
45	58.2	299	10	US-09-989-723-213	Sequence 213, App

Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARNHGSPA 9
||||:||||
Db 97 ARHNGSFA 105

RESULT 2
US-08-790-540A-6
; Sequence 6, Application US/08790540A
; Patent No. US20010011125A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,540A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-790-540A-6

Query Match 81.8%; Score 45; DB 8; Length 117;
Best Local Similarity 80.9%; Pred. No. 0.13;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARNHGSPA 9
||||:||||
Db 97 ARHNGSFA 105

RESULT 3
US-08-791-391A-2
; Sequence 2, Application US/08791391A
; Patent No. US20010016645A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,391A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-391A-2

Query Match 81.8%; Score 45; DB 8; Length 117;
Best Local Similarity 88.9%; Pred. No. 0.13;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNGSFA 9
||||:||||
Db 97 ARHNGSFA 105

RESULT 4
US-08-791-391A-6
; Sequence 6, Application US/08791391A
; Patent No. US20010016645A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,391A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-391A-6

Query Match 81.8%; Score 45; DB 8; Length 117;
Best Local Similarity 88.9%; Pred. No. 0.13;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARNHGSFA 9
 |||||
DB 97 ARHNGSFA 105

RESULT 5
US-09-741-669-368
; Sequence 368, Application US/09741669
; Patent No. US20020022718A1
; GENERAL INFORMATION:
; APPLICANT: Forsyth, R. Allyn
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; TITLE OF INVENTION: Genes identified as required for
; TITLE OF INVENTION: proliferation of E. coli
; FILE REFERENCE: ELITRA.009A
; CURRENT APPLICATION NUMBER: US/09/741,669
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 60/173005
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 481
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 368
; LENGTH: 196
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-741-669-368

Query Match 69.1%; Score 38; DB 10; Length 196;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNHGSF 8
 |||||
DB 105 HNHGSF 110

RESULT 6
US-09-912-020-376
; Sequence 376, Application US/09912020
; Patent No. US20020045592A1
; GENERAL INFORMATION:
; APPLICANT: Zyskind, Judith
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Trawick, John
; APPLICANT: Forsyth, R. Allyn
; APPLICANT: Froelich, Jamie M.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION IN
; TITLE OF INVENTION: ESCHERICHIA COLI
; FILE REFERENCE: ELITRA.001DV1
; CURRENT APPLICATION NUMBER: US/09/912,020
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: 09/492,709
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 60/117,405
; PRIOR FILING DATE: 1999-01-27
; NUMBER OF SEQ ID NOS: 485
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 376
; LENGTH: 196
; TYPE: PRT
; ORGANISM: E. Coli
US-09-912-020-376

Query Match 69.1%; Score 38; DB 10; Length 196;

Best Local Similarity 100.0%; Pred. No. 4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNHGSF 8
 |||||
DB 105 HNHGSF 110

RESULT 7
US-09-981-649A-30
; Sequence 30, Application US/09981649A
; Patent No. US20020132250A1
; GENERAL INFORMATION:
; APPLICANT: Ford et al.
; TITLE OF INVENTION: EGF MOTIF PROTEIN, EGFL6, MATERIALS AND METHODS
; FILE REFERENCE: 28110/37665
; CURRENT APPLICATION NUMBER: US/09/981,649A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 09/687,860
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: US 09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US 09/363,316
; PRIOR FILING DATE: 1999-07-28
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 554
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-981-649A-30

Query Match 69.1%; Score 38; DB 10; Length 554;
Best Local Similarity 70.0%; Pred. No. 12;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNGSFAS 10
 |||||
DB 26 ARHHGLLAS 35

RESULT 8
US-09-864-761-35802
; Sequence 35802, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; FILE REFERENCE: Aeonica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30

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; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 35802
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC011307.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.2
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 11
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 3.8
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 17
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 9.3
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.7
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.8
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 56
; OTHER INFORMATION: EST_HUMAN HIT: AA970601.1, EVALUE 7.00e-18
; OTHER INFORMATION: SWISSPROT HIT: P27793, EVALUE 3.00e-01
US-09-864-761-35802
```

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Query Match 61.8%; Score 34; DB 10; Length 59;
Best Local Similarity 100.0%; Pred. No. 6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 4 NHGSFA 9
Db 16 NHGSFA 21
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```
RESULT 9
US-09-815-242-4953
; Sequence 4953, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10940
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
```

```
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4953
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-815-242-4953
```

```
Query Match 61.8%; Score 34; DB 10; Length 482;
Best Local Similarity 75.0%; Pred. No. 54;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```
Qy 1 ARNHGSF 8
Db 29 ARHNDGEF 36
```

```
RESULT 10
US-09-815-242-10940
; Sequence 10940, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10940
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-815-242-10940
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```
Query Match 61.8%; Score 34; DB 10; Length 491;
Best Local Similarity 75.0%; Pred. No. 55;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```
Qy 1 ARNHGSF 8
Db 37 ARHNDGEF 44
```

RESULT 11
US-09-734-017A-46
; Sequence 46, Application US/09734017A
; Patent No. US20020142422A1
; GENERAL INFORMATION:
; APPLICANT: Lerchl, Jens
; APPLICANT: Renz, Andreas
; APPLICANT: Ehrhardt, Thomas
; APPLICANT: Reindl, Andreas
; APPLICANT: Cirpus, Petra
; APPLICANT: Bischoff, Friedrich
; APPLICANT: Frank, Markus
; APPLICANT: Freund, Annette
; APPLICANT: Duwenig, Elke
; APPLICANT: Schmidt, Ralf-Michael
; TITLE OF INVENTION: Moss genes from Physcomitrella patens encoding proteins involved
; TITLE OF INVENTION: the
; TITLE OF INVENTION: synthesis of amino acids, vitamins, cofactors, nucleotides and
; TITLE OF INVENTION: nucleosides
; FILE REFERENCE: BASF-NAB-1331-99-US
; CURRENT APPLICATION NUMBER: US/09734, 017A
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/171,100
; PRIOR FILING DATE: 1999-12-16
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.1/WordPerfect
; SEQ ID NO 46
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Physcomitrella patens
US-09-734-017A-46

Query Match 60.0%; Score 33; DB 10; Length 182;
Best Local Similarity 70.0%; Pred. No. 29;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARNHGSEFAS 10
||| ||| |
DB 3 ARINNGSEGS 12

RESULT 12
US-09-886-055-21
; Sequence 21, Application US/09886055
; Patent No. US20020132273A1
; GENERAL INFORMATION:
; APPLICANT: STRYER, LUBERT
; APPLICANT: ZOZULYA, SERGEY
; TITLE OF INVENTION: RECEPTOR FINGERPRINTING, SENSORY PERCEPTION, AND
; TITLE OF INVENTION: BIOSENSORS OF CHEMICAL SENSANTS
; FILE REFERENCE: 078003-0277150
; CURRENT APPLICATION NUMBER: US/09/886, 055
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/213,812
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 522
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-886-055-21

Query Match 60.0%; Score 33; DB 10; Length 309;
Best Local Similarity 85.7%; Pred. No. 51;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 NHGSEFAS 10
||| ||| |
DB 268 NHGRFAS 274

RESULT 13
US-09-815-242-10999
; Sequence 10999, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10999
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-09-815-242-10999

Query Match 60.0%; Score 33; DB 10; Length 480;
Best Local Similarity 62.5%; Pred. No. 81;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNHGSEF 8
|:|:|:| |
DB 42 AKHNNGEF 49

RESULT 14
US-09-864-761-34610
; Sequence 34610, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aecomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 34610
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC007638.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 95
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.1
; OTHER INFORMATION: EST_HUMAN HIT: AW937180.1, EVALUATE 1.60e-01
; OTHER INFORMATION: SWISSPROT HIT: P36417, EVALUATE 3.70e+00
US-09-864-761-34610

Query Match 58.2%; Score 32; DB 10; Length 29;
Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 HNHGS 7
| | | | |
Db 16 HNHGS 20

RESULT 15
US-09-864-761-49074
; Sequence 49074, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04

; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 49074
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AP000035.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.71
; OTHER INFORMATION: EST_HUMAN HIT: BE747576.1, EVALUATE 2.20e+00
; OTHER INFORMATION: SWISSPROT HIT: P51882, EVALUATE 3.50e+00
US-09-864-761-49074

Query Match 58.2%; Score 32; DB 10; Length 51;
Best Local Similarity 66.7%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 2 RHNGSFAS 10
| | | | |
Db 7 RHSLSFCS 15

Search completed: November 18, 2002, 19:04:23
Job time : 5.60526 secs

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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:43:42 ; Search time 9.47368 Seconds
(without alignments)
31.058 Million cell updates/sec

Title: US-09-016-061-94

Perfect score: 55

Sequence: 1 ARNHGSPAS 10

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BLOSUM62

Gapop 10.0 , Gapext 0.5

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	38	69.1	213	2	US-08-655-821-16
2	34	61.8	94	3	US-09-147-550-14
3	34	61.8	94	3	US-09-147-550-45
4	34	61.8	94	3	US-09-147-550-48
5	34	61.8	94	3	US-09-147-550-77
6	34	61.8	94	3	US-09-147-550-84
7	34	61.8	94	3	US-09-147-550-90
8	34	61.8	94	3	US-09-147-550-101
9	34	61.8	94	4	US-09-557-917-14
10	34	61.8	94	4	US-09-557-917-45
11	34	61.8	94	4	US-09-557-917-48
12	34	61.8	94	4	US-09-557-917-77
13	34	61.8	94	4	US-09-557-917-84
14	34	61.8	94	4	US-09-557-917-90
15	34	61.8	94	4	US-09-557-917-101
16	34	61.8	99	4	US-09-199-637A-75
17	34	61.8	204	1	US-08-591-989-4
18	33	60.0	907	3	US-08-338-830-26
19	33	60.0	907	3	US-09-020-222-26
20	33	60.0	2109	4	US-08-646-695-6
21	33	60.0	2109	5	PCT-US96-06053-6
22	32	58.2	103	2	US-08-596-319-31
23	32	58.2	120	1	US-08-111-080-28
24	32	58.2	120	1	US-08-211-380-28
25	32	58.2	120	5	PCT-US93-07967-28
26	32	58.2	121	1	US-08-275-053-13
27	32	58.2	231	3	US-08-926-842B-20

28 32 58.2 231 4 US-09-172-952-32 Sequence 32, Appl
29 32 58.2 231 4 US-09-172-952-33 Sequence 33, Appl
30 32 58.2 238 4 US-09-172-952-18 Sequence 18, Appl
31 32 58.2 240 1 US-08-926-842B-21 Sequence 21, Appl
32 32 58.2 384 1 US-08-707-793A-5 Sequence 5, Appl
33 32 58.2 384 1 US-08-707-792A-5 Sequence 5, Appl
34 32 58.2 392 3 US-08-979-917A-2 Sequence 2, Appl
35 32 58.2 393 3 US-08-979-917A-3 Sequence 3, Appl
36 32 58.2 393 4 US-09-252-292C-23 Sequence 23, Appl
37 32 58.2 393 4 US-09-153-599A-11 Sequence 11, Appl
38 32 58.2 443 1 US-07-940-245-2 Sequence 2, Appl
39 32 58.2 443 1 US-08-226-486-2 Sequence 2, Appl
40 32 58.2 466 1 US-08-785-066-2 Sequence 2, Appl
41 32 58.2 466 3 US-09-007-355-2 Sequence 2, Appl
42 32 58.2 466 3 US-08-913-489-2 Sequence 2, Appl
43 32 58.2 479 4 US-09-134-001C-4128 Sequence 4128, Ap
44 32 58.2 536 2 US-08-551-211-3 Sequence 3, Appl
45 32 58.2 630 2 US-08-394-177-5 Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-08-655-821-16
; Sequence 16, Application US/08655821
; Patent No. 5846718
; GENERAL INFORMATION:
; APPLICANT: Zhang, Ying
; APPLICANT: Scorpio, Angelo
; TITLE OF INVENTION: IDENTIFICATION OF PYRAZINAMIDE-RESISTANT
; TITLE OF INVENTION: MYCOBACTERIA AND METHODS FOR TREATING
; TITLE OF INVENTION: MYCOBACTERIAL INFECTIONS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/655,821
; FILING DATE: 31-MAY-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ellison, Eldora L.
; REGISTRATION NUMBER: 39,967
; REFERENCE/DOCKET NUMBER: 07662/003001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 213 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-655-821-16

Query Match 69.1%; Score 38; DB 2; Length 213;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NHGSPAS 10

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DB 57 NHGSPAS 63

RESULT 2
US-09-147-550-14
; Sequence 14, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-14

Query Match 61.8%; Score 34; DB 3; Length 94;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNGSFAS 10
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DB 80 RHNGVFES 88

RESULT 3
US-09-147-550-45
; Sequence 45, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-45

Query Match 61.8%; Score 34; DB 3; Length 94;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNGSFAS 10
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DB 80 RHNGVFES 88

RESULT 4
US-09-147-550-48
; Sequence 48, Application US/09147550

; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-48

Query Match 61.8%; Score 34; DB 3; Length 94;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNGSFAS 10
|||:| | |
DB 80 RHNGVFES 88

RESULT 5
US-09-147-550-77
; Sequence 77, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 77
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-77

Query Match 61.8%; Score 34; DB 3; Length 94;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNGSFAS 10
|||:| | |
DB 80 RHNGVFES 88

RESULT 6
US-09-147-550-84
; Sequence 84, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550

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; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-84

Query Match          61.8%; Score 34; DB 3; Length 94;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RHNHGSFAS 10
Db 80 RHNHGVFES 88

RESULT 7
US-09-147-550-90
; Sequence 90, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 90
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-90

Query Match          61.8%; Score 34; DB 3; Length 94;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RHNHGSFAS 10
Db 80 RHNHGVFES 88

RESULT 8
US-09-147-550-101
; Sequence 101, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17

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; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-101

Query Match          61.8%; Score 34; DB 3; Length 94;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RHNHGSFAS 10
Db 80 RHNHGVFES 88

RESULT 9
US-09-557-917-14
; Sequence 14, Application US/09557917
; Patent No. 6284457
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-14

Query Match          61.8%; Score 34; DB 4; Length 94;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RHNHGSFAS 10
Db 80 RHNHGVFES 88

RESULT 10
US-09-557-917-45
; Sequence 45, Application US/09557917
; Patent No. 6284457
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933

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; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-45

Query Match 61.8%; Score 34; DB 4; Length 94;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNGSFAS 10
|||:| | |
Db 80 RHNYGVFES 88

RESULT 11
US-09-557-917-48
; Sequence 48, Application US/09557917
; Patent No. 6284457
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-48

Query Match 61.8%; Score 34; DB 4; Length 94;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNGSFAS 10
|||:| | |
Db 80 RHNYGVFES 88

RESULT 12
US-09-557-917-77
; Sequence 77, Application US/09557917
; Patent No. 6284457
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19

; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 77
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-77

Query Match 61.8%; Score 34; DB 4; Length 94;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNGSFAS 10
|||:| | |
Db 80 RHNYGVFES 88

RESULT 13
US-09-557-917-84
; Sequence 84, Application US/09557917
; Patent No. 6284457
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-84

Query Match 61.8%; Score 34; DB 4; Length 94;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNGSFAS 10
|||:| | |
Db 80 RHNYGVFES 88

RESULT 14
US-09-557-917-90
; Sequence 90, Application US/09557917
; Patent No. 6284457
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979

; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 90
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-90

Query Match 61.8%; Score 34; DB 4; Length 94;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHHGSPAS 10
| | | | |
Db 80 RHNYGVFES 88

RESULT 15
US-09-557-917-101
; Sequence 101, Application US/09557917
; Patent No. 628457
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-101

Query Match 61.8%; Score 34; DB 4; Length 94;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHHGSPAS 10
| | | | |
Db 80 RHNYGVFES 88

Search completed: November 18, 2002, 17:55:52
Job time : 9.47368 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:47:14 : Search time 10.6579 Seconds
(without alignments)
90.200 Million cell updates/sec

Title: US-09-016-061-96
Perfect score: 58
Sequence: 1 ARNHGFSYS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_73.*
1: p1r1.*
2: p1r2.*
3: p1r3.*
4: p1r4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	72.4	233	2 H82163	arginyl-trna-prote
2	40	69.0	555	2 T21028	hypothetical prote
3	39	67.2	350	2 S76212	hypothetical prote
4	39	67.2	470	2 H71667	glutamate-trna lig
5	38	65.5	191	2 F96634	hypothetical prote
6	38	65.5	195	2 G86742	conserved hypothet
7	38	65.5	196	2 H64968	acetyl CoA acetyl
8	38	65.5	722	2 S84432	hypothetical prote
9	37	63.8	530	2 T01030	hypothetical prote
10	37	63.8	547	2 T48551	fructosidase-like
11	37	63.8	573	2 A85357	receptor-like kina
12	37	63.8	731	1 J26454	probable copper-tr
13	37	63.8	849	2 E82038	GGDEF family prote
14	36	62.1	275	2 S75190	hypothetical prote
15	36	62.1	463	2 D98104	protein W10G11.19
16	36	62.1	473	2 D70405	glutamate-trna lig
17	36	62.1	547	2 AC0405	glutamate hydratase
18	36	62.1	548	1 B44511	fumarate hydratase
19	36	62.1	548	2 H91266	fumarate hydratase
20	36	62.1	548	2 E86107	hypothetical prote
21	36	62.1	778	2 D95912	probable membrane
22	35	60.3	86	2 A81873	hypothetical prote
23	35	60.3	108	2 C72852	AcOrf-19 protein -
24	35	60.3	108	2 D44221	orf4 protein - Aut
25	35	60.3	110	2 T41765	ACMNPV orf19 - Bom
26	35	60.3	113	2 S26468	1g heavy chain v r
27	35	60.3	272	2 S27819	vitelline B1 precu
28	35	60.3	272	2 S27820	vitelline B2 precu
29	35	60.3	349	2 S15011	mbh1 protein - mou

30	35	60.3	352	1 A39834	actin-capping prot
31	35	60.3	448	1 A60003	nucleocapsid prote
32	35	60.3	543	2 T27190	hypothetical prote
33	35	60.3	552	2 T27191	hypothetical prote
34	35	60.3	659	2 S30859	hypothetical prote
35	35	60.3	696	2 T48432	maturase-like prot
36	35	60.3	1466	2 T17138	CL1AA protein - ra
37	35	60.3	1467	2 T18411	latrophilin-1, bra
38	35	60.3	1471	2 T17149	CL1BA protein - ra
39	35	60.3	1472	2 T18413	latrophilin-1, bra
40	35	60.3	1510	2 T17145	CL1AB protein - ra
41	35	60.3	1515	2 T17156	CL1BB protein - ra
42	35	60.3	2470	2 I50726	cation-independent
43	34.5	59.5	308	2 E81288	hypothetical prote
44	34	58.6	139	2 G29380	1g heavy chain pre
45	34	58.6	140	2 I37782	1g variable region

ALIGNMENTS

RESULT 1
H82163
arginyl-trna-protein transferase-related protein VCL1736 [imported] - Vibrio cholerae
C:Species: Vibrio cholerae
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C:Accession: H82163
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers
I, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A>Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: H82163
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-233 <HEL>
A:Cross-References: GB:AE004251; GB:AE003852; NID:g9656248; PIDN:AAF94886.1; GSPDB:GN
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VCL1736
A:Map position: 1

Query Match 72.4%; Score 42; DB 2; Length 233;
Best Local Similarity 77.8%; Pred. No. 3 9;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARNHGFSY 9
||| ||| |
Db 117 ARHRHGSMY 125

RESULT 2
T21028
hypothetical protein F16H6.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T21028
R:Matthews, L.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z19362
A:Accession: T21028
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-555 <WIL>
A:Cross-References: EMBL:Z81506; PIDN:CAB04128.1; GSPDB:GN00023; CESP:F16H6.1
A:Experimental source: clone F16H6
C:Genetics:
A:Gene: CESP:F16H6.1
A:Map position: 5
A:Introns: 123/1; 318/3

Query Match 69.0%; Score 40; DB 2; Length 555;

Best Local Similarity 87.5%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 HHNGSFYS 10

|||||

Db 314 HNSGSFYS 321

RESULT 3

S76212

hypothetical protein - *Synechocystis* sp. (strain PCC 6803)

C:Species: *Synechocystis* sp.

A:Variety: PCC 6803

C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999

C:Accession: S76212

R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asanizu, E.; Nakamura, Y.; Miyajima, N.;

O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda

DNA Res. 3, 109-136, 1996

A:Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*

S.

A:Reference number: S74322; MUID:97061201; PMID:8905231

A:Accession: S76212

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-350 <KAN>

A:Cross-references: EMBL:D90914; GB:AB001339; NID:gl653477; PIDN:BAAL8471.1; PID:dl01920

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 67.2%; Score 39; DB 2; Length 350;

Best Local Similarity 71.4%; Pred. No. 20;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 HHNGSFY 9

|||||

Db 247 HHNGNY 253

RESULT 4

H71667

glutamate-tRNA ligase (EC 6.1.1.17) (gltX2) RP623 - *Rickettsia prowazekii*

C:Species: *Rickettsia prowazekii*

C:Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 03-Jun-2002

C:Accession: H71667

R:Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, U

Nature 396, 133-140, 1998

A:Title: The genome sequence of *Rickettsia prowazekii* and the origin of mitochondria.

A:Reference number: A71630; MUID:99039499; PMID:9823893

A:Accession: H71667

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-470 <AND>

A:Cross-references: GB:AJ235272; GB:AJ235269; NID:g3861033; PIDN:CAA15066.1; PID:g386116

A:Experimental source: strain Madrid E

C:Genetics:

A:Gene: gltX2; RP623

C:Superfamily: glutamate-tRNA ligase; glutamine-tRNA ligase homology

C:Keywords: aminocacyl-tRNA synthetase; ligase; protein biosynthesis

F;4-281/Domain: glutamine-tRNA ligase homology <EGL>

Query Match 67.2%; Score 39; DB 2; Length 470;

Best Local Similarity 66.7%; Pred. No. 26;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARNHGSFY 9

|||||

Db 31 ARHNGKFF 39

RESULT 5

F96634

hypothetical protein T7P1.6 [imported] - *Arabidopsis thaliana*

C:Species: *Arabidopsis thaliana* (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C:Accession: F96634

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maitl, R.; Marzia

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: F96634

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-191 <STO>

A:Cross-references: GB:AE005173; NID:g6751683; PIDN:AAF27666.1; GSPDB:GN00141

C:Genetics:

A:Gene: T7P1.6

A:Map position: 1

Query Match 65.5%; Score 38; DB 2; Length 191;

Best Local Similarity 75.0%; Pred. No. 16;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HHNGSFYS 10

|||||

Db 56 HSHASFS 63

RESULT 6

G86742

conserved hypothetical protein yjgF [imported] - *Lactococcus lactis* subsp. *lactis* (st

C:Species: *Lactococcus lactis* subsp. *lactis*

C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 17-May-2002

C:Accession: G86742

R:Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Eh

Genome Res. 11, 731-753, 2001

A:Title: The complete genome sequence of the lactic acid bacterium *Lactococcus lactis*

A:Reference number: A86625; MUID:21235186; PMID:11337471

A:Accession: G86742

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-195 <STO>

A:Cross-references: GB:AE005176; PID:g12723879; PIDN:AAK05041.1; GSPDB:GN00146

A:Experimental source: strain IL1403

C:Genetics:

A:Gene: yjgF

C:Superfamily: hypothetical protein b1011

Query Match 65.5%; Score 38; DB 2; Length 195;

Best Local Similarity 66.7%; Pred. No. 17;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARNHGSFY 9

|||||

Db 103 AKHNGAFY 111

RESULT 7

H64968

acetyl CoA acetyltransferase - *Escherichia coli* (strain K-12)

C:Species: *Escherichia coli*

C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002

C:Accession: H64968; I69646; I69656

R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;

.A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A:Title: The complete genome sequence of *Escherichia coli* K-12.

A:Reference number: A64720; MUID:97426617; PMID:9278503

A:Accession: H64968

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-196 <BLAT>
 A:Cross-references: GB:AB000294; GB:U00096; NID:g1788338; PIDN:AAC75094.1; PID:g1788345;
 A:Experimental source: strain K-12, substrain MG1655
 R:Yao, Z.; Valvano, M.A.
 J. Bacteriol. 176, 4133-4143, 1994
 A:Title: Genetic analysis of the O-specific lipopolysaccharide biosynthesis region (rfb) erythrogen Y and 4a.
 A:Reference number: 155053; MUID:94292434; PMID:7517390
 A:Accession: 169646
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-167, 'LFRKYCHC', 177-186, 'IMR', 190-196 <RES>
 A:Cross-references: EMBL:U03041; NID:g501028; PIDN:AAC31635.1; PID:g510256
 R:Stevenson, G.; Neal, B.; Liu, D.; Hobbs, M.; Packer, N.H.; Batley, M.; Redmond, J.W.;
 J. Bacteriol. 176, 4144-4156, 1994
 A:Title: Structure of the O antigen of *Escherichia coli* K-12 and the sequence of its rfb
 A:Reference number: 155054; MUID:94292435; PMID:7517391
 A:Accession: 169656
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-167, 'LFRKYCHC', 177-186, 'IMR', 190-196 <RE2>
 A:Cross-references: EMBL:U09876; NID:g508236; PID:g508245
 C:Genetics:
 A:Gene: yefH
 A:Map position: 45 min
 C:Superfamily: galactoside acetyltransferase
 Query Match 65.5%; Score 38; DB 2; Length 196;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 HHNGSF 8
 Db 105 HHNGSF 110
 RESULT 8
 S64492
 hypothetical protein YGR178c - yeast (*Saccharomyces cerevisiae*)
 N:Alternate names: hypothetical protein G7139
 C:Species: *Saccharomyces cerevisiae*
 C:Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 29-Oct-1999
 C:Accession: S64492
 R:Hebling, U.; Hofmann, B.; Delli, H.
 submitted to the Protein Sequence Database, May 1996
 A:Reference number: S64003
 A:Accession: S64492
 A:Molecule type: DNA
 A:Residues: 1-722 <HEB>
 A:Cross-references: EMBL:Z72963; NID:g1323314; PIDN:CAA97204.1; PID:g243559; PID:g132331
 A:Experimental source: strain S288C
 C:Genetics:
 A:Gene: SGD:PBPI
 A:Cross-references: SGD:S0003410; MIPS:YGR178c
 A:Map position: 7R
 Query Match 65.5%; Score 38; DB 2; Length 722;
 Best Local Similarity 75.0%; Pred. No. 60;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 RHNGSPFY 9
 Db 474 RHNGSPFY 481
 RESULT 9
 T01030
 hypothetical protein YUP8H12R.13 - *Arabidopsis thaliana*
 C:Species: *Arabidopsis thaliana* (mouse-ear cress)
 C:Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 22-Oct-1999
 C:Accession: T01030
 R:Theologis, A.; Vysotskaya, V.S.; Osborne, B.I.; Schwartz, J.R.; Federspiel, N.A.; Kwan
 Oefner, P.; Davis, R.W.

submitted to the EMBL Data Library, May 1998
 A:Description: *Arabidopsis thaliana* chromosome 1 YAC YUP8H12R sequence.
 A:Reference number: Z14227
 A:Accession: T01030
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-530 <THE>
 A:Cross-references: EMBL:AC002986; NID:g2494106; PID:g3152559; GSPDB:GN00059; ATSP:YU
 C:Genetics:
 A:Gene: ATSP:YUP8H12R.13
 A:Map position: 1
 A:Introns: 37/3; 77/1; 100/3; 219/3; 380/3; 451/3; 499/3
 Query Match 63.8%; Score 37; DB 2; Length 530;
 Best Local Similarity 62.5%; Pred. No. 67;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 3 HHNGSPFY 10
 Db 192 HHNNYYS 199
 RESULT 10
 T48551
 fructosidase-like protein - *Arabidopsis thaliana*
 N:Alternate names: protein F14F18.90
 C:Species: *Arabidopsis thaliana* (mouse-ear cress)
 C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 19-May-2000
 C:Accession: T48551
 R:Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancro
 submitted to the Protein Sequence Database, April 2000
 A:Reference number: Z24490
 A:Accession: T48551
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-547 <BEV>
 A:Cross-references: EMBL:AL163812
 A:Experimental source: cultivar Columbia; BAC clone F14F18
 C:Genetics:
 A:Map position: 5
 A:Introns: 31/1; 319/3; 373/3; 453/2; 483/3
 A:Note: F14F18.90
 C:Superfamily: beta-fructofuranosidase
 Query Match 63.8%; Score 37; DB 2; Length 547;
 Best Local Similarity 55.6%; Pred. No. 69;
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 QY 2 RHNGSPFY 10
 Db 275 RYDHGTFFA 283
 RESULT 11
 A85357
 receptor-like kinase homolog [imported] - *Arabidopsis thaliana*
 C:Species: *Arabidopsis thaliana* (mouse-ear cress)
 C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
 C:Accession: A85357
 R:anonymous, The European Union *Arabidopsis* Genome Sequencing Consortium, The Cold Sp
 Nature 402, 769-777, 1999
 A:Title: Sequence and analysis of chromosome 4 of the plant *Arabidopsis thaliana*.
 A:Reference number: A85001; MUID:20083488; PMID:10617198
 A:Accession: A85357
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-573 <STO>
 A:Cross-references: GB:NC_001268; NID:g7269953; PIDN:CAB79770.1; GSPDB:GN00140
 C:Genetics:
 A:Gene: At4g30520
 A:Map position: 4
 Query Match 63.8%; Score 37; DB 2; Length 573;

```
Best Local Similarity 66.7%; Pred. No. 72;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARHNHGSFY 9
   | | | | |
Db 508 ASHNSHFY 516

RESULT 12
JC2464
probable copper-transporting ATPase (EC 3.6.1.-) HRA-1 - Enterobacteriaceae spp.
C:Species: Enterobacteriaceae spp.
C:Date: 16-Oct-1998 #sequence_revision 16-Oct-1998 #text_change 18-Jun-1999
C:Accession: JC2464
R:Trenor III., C.; Lin, W.; Andrews, N.C.
Biochem. Biophys. Res. Commun. 205, 1644-1650, 1994
A:Title: Novel bacterial P-type ATPases with histidine-rich heavy-metal-associated sequence
A:Reference number: JC2464; MUID:95110304; PMID:7811248
A:Accession: JC2464
A:Molecule type: mRNA
A:Residues: 1-731 <TR>
A:Cross-references: GB:U16658; NID:9643612; PIDN:AAAG2113.1; PID:9643613
A:Experimental source: human small intestine cDNA library
A:Note: the source species is uncertain; the cloned sequence did not hybridize with human
C:Superfamily: Enterococcus copper-transporting ATPase copB; ATPase nucleotide-binding domain
C:Keywords: ATP; copper transport; hydrolase; ion transport; phosphoprotein; transmembrane
F:7-92/Region: His-rich
F:135-477/Domain: ATPase transduction domain homology <ATT>
F:544-685/Domain: ATPase nucleotide-binding domain homology <ATN>
F:287/Active site: Glu #status predicted
F:431/Active site: Asp (aspartylphosphate intermediate) #status predicted

Query Match 63.8%; Score 37; DB 1; Length 731;
Best Local Similarity 75.0%; Pred. No. 91;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNHGSF 8
   | | | | |
Db 88 AHHHGSF 95

RESULT 13
EG2038
GGDEF family protein VC2750 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C:Accession: EG2038
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
L., R.K.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: AB2035; MUID:20406833; PMID:10952301
A:Accession: EG2038
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-849 <HEI>
A:Cross-references: GB:AE004340; GB:AE003852; NID:g9657344; PIDN:AAF95889.1; GSPDB:GN001
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC2750
A:Map position: 1

Query Match 63.8%; Score 37; DB 2; Length 849;
Best Local Similarity 70.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARHNHGSFYS 10
   | | | | |
Db 572 AEHTHISFYS 581

RESULT 14
```

```
S75190
hypothetical protein sir2042 - Synechocystis sp. (strain PCC 6803)
C:Species: Synechocystis sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C:Accession: S75190
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima,
O., K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocys
s.
A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S75190
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-275 <KAN>
A:Cross-references: EMBL:D90903; GB:AB001339; NID:gl652127; PIDN:BAAL7104.1; PID:gl65
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 62.1%; Score 36; DB 2; Length 275;
Best Local Similarity 62.5%; Pred. No. 53;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNHGSFY 9
   : | | | | |
Db 253 QHNHGQLY 260

RESULT 15
D88104
protein W10G11.19 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C:Accession: D88104
R:Anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating bio
A:Reference number: A75000; MUID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/projects/C-
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999;
A:Accession: D88104
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-463 <STO>
A:Cross-references: GB:chr_II; PIDN:AB95082.1; PID:g2746940; GSPDB:GN000020; CESP:W10G
C:Genetics:
A:Gene: W10G11.19
A:Map position: 2

Query Match 62.1%; Score 36; DB 2; Length 463;
Best Local Similarity 56.7%; Pred. No. 88;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNHGSFY 9
   | | | | |
Db 121 ARENHGRFH 129

Search completed: November 18, 2002, 17:57:23
Job time : 11.6579 secs
```

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:33:36 ; Search time 5.39474 Seconds
(without alignments)
76.883 Million cell updates/sec

Title: US-09-016-061-96
Perfect score: 58
Sequence: 1 ARNHGSFYS 10

Scoring table:
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	39	67.2	470	1 SYE2_RICPR	Q9ZCT8 rickettsia
2	38	55.5	196	1 WBBJ_ECOLI	P37750 escherichia
3	38	65.5	722	1 PBP1_YEAST	P53297 saccharomyc
4	36	62.1	275	1 YK42_SYNV3	P73079 synechocyst
5	36	62.1	473	1 SYE_AQUAE	O67271 aquifex aeo
6	36	62.1	548	1 FUMB_ECOLI	P14407 escherichia
7	36	62.1	627	1 TSD2_ABIGR	O24474 abies grand
8	35	60.3	108	1 Y019_NPVAC	P41424 autographa
9	35	60.3	197	1 EGG5_FASHE	P07915 fasciola he
10	35	60.3	218	1 Y4VH_RHTSN	Q53216 rhizobium s
11	35	60.3	309	1 TSA2_HUMAN	Q8WYR4 homo sapien
12	35	60.3	352	1 CAPG_MOUSE	P24452 mus musculu
13	35	60.3	448	1 NCAP_CVROC	P33469 human coron
14	35	60.3	567	1 CC45_XENLA	Q9YH26 xenopus lae
15	35	60.3	659	1 RA24_YEAST	P32641 saccharomyc
16	34	58.6	160	1 LSPA_BUCAI	P57248 buchnera ap
17	34	58.6	177	1 PTH_BUCAI	P57287 buchnera ap
18	34	58.6	323	1 CCSA_LOTJA	Q9BBP4 lotus japon
19	34	58.6	349	1 F16P_NOSPU	P48847 nostoc punc
20	34	58.6	435	1 PURA_SPICI	P52150 spiroplasma
21	34	58.6	491	1 SYE_LISIN	Q92138 listeria in
22	34	58.6	491	1 SYE_LISMO	Q8YAB3 listeria mo
23	34	58.6	604	1 GLAS_DROME	P13360 drosophila
24	34	58.6	718	1 LSP2_DROME	Q24388 drosophila
25	34	58.6	1446	1 IE18_PRVKA	P33479 pseudorabie
26	34	58.6	1461	1 IE18_PRVIF	P11675 pseudorabie
27	33	56.9	81	1 YWR4_CAEEL	Q10927 caenorhabdi
28	33	56.9	159	1 CUP9_DROME	P27781 drosophila
29	33	56.9	225	1 CD9_MOUSE	P40240 mus musculu
30	33	56.9	284	1 YNB9_YEAST	P53975 saccharomyc
31	33	56.9	284	1 YND3_YEAST	P53964 saccharomyc
32	33	56.9	322	1 FATB_VIBAN	P11460 vibrio angu
33	33	56.9	347	1 UL33_HSV6U	P52380 human herpe

Query Match 67.2%; Score 39; DB 1; Length 470;
Best Local Similarity 66.7%; Pred. No. 5.4;

34	33	56.9	394	1 IPOUL_DROME	P24350 drosophila
35	33	56.9	480	1 SYE_HAEIN	P43818 haemophilus
36	33	56.9	486	1 GATC_DROME	P91623 drosophila
37	33	56.9	502	1 KIR3_MOUSE	O61288 mus musculu
38	33	56.9	503	1 KIR3_HUMAN	P37023 homo sapien
39	33	56.9	505	1 KIR3_RAT	P80203 rattus norv
40	33	56.9	596	1 GLMS_HELPJ	Q9ZJ94 h glucosami
41	33	56.9	596	1 GLMS_HELPJ	O26060 h glucosami
42	33	56.9	692	1 AMO_PICAN	P12807 plichia angu
43	33	56.9	783	1 FAND_ECOLI	P12050 escherichia
44	33	56.9	798	1 YLPN_CAEEL	Q20296 caenorhabdi
45	33	56.9	846	1 AMDM_SCHPO	P50998 schizosacch

ALIGNMENTS

RESULT 1
SYE2_RICPR STANDARD; PRT; 470 AA.
AC Q9ZCT8;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Glutamyl-tRNA synthetase 2 (EC 6.1.1.17) (Glutamate--tRNA ligase 2)
DE (GLURS 2).
GN GLTX2 OR RP623.
OS Rickettsia prowazekii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsieae; Rickettsia.
OX NCBI_TaxID=782;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Madrid E;
RX MEDLINE=99039499; PubMed=9823893;
RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,
RA Sichteritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
RT "The genome sequence of Rickettsia prowazekii and the origin of mitochondria";
RL Nature 396:133-140(1998).
CC -!- CATALYTIC ACTIVITY: ATP + L-glutamate + tRNA(Glu) -> AMP +
CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
CC -----
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CC -----
CC EMBL; AJ235272; CAA15066.1; -.
DR HSP; P27000; 1GLN.
DR InterPro; IPR004527; GLTX_bact.
DR InterPro; IPR000924; Glu_tRNA-synt_lc.
DR InterPro; IPR001412; tRNA-synt_I.
DR Pfam; PF00749; tRNA-synt_lc; 1.
DR PRINTS; PR00987; TRNASYNTHGLU.
DR TIGRFAMs; TIGR00464; gltx_bact; 1.
DR PROSITE; PS00178; AA_TRNA_LIGASE_I; FALSE_NEG.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
Complete proteome.
FT SITE 10 20 "HIGH" REGION.
FT SITE 239 243 "KMSKS" REGION.
FT BINDING 242 242 ATP (BY SIMILARITY).
FT BINDING 242 242 ATP (BY SIMILARITY).
SQ SEQUENCE 470 AA; 53696 MW; DFICE50A20B8A9FD CRC64;

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Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 1 ARHNGSFY 9
|||||:
Db 31 ARHNGKFF 39

RESULT 2
WBBJ_ECOLI
ID WBBJ_ECOLI STANDARD; PRT; 196 AA.
AC P37750; P76375;
DT 01-OCT-1994 (Rel. 30, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE putative lipopolysaccharide biosynthesis O-acetyl transferase wbbJ
DE (EC 2.3.1.-)
GN WBBJ OR B2033.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / W3110;
RX MEDLINE=94292434; PubMed=7517390;
RA Yao Z., Valvano M.A.;
RT "Genetic analysis of the O-specific lipopolysaccharide biosynthesis
RT region (rfb) of Escherichia coli K-12 W3110: identification of genes
RT that confer group 6 specificity to Shigella flexneri serotypes Y and
RT 4a.";
RL J. Bacteriol. 176:4133-4143(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / W31;
RX MEDLINE=94292435; PubMed=7517391;
RA Stevenson G., Neal B., Liu D., Hobbs M., Packer N.H., Batley M.,
RA Redmond J.W., Lindquist L., Reeves P.R.;
RT "Structure of the O antigen of Escherichia coli K-12 and the sequence
RT of its rfb gene cluster.";
RN [3]
RP REVISIONS TO 168-176 AND 187-189.
RC STRAIN=K12 / W31;
RX Stevenson G.;
RA Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RN [5]
RP Science 277:1453-1474(1997).
RC SEQUENCE FROM N.A.
RX STRAIN=K12;
RX MEDLINE=97251358; PubMed=9097040;
RA Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T.,
RA Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T.,
RA Saito N., Sempel G., Seki Y., Sivasubram S., Tagami H.,
RA Takeda J., Takemoto K., Wada C., Yamamoto Y., Horuchi T.;
RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 40.1-50.0 min region on the linkage map.";
RL DNA Res. 3:379-392(1996).
CC -1- FUNCTION: PUTATIVE O-ACETYLTRANSFERASE THAT TRANSFERS AN O-ACETYL
CC 2N THE O ANTIGEN.
CC -1- PATHWAY: Lipopolysaccharide biosynthesis.
CC -1- SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NDL FAMILY OF
CC ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).

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CC -----
DR EMBL; U03041; AAC31635.1; -.
DR EMBL; U09876; AAB88406.1; -.
DR EMBL; A5000294; AAC75094.1; -.
DR EMBL; D90841; BAA15875.1; -.
DR EMBL; D90842; BAA15887.1; -.
DR EcoGene; EG11984; wbbJ.
DR InterPro; IPR001451; Hexapep_transf.
DR Pfam; PF00132; hexapep; 4.
DR PROSITE; PS00101; HEXAPEP_TRANSFERASES; FALSE_NEG.
KW Lipopolysaccharide biosynthesis; Transferase; Acyltransferase; Repeat;
KW Complete proteome.
FT CONFLICT 168 176 SIPENTVIA -> LFRKYCHC (IN REF. 1).
FT CONFLICT 187 189 NHE -> IMR (IN REF. 1).
SQ SEQUENCE 196 AA; 21675 MW; D1C2FA7D3B29A1B1 CRC64;
Query Match 65.5%; Score 38; DB 1; Length 196;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 HNHGSF 8
|||||
Db 105 HNHGSF 110

RESULT 3
PBPL_YEAST
ID PBPL_YEAST STANDARD; PRT; 722 AA.
AC P53297;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE PAB1-binding protein 1.
GN PBPL OR MRS16 OR YGR178C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Hebling U., Hofmann B., Delius H.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=DBY747;
RA Mecklenbrauer I.;
RT "Sequencing and characterization of a suppressor of the pet- phenotype
RT in a Saccharomyces cerevisiae strain without mitochondrial group II
RT introns.";
RL Thesis (1996), Vienna Biocentre, Austria.
RN [3]
RA CHARACTERIZATION.
RX MEDLINE=99038243; PubMed=9819425;
RA Mangus D.A., Amrani N., Jacobson A.;
RT "Pbplp, a factor interacting with Saccharomyces cerevisiae poly(A)-
RT binding protein, regulates polyadenylation.";
RL Mol. Cell. Biol. 18:7383-7396(1998).
CC -1- FUNCTION: APPEARS TO PROMOTE PROPER POLYADENYLATION. IN THE
CC ABSENCE OF PBPLP, THE 3'TERMINI OF PRE-MRNAS ARE PROPERLY CLEAVED
CC BUT LACK FULL-LENGTH POLY(A) TAILS. MAY ACT TO REPRESS THE ABILITY
CC OF PAB1 TO NEGATIVELY REGULATE POLYADENYLATION.
CC -1- SUBUNIT: INTERACTS WITH PAB1.
CC -1- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
CC -----
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 CC -----
 DR EMBL: Z72963; CAA97204.1; -;
 DR EMBL: U46931; AAB94294.1; -;
 DR SGD: S0003410; PBPL.
 KW Nuclear protein.
 SQ SEQUENCE 722 AA; 78781 MW; 92005F3A2346193E CRC64;
 Query Match 55.5%; Score 38; DB 1; Length 722;
 Best Local Similarity 75.0%; Pred. No. 13;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 RHNHGSFY 9
 Db 474 RHNHGSFF 481
 RESULT 4
 YK42_SYNY3
 ID YK42_SYNY3 STANDARD; PRT; 275 AA.
 AC P73079;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Hypothetical protein slr2042.
 GN SLR2042.
 OS Synechocystis sp. (strain PCC 6803).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
 OX NCBI_TaxID=1148;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97061201; PubMed=8905231;
 RA Kaneko T., Sato S., Kotani H., Tanaka A., Asanizu E., Nakamura Y.,
 RA Miyajima N., Hirose M., Sugita M., Sasamoto S., Kimura T.,
 RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
 RA Shimizu S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
 RA Tabata S.,
 RA Sequence analysis of the genome of the unicellular cyanobacterium
 RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
 RT entire genome and assignment of potential protein-coding regions.;
 RL DNA Res. 3:109-136(1996).
 CC -!- SIMILARITY: TO E.COLI YEF1.
 CC -----
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 CC -----
 DR EMBL: D90903; BAA17104.1; -;
 DR Hypothetical protein: Complete proteome.
 KW Hypothetical protein: Complete proteome.
 SQ SEQUENCE 275 AA; 31929 MW; 3A46776EA239BD9E CRC64;
 Query Match 62.1%; Score 36; DB 1; Length 275;
 Best Local Similarity 62.5%; Pred. No. 11;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 2 RHNHGSFY 9
 Db 253 QHNHGQLY 260
 RESULT 5
 SYE_AQUAE
 ID SYE_AQUAE STANDARD; PRT; 473 AA.
 AC O67271;

DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Glutamyl-tRNA synthetase (EC 6.1.1.17) (Glutamate--tRNA ligase)
 DE (GluRS).
 GN GLTX OR AQ_1221.
 OS Aquifex aeolicus.
 OC Bacteria; Aquificae; Aquificae (class); Aquificales; Aquificaceae;
 OC Aquifex.
 OX NCBI_TaxID=63363;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VF5;
 RA DECKERT G., WARREN P.V., GAESTERLAND T., YOUNG W.G., LENOX A.L.,
 RA GRAHAM D.E., OVERBECK R., SNEAD M.A., KELLER M., AUJAY M., HUBER R.,
 RA FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.;
 RT "The complete genome of the hyperthermophilic bacterium Aquifex
 RT aeolicus";
 RL Nature 392:353-358(1998).
 CC -!- CATALYTIC ACTIVITY: ATP + L-glutamate + tRNA(Glu) = AMP +
 CC diphosphate + L-glutamyl-tRNA(Glu).
 CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
 CC -----
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 CC -----
 DR EMBL: AE000729; AAC07230.1; -;
 DR HSSP; P27000; IGLN.
 DR InterPro; IPR004527; GLTX_bact.
 DR InterPro; IPR000924; Glu_tRNA-synt_1c.
 DR InterPro; IPR001412; tRNA-synt_1.
 DR Pfam; PF00749; tRNA-synt_1c; 1.
 DR PRINTS; PR00987; TRNASYNTHGLU.
 DR TIGRFAMS; TIGR00464; gltx_bact; 1.
 DR PROSITE; PS00178; AA_TRNA_LIGASE_1; 1.
 KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
 KW Complete proteome.
 FT SITE 10 20 "HIGH" REGION.
 FT SITE 242 246 "KMSKS" REGION.
 FT BINDING 245 245 ATP (BY SIMILARITY).
 SQ SEQUENCE 473 AA; 55121 MW; 5CB4D1590973E07A CRC64;
 Query Match 62.1%; Score 36; DB 1; Length 473;
 Best Local Similarity 75.0%; Pred. No. 20;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ARNHGSGF 8
 Db 31 ARHNGGFF 38
 RESULT 6
 FUMB_ECOLI
 ID FUMB_ECOLI STANDARD; PRT; 548 AA.
 AC P14407; P78139;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Fumarate hydratase class I, anaerobic (EC 4.2.1.2) (Fumarase).
 GN FUMB OR B4122.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 RN [1]

```
RP SEQUENCE FROM N.A.
RC STRAIN-K12;
RX MEDLINE=89255123; PubMed=2656658;
RT "Nucleotide sequence of the FNR-regulated fumarase gene (fumB) of
RT Escherichia coli K-12";
RL J. Bacteriol. 171:3494-3503(1989).
RN [2]

RP SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655;
RX MEDLINE=95334362; PubMed=7610040;
RA Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,
RA Blattner F.R.;
RT "Analysis of the Escherichia coli genome VI: DNA sequence of the
RT region from 92.8 through 100 minutes.";
RL Nucleic Acids Res. 23:2105-2119(1995).
CC -1- FUNCTION: IT FUNCTIONS IN THE GENERATION OF FUMARATE FOR USE AS AN
CC ANAEROBIC ELECTRON ACCEPTOR.
CC -1- CATALYTIC ACTIVITY: (S)-malate = fumarate + H(2)O.
CC -1- COFACTOR: BINDS 1 4Fe-4S CLUSTER.
CC -1- ENZYME REGULATION: SUBJECT TO ANAEROBIC REPRESSION.
CC -1- PATHWAY: FERMENTATIVE PATHWAY THAT LEADS TO THE PRODUCTION OF
CC SUCCINATE.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SIMILARITY: TO OTHER THERMOLABILE CLASS I FUMARASES.
CC
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CC -----
DR EMBL: M27058; AAA23827.1; ..
DR EMBL: U14003; AAA97022.1; ..
DR EMBL: AE000485; AAC77083.1; ..
DR PIR: B44511; B44511.
DR EcoGene; EG10357; fumB.
DR InterPro; IPR000362; Fumarate_lyase.
DR InterPro; IPR004646; TtdA_fumA_fumB.
DR InterPro; IPR004647; TtdB_fumA_fumB.
DR Pfam; PF00206; lyase_1; 1.
DR TIGRFAMS; TIGR00722; ttdA_fumA_fumB; 1.
DR TIGRFAMS; TIGR00723; ttdB_fumA_fumB; 1.
DR PROSITE; PS00163; FUMARATE_LYASES; 1.
KW Lyase; Tricarboxylic acid cycle; Iron-sulfur; 4Fe-4S;
KW Complete proteome.
FT METAL 318 318 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT ACT_SITE 397 397 POTENTIAL.
FT BINDING 463 463 CARBOXYL GROUP (POTENTIAL).
FT CONFLICT 50 50 V -> L (IN REF. 2; AAC77083).
SQ SEQUENCE 548 AA; 60091 MW; 336854D8FA5551AB CRC64;

Query Match 62.1%; Score 36; DB 1; Length 548;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARNHGGSFY 9
DB 473 ACKHGGFY 481

RESULT 7
TS2D_ABIGR STANDARD; PRT; 627 AA.
AC O24474;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Myrcene synthase, chloroplast precursor (EC 4.2.3.15).
GN AC2.2.
OS Abies grandis (Grand fir).

RP SEQUENCE FROM N.A.
RC STRAIN-K12;
RX MEDLINE=89255123; PubMed=2656658;
RT "Nucleotide sequence of the FNR-regulated fumarase gene (fumB) of
RT Escherichia coli K-12";
RL J. Bacteriol. 171:3494-3503(1989).
RN [2]

RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RX MEDLINE=97413772; PubMed=9268308;
RA Bohlmann J., Steele C.L., Croteau R.;
RT "Monoterpene synthases from grand fir (Abies grandis). cDNA isolation,
RT characterization, and functional expression of myrcene synthase, (-)-
RT (4S)-limonene synthase, and (-)-(1S,5S)-pinene synthase.";
RL J. Biol. Chem. 272:21784-21792(1997).
CC -1- FUNCTION: Involved in defensive oleoresin formation in conifers in
CC response to insect attack or other injury. Involved in monoterpene
CC (C10) olefins biosynthesis.
CC -1- CATALYTIC ACTIVITY: Geranyl diphosphate = myrcene + diphosphate.
CC -1- COFACTOR: Manganese and potassium.
CC -1- PATHWAY: Oleoresinosis.
CC -1- SUBCELLULAR LOCATION: Chloroplast.
CC -1- INDUCTION: By wounding.
CC -1- SIMILARITY: BELONGS TO THE TERPENE SYNTHASE FAMILY.
CC
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CC -----
DR EMBL: U87908; AAB71084.1; ..
DR HSP; Q40377; 5EAS.
DR InterPro; IPR001906; Terp_synth-like.
DR Pfam; PF01397; Terpene_synth; 1.
KW Lyase; Manganese; Transit peptide; Chloroplast.
FT TRANSIT 1 ? CHLOROPLAST (POTENTIAL).
FT CHAIN ? 627 MYRCENE SYNTHASE.
FT ACT_SITE 523 523 BY SIMILARITY.
FT ACT_SITE 600 600 BY SIMILARITY.
FT ACT_SITE 604 604 BY SIMILARITY.
SQ SEQUENCE 627 AA; 72478 MW; 2E0DA4920C971FD CRC64;

Query Match 62.1%; Score 36; DB 1; Length 627;
Best Local Similarity 60.0%; Pred. No. 27;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARNHGGSFYS 10
DB 340 ARRHVEFT 349

RESULT 8
Y019_NPVAC STANDARD; PRT; 108 AA.
AC P41424;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Hypothetical 12.2 kDa protein in EST-IAP1 intergenic region (ORF4).
OS Autographa californica nuclear polyhedrosis virus (AcMNPV).
CC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
CC Nucleopolyhedrovirus.
CC NCBI_TaxID=46015;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C6;
RX MEDLINE=94303173; PubMed=8030224;
RA Ayres M.D., Howard S.C., Kuzio J., Lopez-Ferber M., Possee R.D.;
RT "The complete DNA sequence of Autographa californica nuclear
RT polyhedrosis virus.";
RL Virology 202:586-605(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=E2;
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OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Abies.
OX NCBI_TaxID=46611;
RN [1]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RX MEDLINE=97413772; PubMed=9268308;
RA Bohlmann J., Steele C.L., Croteau R.;
RT "Monoterpene synthases from grand fir (Abies grandis). cDNA isolation,
RT characterization, and functional expression of myrcene synthase, (-)-
RT (4S)-limonene synthase, and (-)-(1S,5S)-pinene synthase.";
RL J. Biol. Chem. 272:21784-21792(1997).
CC -1- FUNCTION: Involved in defensive oleoresin formation in conifers in
CC response to insect attack or other injury. Involved in monoterpene
CC (C10) olefins biosynthesis.
CC -1- CATALYTIC ACTIVITY: Geranyl diphosphate = myrcene + diphosphate.
CC -1- COFACTOR: Manganese and potassium.
CC -1- PATHWAY: Oleoresinosis.
CC -1- SUBCELLULAR LOCATION: Chloroplast.
CC -1- INDUCTION: By wounding.
CC -1- SIMILARITY: BELONGS TO THE TERPENE SYNTHASE FAMILY.
CC
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CC -----
DR EMBL: U87908; AAB71084.1; ..
DR HSP; Q40377; 5EAS.
DR InterPro; IPR001906; Terp_synth-like.
DR Pfam; PF01397; Terpene_synth; 1.
KW Lyase; Manganese; Transit peptide; Chloroplast.
FT TRANSIT 1 ? CHLOROPLAST (POTENTIAL).
FT CHAIN ? 627 MYRCENE SYNTHASE.
FT ACT_SITE 523 523 BY SIMILARITY.
FT ACT_SITE 600 600 BY SIMILARITY.
FT ACT_SITE 604 604 BY SIMILARITY.
SQ SEQUENCE 627 AA; 72478 MW; 2E0DA4920C971FD CRC64;

Query Match 62.1%; Score 36; DB 1; Length 627;
Best Local Similarity 60.0%; Pred. No. 27;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARNHGGSFYS 10
DB 340 ARRHVEFT 349

RESULT 8
Y019_NPVAC STANDARD; PRT; 108 AA.
AC P41424;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Hypothetical 12.2 kDa protein in EST-IAP1 intergenic region (ORF4).
OS Autographa californica nuclear polyhedrosis virus (AcMNPV).
CC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
CC Nucleopolyhedrovirus.
CC NCBI_TaxID=46015;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C6;
RX MEDLINE=94303173; PubMed=8030224;
RA Ayres M.D., Howard S.C., Kuzio J., Lopez-Ferber M., Possee R.D.;
RT "The complete DNA sequence of Autographa californica nuclear
RT polyhedrosis virus.";
RL Virology 202:586-605(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=E2;
```

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RX MEDLINE=93079853; PubMed=1333113;
RA Braunagel S.C., Daniel K.D., Reilly L.M., Guarino L.A., Hong T.,
RT Summers M.D.;
RA "Sequence, genomic organization of the EcoRI-A fragment of Autographa
RT californica nuclear polyhedrosis virus, and identification of a
RT viral-encoded protein resembling the outer capsid protein VP8 of
RT rotavirus.";
RL Virology 191:1003-1008(1992).
CC -!- SIMILARITY: TO CORRESPONDING ORF IN OPMPNV.
CC -----
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CC -----
DR EMBL; L22858; AAA66649.1; -.
DR EMBL; M96361; AAA66789.1; -.
DR PIR; D44221; D44221.
KW Hypothetical protein.
FT CONFLICT 6 A -> R (IN REF. 2).
SQ SEQUENCE 108 AA; 12162 MW; 8363B15DF72486A1 CRC64;

Query Match 60.3%; Score 35; DB 1; Length 108;
Best Local Similarity 66.7%; Pred. No. 6.2;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARNHGVSFY 9
| | | | |
Db 25 ANRHHGSFY 33

RESULT 9
EGGS_FASHE
ID EGGS_FASHE STANDARD; PRT; 197 AA.
AC P07915;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Putative eggshell protein precursor.
OS Fasciola hepatica (Liver fluke)
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
OC Echinostomida; Echinostomata; Fascioloidae; Fasciolidae; Fasciola.
OX NCBI_TaxID=6192;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87175670; PubMed=3470798;
RA Zurita M., Bieber D., Ringold G., Mansour T.E.;
RT "Cloning and characterization of a female genital complex cDNA from
RT the liver fluke Fasciola hepatica.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:2340-2344(1987).
CC -----
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CC -----
DR EMBL; M15871; AAA29138.1; -.
DR Eggshell; Signal.
FT SIGNAL 1 17
FT CHAIN 18 197 PUTATIVE EGG SHELL PROTEIN.
SQ SEQUENCE 197 AA; 22470 MW; 72033ED203FC1A3E CRC64;

Query Match 60.3%; Score 35; DB 1; Length 197;
Best Local Similarity 75.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARNHGVSF 8
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Db 17 ARHPHGKF 24
| | | | |
RESULT 10
Y4VH_RHISN
ID Y4VH_RHISN STANDARD; PRT; 218 AA.
AC Q53216;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE Hypothetical 24.6 kDa protein Y4VH.
GN Y4VH.
OS Rhizobium sp. (strain NGR234).
CG Plasmid sym pNGR234a.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=394;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97305956; PubMed=9163424;
RA Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
RA Perret X.;
RT "Molecular basis of symbiosis between Rhizobium and legumes.";
RL Nature 387:394-401(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96389014; PubMed=8796346;
RA Freiberg C., Perret X., Broughton W.J., Rosenthal A.;
RT "Sequencing the 500-kb GC-rich symbiotic replicon of Rhizobium sp.
RT NGR234 using dye terminators and a thermostable 'sequenase': a
RT beginning.";
RL Genome Res. 6:590-600(1996).
CC -!- SIMILARITY: NONE OBVIOUS.
CC -----
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CC -----
DR EMBL; Z68203; CAA92423.1; -.
DR EMBL; AE000101; AAB91896.1; -.
KW Hypothetical protein; Plasmid.
SQ SEQUENCE 218 AA; 24594 MW; 501C6CB38A09A2E5 CRC64;

Query Match 60.3%; Score 35; DB 1; Length 218;
Best Local Similarity 75.0%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARNHGVSF 8
| | | | |
Db 68 ARDNHGSY 75

RESULT 11
TSA2_HUMAN
ID TSA2_HUMAN STANDARD; PRT; 309 AA.
AC Q8WYR4;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Testis-specific gene A2 (Male meiotic metaphase chromosome-associated
DE acidic protein) (Meichroacidin).
GN TSA2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
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RC TISSUE-Testis;
RX MEDLINE=98246622; PubMed=9578619;
RA Tsuchida J., Nishina Y., Wakabayashi N., Nozaki M., Sakai Y.,
RA Nishimune Y.;
RT "Molecular cloning and characterization of melchroacidin (male meiotic
RT metaphase chromosome-associated acidic protein).";
RL Dev. Biol. 197; 67-76(1998).
RN [2]
RN SEQUENCE FROM N.A.
RP TISSUE-Testis;
RC Shimizu N., Kudoh J., Shibuya K.;
RA Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RL -!- FUNCTION: May play an important role in male meiosis (By
CC similarity).
CC
CC -!- SUBCELLULAR LOCATION: Cytoplasmic in late spermatocytes, secondary
CC spermatocytes and round spermatids. Gathered around metaphase
CC chromosomes during meiotic divisions (By similarity).
CC
CC -!- TISSUE SPECIFICITY: Testis specific.
CC
CC -!- SIMILARITY: CONTAINS 6 MORN REPEATS.
CC
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CC
CC EMBL; AB065336; BAB3694.1; -.
DR EMBL; AB041016; BAB2995.1; -.
DR Genew; HGNC:12371; TSGA2.
DR InterPro; IPR003409; MORN.
DR Pfam; PF02493; MORN; 6.
KW Meiosis; Repeat.
FT DOMAIN 195 201 POLY-GLU.
FT DOMAIN 298 301 POLY-GLU.
FT REPEAT 20 43 MORN REPEAT 1.
FT REPEAT 44 66 MORN REPEAT 2.
FT REPEAT 67 89 MORN REPEAT 3.
FT REPEAT 90 112 MORN REPEAT 4.
FT REPEAT 113 135 MORN REPEAT 5.
FT REPEAT 159 181 MORN REPEAT 6.
SQ SEQUENCE 309 AA; 35124 MW; 09A20A766D5A6A88 CRC64;

Query Match 60.3%; Score 35; DB 1; Length 309;
Best Local Similarity 62.5%; Pred. No. 19;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNGSFY 9
|| || |
Db 99 RHGHGVY 106

RESULT 12
CAPG_MOUSE STANDARD; PRT; 352 AA.
AC P24452;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Macrophage capping protein (Myc basic motif homolog-1) (Actin-capping
DE protein GCAP39).
DE CAPG OR MBH1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A.
RP STRAIN=N1H Swiss;
RX MEDLINE=91184120; PubMed=1849072;
RA Prendergast G.C., Ziff E.B.;
RT "Mbh 1: a novel gelsolin/severin-related protein which binds actin in

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RT vitro and exhibits nuclear localization in vivo.";
RN EMBO J. 10:757-766(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-Kidney;
RX MEDLINE=91075231; PubMed=2255912;
RA Yu F.-X., Johnston P.A., Suedhof T.C., Yin H.L.;
RT "gcap39, a calcium ion- and polyphosphoinositide-regulated actin
RT capping protein.";
RL Science 250:1413-1415(1990).
RN [3]
RN PARTIAL SEQUENCE.
RX MEDLINE=91009264; PubMed=2211671;
RA Johnston P.A., Yu F.-X., Reynolds G.A., Yin H.L., Moomaw C.R.,
RA Slaughter C.A., Suedhof T.C.;
RT "Purification and expression of gCap39. An intracellular and secreted
RT Ca2(+)-dependent actin-binding protein enriched in mononuclear
RT phagocytes.";
RL J. Biol. Chem. 265:17946-17952(1990).
RN [4]
RN SUBCELLULAR LOCATION.
RX MEDLINE=94123352; PubMed=8293478;
RA Onoda K., Yu F.-X., Yin H.L.;
RT "gCap39 is a nuclear and cytoplasmic protein.";
RL Cell Motil. Cytoskeleton 26:227-238(1993).
CC -!- FUNCTION: CALCIUM-SENSITIVE PROTEIN WHICH REVERSIBLY BLOCKS THE
CC BARBED ENDS OF ACTIN FILAMENTS BUT DOES NOT SEVER PREFORMED ACTIN
CC FILAMENTS. MAY PLAY AN IMPORTANT ROLE IN MACROPHAGE STRUCTURE. MAY
CC PLAY A ROLE IN REGULATING CYTOPLASMIC AND/OR NUCLEAR STRUCTURES
CC THROUGH POTENTIAL INTERACTIONS WITH ACTIN. MAY BIND DNA. UNCAPPING
CC OCCURS EITHER WHEN CA(2+) FALLS OR WHEN THE CONCENTRATION OF
CC POLYPHOSPHOINOSITIDE RISES, BOTH AT LOW AND HIGH CA(2+).
CC -!- SUBCELLULAR LOCATION: NUCLEAR, CYTOPLASMIC AND SECRETED. NUCLEAR
CC GCAP39 REDISTRIBUTES THROUGHOUT THE CYTOPLASM DURING MITOSIS AND
CC IS EXCLUDED FROM REGIONS CONTAINING CHROMOSOMES.
CC -!- TISSUE SPECIFICITY: PRESENT IN A LARGE VARIETY OF TISSUES AND IS
CC PARTICULARLY ABUNDANT IN KIDNEY AND LUNG.
CC -!- PTM: PHOSPHORYLATED. NUCLEAR GCAP39 IS MORE HIGHLY PHOSPHORYLATED
CC THAN CYTOPLASMIC GCAP39.
CC -!- SIMILARITY: BELONGS TO THE VILLIN/GELSOLIN FAMILY.
CC -!- SIMILARITY: CONTAINS 3 GELSOLIN-LIKE REPEATS.
CC -!- CAUTION: THIS PROTEIN WAS ORIGINALLY THOUGHT TO BE A DNA-BINDING
CC PROTEIN WITH A HELIX-LOOP-HELIX DOMAIN.
CC
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CC
CC EMBL; X54511; CAA38370.1; -.
DR PIR; A39834; A39834.
DR PIR; S15011; S15011.
DR HSP; P10733; 1SVR.
DR MGD; MGI:1098259; Capg.
DR InterPro; IPR001974; Gelsolin.
DR Pfam; PF00626; Gelsolin; 3.
DR SMART; SM00262; GEL; 3.
KW Nuclear protein; Actin-binding; Repeat; Phosphorylation.
FT DOMAIN 139 148 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT REPEAT 27 75 GELSOLIN-LIKE 1.
FT REPEAT 150 190 GELSOLIN-LIKE 2.
FT REPEAT 265 311 GELSOLIN-LIKE 3.
FT CONFLICT 32 32 V -> W (IN REF. 1).
FT CONFLICT 98 98 V -> L (IN REF. 1).
FT CONFLICT 117 117 MISSING (IN REF. 1).
FT CONFLICT 122 135 VESAPHTKTSARG -> GRVGISQNLRAIP (IN
FT REF. 1).
FT CONFLICT 156 156 P -> A (IN REF. 1).
FT CONFLICT 245 245 Q -> E (IN REF. 3).
FT CONFLICT 247 248 MISSING (IN REF. 1 AND 3).

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CC -----
DR EMBL; U18922; AAB64700.1; -
DR PIR; S30859; S30859.
DR SGD; S0000975; RAD24.
DR InterPro; IPR000862; RFCdomain.
DR InterPro; IPR004582; Rad24.
DR Pfam; PF03215; Rad17; 1.
DR TIGRFAMS; TIGR00602; rad24; 1.
KW DNA damage; DNA repair; Nuclear protein; Cell cycle.
SQ SEQUENCE 659 AA; 75726 MW; 130FE54875CAA930 CRC64;

Query Match 60.3%; Score 35; DB 1; Length 659;
Best Local Similarity 71.4%; Pred. No. 44;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNHGSFY 9
||||:|
Db 436 HNHGTVY 442

Search completed: November 18, 2002, 17:51:41
Job time : 6.39474 secs

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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:40:56 ; Search time 22.3684 Seconds
(without alignments)
92.115 Million cell updates/sec

Title: US-09-016-061-96

Perfect score: 58

Sequence: 1 ARNHGSGFYS 10

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL.21.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_tvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	77.6	1108	10 Q9FNQ7	Q9fnq7 arabidopsis
2	42	72.4	233	16 Q9KRA6	Q9kra6 vibrio chol
3	40	69.0	555	5 Q9XV91	Q9xv91 caenorhabdi
4	39	67.2	350	16 P74376	P74376 synecocyst
5	39	67.2	444	2 Q9AKB5	Q9akb5 rickettsia
6	39	67.2	1471	16 Q8XKN0	Q8xkn0 clostridium
7	38	65.5	191	10 Q9C960	Q9c960 arabidopsis
8	38	65.5	195	16 Q9CG29	Q9c929 lactococcus
9	38	65.5	278	5 Q9VP63	Q9vp63 drosophila
10	38	65.5	839	10 Q9LIES	Q9lies arabidopsis
11	37	63.8	270	16 Q92LS4	Q92ls4 rhizobium m
12	37	63.8	326	16 Q9RJG3	Q9rjg3 streptomyce
13	37	63.8	354	4 Q96EK9	Q96ek9 homo sapien
14	37	63.8	528	10 Q9FPE7	Q9fpe7 arabidopsis
15	37	63.8	530	10 Q64526	Q64526 arabidopsis
16	37	63.8	547	10 Q9LX11	Q9lyl1 arabidopsis

17	37	63.8	550	10 Q8W4S6	Q8w4s6 arabidopsis
18	37	63.8	573	10 Q9M0A8	Q9m0a8 arabidopsis
19	37	63.8	583	5 Q9VHN8	Q9vhn8 drosophila
20	37	63.8	648	10 Q8VYT3	Q8vyt3 arabidopsis
21	37	63.8	710	2 Q8VPE6	Q8vpe6 enterococcu
22	37	63.8	731	2 Q59369	Q59369 escherichia
23	37	63.8	849	16 Q9KNI8	Q9kni8 vibrio chol
24	37	63.8	939	4 Q9H088	Q9h088 homo sapien
25	36	62.1	227	5 Q9VNI9	Q9vni9 drosophila
26	36	62.1	235	10 Q94KA4	Q94ka4 picea abies
27	36	62.1	316	11 Q8R256	Q8r256 mus musculu
28	36	62.1	339	2 Q9XD85	Q9xd85 corynebacte
29	36	62.1	343	10 Q94LN9	Q94ln9 oryza sativ
30	36	62.1	508	5 Q44923	Q44923 caenorhabdi
31	36	62.1	547	16 Q8ZBR9	Q8zbr9 yersinia pe
32	36	62.1	548	16 Q8X591	Q8x591 escherichia
33	36	62.1	623	16 Q8XVB0	Q8xvb0 ralstonia s
34	36	62.1	778	16 Q92VY3	Q92vy3 rhizobium m
35	36	62.1	893	3 Q8TGD5	Q8tgd5 aspergillus
36	36	62.1	2820	5 Q9VLT6	Q9vlt6 drosophila
37	35	60.3	85	7 Q95HR7	Q95hr7 peromyscus
38	35	60.3	86	16 Q9JU21	Q9ju21 neisseria m
39	35	60.3	89	7 Q19495	Q19495 gallus gall
40	35	60.3	110	12 Q92387	Q92387 bombyx mori
41	35	60.3	134	10 Q8S4F4	Q8s4f4 areca catec
42	35	60.3	157	5 Q9VNB9	Q9vnb9 drosophila
43	35	60.3	272	5 Q24950	Q24950 fasciola he
44	35	60.3	272	5 Q24951	Q24951 fasciola he
45	35	60.3	305	10 Q8RUD9	Q8rud9 glycine max

ALIGNMENTS

RESULT 1

Q9FNQ7 PRELIMINARY; PRF: 1108 AA.
ID Q9FNQ7
AC Q9FNQ7
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Similarity to histone deacetylase.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=98069011; PubMed=9405937;
RA Kotani H., Nakamura Y., Sato S., Kaneko T., Asamizu E., Miyajima N.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. II.
RT Sequence features of the regions of 1,044,062 bp covered by thirteen
RT physically assigned pl clones.";
RL DNA Res. 4:291-300(1997).
DR EMBL: AB006696; BAB10370.1; -
DR InterPro: IPR000286; His_deacetylase.
DR Pfam: PF00850; Hist_deacetyl; 2.
DR PRINTS: PR01270; HDASUPER.
SQ SEQUENCE 1108 AA; 123609 MW; 9BCF5A2BCD90A1E2 CRC64;

Query Match 77.6%; Score 45; DB 10; Length 1108;
Best Local Similarity 87.5%; Pred. No. 10;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Caps 0;

QY 2 RHNHGSFY 9

Db 255 RHDHGSFY 262

RESULT 2

Q9KRA6
ID Q9KRA6 PRELIMINARY; PRT; 233 AA.
AC Q9KRA6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Arginyl-tRNA-protein transferase-related protein.
GN VCI736.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EL TOR N16961 / SEROTYPE O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
cholerae";
RL Nature 406:477-483(2000).
DR EMBL: AE004251; AAF94886.1; -.
DR TIGR: VCI736; -.
KW Transferase; Complete proteome.
SQ SEQUENCE 233 AA; 27350 MW; AEB6E95905EC2C3C CRC64;

Query Match 72.4%; Score 42; DB 16; Length 233;
Best Local Similarity 77.8%; Pred. No. 7.1;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARNHGSPY 9
||| ||| |
Db 117 ARHRGSMY 125

RESULT 3
Q9XV91
ID Q9XV91 PRELIMINARY; PRT; 555 AA.
AC Q9XV91;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE F16H6.1 protein.
DE F16H6.1 protein.
GN F16H6.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Matthews L.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
investigating biology";
RL Science 282:2012-2018(1998).
CC -1- SIMILARITY: CONTAINS 2 CUB DOMAINS.
DR EMBL: Z81506; CAB04128.1; -.
DR HSSP; P23807; lixx.
DR InterPro; IPR000859; CUB_domain.
DR Pfam; PF00431; CUB; 2.
DR Pfam; PF00059; lectin_C; 2.
DR SMART; SM00034; CLECT; 2.
DR SMART; SM00042; CUB; 2.
DR PROSITE; PS01180; CUB; 2.

DR PROSITE; PS00615; C_TYPE_LECTIN_1; UNKNOWN_1.
DR PROSITE; PS0041; C_TYPE_LECTIN_2; 2.
SQ SEQUENCE 555 AA; 60401 MW; 00B58D22B2E14EDC CRC64;

Query Match 69.0%; Score 40; DB 5; Length 555;
Best Local Similarity 87.5%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNHGSPYS 10
|| |||||
Db 314 HNSGSPYS 321

RESULT 4
P74376
ID P74376 PRELIMINARY; PRT; 350 AA.
AC P74376;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical protein sl10428.
GN SL10428.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hirose M., Sugita M., Sugita M., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
RA Shimpou S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
Synechocystis sp. strain PCC6803. II. Sequence determination of the
entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
DR EMBL; D90914; BAA18471.1; -.
DR InterPro; IPR005123; 2OG-FeII_Oxy.
DR Pfam; PF03171; 2OG-FeII_Oxy; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 350 AA; 40262 MW; 29E436C5B44839DC CRC64;

Query Match 67.2%; Score 39; DB 16; Length 350;
Best Local Similarity 71.4%; Pred. No. 38;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNHGSPY 9
||| |||
Db 247 HNHGNYV 253

RESULT 5
Q9AKB5
ID Q9AKB5 PRELIMINARY; PRT; 444 AA.
AC Q9AKB5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Glutamyl-tRNA synthetase (Fragment).
GN GLTX2.
OS Rickettsia typhi.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=785;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WILMINGTON;
RX MEDLINE=21219194; PubMed=11319266;
RA Andersson J.O., Andersson S.G.E.;
RT "Pseudogenes, junk DNA and the dynamics of Rickettsia genomes.";
RL Mol. Biol. Evol. 18:829-839(2001).
DR EMBL; AJ293325; CAC33753.1; -.

DR HSSP: P27000; IGLN.
 DR InterPro: IPR004527; GltX_bact.
 DR InterPro: IPR000924; Glu_tRNA-synt_1c.
 DR Pfam: PF00749; tRNA-synt_1c; 1.
 DR PRINTS: PR00987; TRNASYNTHGLU.
 DR TIGRFAMS: TIGR00464; gltx_bact; 1.
 KW Aminocacyl-tRNA synthetase.
 FT NON_TER 1
 SQ SEQUENCE 444 AA; 50791 MW; FF00E12E10FD6FCB CRC64;

Query Match 67.2%; Score 39; DB 2; Length 444;
 Best Local Similarity 66.7%; Pred. No. 48;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARNHGSEFY 9
 ||||| 1:
 Db 6 ARHNGREF 14

RESULT 6

Q8XKNO ID Q8XKNO PRELIMINARY; PRT; 1471 AA.
 AC Q8XKNO;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Hypothetical protein CPE1364.
 GN CPE1364.
 OS Clostridium perfringens.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
 OC Clostridiales; Clostridiaceae; Clostridium.
 OX NCBI_TaxID=1502;

[1]

RP SEQUENCE FROM N.A.
 RC STRAIN=13 / TYPE A;
 RX PubMed=11792842;
 RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
 RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
 RT "Complete genome sequence of Clostridium perfringens, an anaerobic
 flesh-eater.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).

DR EMBL: AP003190; BAB81070.1; -.
 DR InterPro: IPR000515; BPD_transp.
 DR InterPro: IPR001064; Crystallin.
 DR InterPro: IPR000719; Euk_pkkinase.
 DR InterPro: IPR000421; FA58_C.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR001540; GH_20.
 DR Pfam: PF00734; F5_F8_type_C; 1.
 DR Pfam: PF00041; fn3; 1.
 DR Pfam: PF00728; Glyco_hydro_20; 1.
 DR SMART: SM00060; FN3; 1.
 DR PROSITE: PS00402; BPD_TRANS INN MEMBR; UNKNOWN_1.
 DR PROSITE: PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 1471 AA; 164321 MW; 540A078FD935D4EF CRC64;

Query Match 67.2%; Score 39; DB 16; Length 1471;
 Best Local Similarity 70.0%; Pred. No. 1.6e+02;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARNHGSEFY 10
 ||||| 1:
 Db 518 ATHTGTAFYS 527

RESULT 7

Q9C960 ID Q9C960 PRELIMINARY; PRT; 191 AA.
 AC Q9C960;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Hypothetical 21.5 kDa protein.
 GN T7Pl.6.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RX MEDLINE=21016719; PubMed=11130712;
 RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
 RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
 RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
 RA Chung M.K., Conn L., Conway A.B., Creasy T.H., Dewar K.,
 RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
 RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
 RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
 RA Kim C.J., Koo H.L., Kremenetska I., Kurtz D.B., Kwan A., Lam B.,
 RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
 RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marzilli A.,
 RA Militischer J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
 RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
 RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
 RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
 RA Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
 RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
 RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
 thaliana";
 RL Nature 408:816-820(2000).
 DR EMBL: AC018908; AAG51643.1; -.
 DR InterPro: IPR002100; TF_MADSbox.
 DR Pfam: PF00319; SRF-TF; 1.
 DR PRINTS: PR00404; MADS_DOMAIN.
 DR SMART: SM00432; MADS; 1.
 DR PROSITE: PS50066; MADS_BOX_2; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 191 AA; 21501 MW; BF92CEBA222421D1 CRC64;

Query Match 65.5%; Score 38; DB 10; Length 191;
 Best Local Similarity 75.0%; Pred. No. 31;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNHGSEFY 10
 |.1.1111
 Db 56 HSHASFY 63

RESULT 8
 Q9CGZ9 ID Q9CGZ9 PRELIMINARY; PRT; 195 AA.
 AC Q9CGZ9;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Hypothetical protein yjgF.
 GN YJGF OR LL0943.
 OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
 OC Streptococcaceae; Lactococcus.
 OX NCBI_TaxID=1360;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LL403;
 RX MEDLINE=21235186; PubMed=11337471;
 RA Bolotin A., Wincker P., Mauger S., Jaillon O., Malarne K.,
 RA Weissenbach J., Ehrlich S.D., Sorokin A.;
 RT "The complete genome sequence of the lactic acid bacterium Lactococcus
 lactis ssp. lactis LL403.";
 RL Genome Res. 11:731-753(2001).
 DR EMBL: AE006328; AAK05041.1; -.
 DR InterPro: IPR000868; Isochorismatase.

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DR Pfam: PF00857; Isochorismatase; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 195 AA; 21535 MW; A408E9F70EC7B43F CRC64;

Query Match 65.5%; Score 38; DB 16; Length 195;
Best Local Similarity 66.7%; Pred. No. 31;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ARNHGGSFY 9
   I::I I::I
Db 103 AKHNGAFY 111

RESULT 9
Q9VP63 PRELIMINARY; PRT; 278 AA.
ID Q9VP63
AC Q9VP63
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE CG9391 protein (RE10407p).
GN CG9391.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrier S., Fleischmann W.,
RA Folsler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J., Weng H.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,

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RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AE003594; AAF51693.1; -.
DR EMBL: AY071022; AAL48644.1; -.
DR HSSP: P29218; 1IMP.
DR FlyBase: FBgn0037063; CG9391.
DR InterPro: IPR000760; Inositol_P.
DR Pfam: PF00459; inositol_P: 1.
DR PROSITE: PS00629; IMP_1; 1.
DR PROSITE: PS00630; IMP_2; 1.
SQ SEQUENCE 278 AA; 30626 MW; B5AEEC2445A72D99 CRC64;

Query Match 65.5%; Score 38; DB 5; Length 278;
Best Local Similarity 60.0%; Pred. No. 45;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ARNHGGSFY 10
   I::I I::I
Db 136 ARRGHGAFFN 145

RESULT 10
Q9LIE5 PRELIMINARY; PRT; 839 AA.
ID Q9LIE5
AC Q9LIE5
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Far-red impaired response protein, mutator-like transposase-like
DE protein, phytochrome A signaling protein-like.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=20363099; PubMed=10907853;
RA Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.
RT Sequence features of the regions of 4,251,695 bp covered by ninety PL,
RT TAC and BAC clones."
RL DNA Res. 7:217-221(2000).
DR EMBL: AP001306; BAB03065.1; -.
DR InterPro: IPR004330; FAR1.
DR InterPro: IPR001000; Glyco_hydro_10.
DR Pfam: PF03101; FAR1; 1.
DR PROSITE: PS00591; GLYCOSYL_HYDROL_F10; UNKNOWN1.
SQ SEQUENCE 839 AA; 95996 MW; CBBF60DF8B6797F8 CRC64;

Query Match 65.5%; Score 38; DB 10; Length 839;
Best Local Similarity 75.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARNHGGSF 8
   I::I I::I
Db 274 SRHNGGSF 281

RESULT 11
Q92LS4 PRELIMINARY; PRT; 270 AA.
ID Q92LS4
AC Q92LS4;

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DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Putative sugar kinase protein.
GN R02955 OR SMC03138.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21396507; PubMed=11481430;
RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
RA Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
RA Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
RA Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,
RA Renard C., Thebaud P., Vandenbol M., Weidner S., Galibert F.;
RT "Analysis of the chromosome sequence of the legume symbiont
RT Sinorhizobium meliloti strain 1021.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
DR EMBL; AL591792; CAC47534.1; -.
DR InterPro; IPR002173; PfkB.
DR Pfam; PF00294; pfkB; 1.
DR PROSITE; PS00583; PFKB_KINASES_1; UNKNOWN_1.
DR PROSITE; PS00584; PFKB_KINASES_2; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 270 AA; 27995 MW; D14EB093C720B4C CRC64;

Query Match 63.8%; Score 37; DB 16; Length 270;
Best Local Similarity 77.8%; Pred. No. 66;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARNHGSPFY 9
DB 38 ARLGHSFY 46

RESULT 12
ID Q9RJG3 PRELIMINARY; PRT; 326 AA.
AC Q9RJG3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative araC family transcriptional regulator.
GN SCO0471 OR SCF76.11.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae.
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Murphy L., Harris D.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RX MEDLINE=97000351; PubMed=8843436;
RA Redenbach M., Kieser H.M., Denapante D., Eichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL Mol. Microbiol. 21:77-96(1996).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;

Query Match 63.8%; Score 37; DB 16; Length 270;
Best Local Similarity 77.8%; Pred. No. 66;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARNHGSPFY 9
DB 38 ARLGHSFY 46

RESULT 13
ID Q96EK9 PRELIMINARY; PRT; 354 AA.
AC Q96EK9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Similar to RIKEN cDNA 1110001A12 gene (Hypothetical 38.6 kDa
DE protein).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SKIN;
RA Strausberg R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Zhang W., Li N., Wan T., Zhang J., Cao X.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC012173; AAH12173.1; -.
DR EMBL; AF327348; AAL56009.1; -.
KW Hypothetical protein.
SQ SEQUENCE 354 AA; 38615 MW; 877F297D28AF1E24 CRC64;

Query Match 63.8%; Score 37; DB 4; Length 354;
Best Local Similarity 60.0%; Pred. No. 87;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARNHGSPFY 10
DB 196 ARHGSPFY 205

RESULT 14
ID Q9FPE7 PRELIMINARY; PRT; 528 AA.
AC Q9FPE7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

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DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical 59.5 kDa protein.
GN YUP8H12R.13.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
RA Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,
RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
RA Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RT "Full length cDNA of gene YUP8H12R.13 (GI:7487895).";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF326910; AAC1492.1; -;
DR InterPro: IPR001064; Crystallin.
DR PROSITE: PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 528 AA; 59549 MW; DF4365FFFE014DF0 CRC64;

Query Match 63.8%; Score 37; DB 10; Length 528;
Best Local Similarity 62.5%; Pred. No. 1.3e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNHGSFYS 10
||| :|||
DB 190 HNHNNYYS 197

RESULT 15
O64526 PRELIMINARY; PRT; 530 AA.
AC O64526;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE YUP8H12R.13 protein.
GN YUP8H12R.13.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Theologis A., Vysotskaia V.S., Osborne B.I., Schwartz J.R.,
RA Federspiel N.A., Kwan A., Toriumi M., Yu G., Oji, O., Araujo R.,
RA Chung E., Dewar K., Dietrich F., Ecker J.R., Marziani A., Oefner P.,
RA Davis R.W.;
RT "Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence.";
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Theologis A.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC002986; AAC17040.1; -;
DR InterPro: IPR001064; Crystallin.
DR PROSITE: PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
SQ SEQUENCE 530 AA; 59679 MW; E326AA0A6958F910 CRC64;

Query Match 63.8%; Score 37; DB 10; Length 530;
Best Local Similarity 62.5%; Pred. No. 1.3e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNHGSFYS 10
||| :|||

Db 192 HNHNNYYS 199
Search completed: November 18, 2002, 17:54:40
Job time : 24.3684 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:31:45 ; Search time 29.3421 Seconds
(without alignments)
45.413 Million cell updates/sec

Title: US-09-016-061-96
Perfect score: 58
Sequence: 1 ARNHCSFYS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	58	100.0	10	19	AAW76038
2	58	100.0	10	22	AAW76038
3	52	89.7	10	19	AAW76040
4	52	89.7	10	22	AAW76038
5	49	84.5	10	19	AAW76037
6	49	84.5	10	22	AAW76039
7	48	82.8	10	19	AAW76039
8	48	82.8	10	19	AAW76023
9	48	82.8	10	22	AAW76038
10	48	82.8	10	22	AAW76037

11	47	81.0	10	19	AAW76020	LM609 grafted anti
12	47	81.0	10	22	AAW76038	Mutant VH CDR3 pep
13	43	74.1	10	19	AAW76024	LM609 grafted anti
14	43	74.1	10	22	AAW76038	Mutant VH CDR3 pep
15	41	70.7	10	19	AAW76022	LM609 grafted anti
16	41	70.7	10	19	AAW76025	LM609 grafted anti
17	41	70.7	10	19	AAW76026	LM609 grafted anti
18	41	70.7	10	19	AAW76027	LM609 grafted anti
19	41	70.7	10	19	AAW76028	LM609 grafted anti
20	41	70.7	10	19	AAW76029	LM609 grafted anti
21	41	70.7	10	19	AAW76030	LM609 grafted anti
22	41	70.7	10	19	AAW76010	LM609 grafted anti
23	41	70.7	10	22	AAW76038	Mutant VH CDR3 pep
24	41	70.7	10	22	AAW76038	Mutant VH CDR3 pep
25	41	70.7	10	22	AAW76038	Mutant VH CDR3 pep
26	41	70.7	10	22	AAW76038	Mutant VH CDR3 pep
27	41	70.7	10	22	AAW76038	Mutant VH CDR3 pep
28	41	70.7	10	22	AAW76038	Mutant VH CDR3 pep
29	41	70.7	10	22	AAW76038	Mutant VH CDR3 pep
30	41	70.7	10	22	AAW76038	Mutant VH CDR3 pep
31	41	70.7	117	19	AAW76001	Vitaxin antibody h
32	41	70.7	117	19	AAW76003	LM609 antibody h
33	41	70.7	117	20	AAW06381	Murine monoclonal
34	41	70.7	117	20	AAW06387	Humanised LM609 an
35	41	70.7	117	22	AAW63587	A heavy chain vari
36	41	70.7	117	22	AAW63589	A heavy chain vari
37	41	70.7	117	22	AAW63589	Vitaxin heavy chai
38	41	70.7	117	22	AAW6384	Antibody LM609 hea
39	41	70.7	118	20	AAW06384	Humanised LM609 an
40	41	70.7	118	20	AAW06385	Humanised LM609 an
41	41	70.7	118	20	AAW06386	Humanised LM609 an
42	41	70.7	118	20	AAW06386	Humanised LM609 an
43	41	70.7	130	20	AAW06379	Murine monoclonal
44	40	69.0	33	23	ABP41652	Human ovarian anti
45	38	65.5	10	19	AAW76021	LM609 grafted anti

ALIGNMENTS

RESULT 1
AAW76038
ID AAW76038 standard; Protein; 10 AA.
XX
AC AAW76038;
XX
DT 02-NOV-1998 (first entry)
XX
DE LM609 grafted antibody V-H region CDR3 protein fragment #14.
XX
KW Vitaxin; antibody; variable region; heavy chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
XX
OS Mus sp.
XX
PN WO9833919-A2.
XX
PD 06-AUG-1998.
XX
PF 30-JAN-1998; 98WO-US01826.
XX
PR 30-JAN-1997; 97US-0791391.
XX
PA (IXSY-) IXSYS INC.
XX
PI Glaser SM, Huse WD;
XX
DR WPI; 1998-437472/37.
DR N-PSDB; AAW49875.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
PS Claim 62; Page 43; 129pp; English.
XX
CC AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease. Specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
CC antibodies contain non-murine framework regions so are suitable for use
CC in humans. Enhanced types of LM609 have affinity more than 90 times
CC greater than that of parent the parent antibody.
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 58; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00055;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARNHGGSFYS 10
|||||
Db 1 ARNHGGSFYS 10

RESULT 2
AAB61396
ID AAB61396 standard; peptide; 10 AA.
XX
AC AAB61396;
XX
XX 03-APR-2001 (first entry)
XX
DE Multiple mutant VH CDR3 #2.
XX
XX LM609; grafted antibody; alphaVbeta_3 integrin; angiogenesis;
KW inflammatory; cancer; retina; restenosis; osteoporosis.
XX
XX Unidentified.
XX
XX WO200078815-A1.
XX
XX 28-DEC-2000.
XX
XX 23-JUN-2000; 2000WO-US17454.
XX
XX 24-JUN-1999; 99US-0339922.
XX
XX (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX
XX Huse WD, Wu H;
XX
XX WPI; 2001-050110/06.
XX
XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
PT osteoporosis -
XX
XX Disclosure; Page 42; 132pp; English.
XX
XX The present invention relates to enhanced LM609 grafted antibodies
CC exhibiting selective binding affinity to alphavbeta_3 integrin or
CC their functional fragments. The antibodies or their functional
CC fragments can be used in the diagnosis and treatment of
CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory

CC diseases (such as psoriasis and chronic articular rheumatism),
CC disorders associated with inappropriate or inopportune invasion of
CC vessels (such as diabetic retinopathy, neovascular glaucoma and
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
CC diseases (such as macular degeneration), restenosis and
CC osteoporosis.
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 58; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00055;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARNHGGSFYS 10
|||||
Db 1 ARNHGGSFYS 10

RESULT 3
AAW76040
ID AAW76040 standard; Protein; 10 AA.
XX
AC AAW76040;
XX
XX 02-NOV-1998 (first entry)
XX
XX LM609 grafted antibody V-H region CDR3 protein fragment #16.
XX
XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
XX
XX Mus sp.
OS
XX WO9833919-A2.
XX
XX 06-AUG-1998.
XX
XX 30-JAN-1998; 98WO-US01826.
XX
XX 30-JAN-1997; 97US-0791391.
XX
XX (IXSY-) IXSYS INC.
XX
XX Glaser SM, Huse WD;
PI
XX N-PSDB; AAV49877.
DR
XX WPI; 1998-437472/37.
XX
XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
XX Claim 62; Page 43; 129pp; English.
PS
XX AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease. Specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
CC antibodies contain non-murine framework regions so are suitable for use
CC in humans. Enhanced types of LM609 have affinity more than 90 times
CC greater than that of parent the parent antibody.
XX
SQ Sequence 10 AA;

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Query Match      89.7%; Score 52; DB 19; Length 10;
Best Local Similarity 90.0%; Pred. NO. 0.0064;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNHGSFYS 10
DB 1 ARHNHGSFYS 10
    ||||:|||||
RESULT 4
AAB61398
ID AAB61398 standard; peptide; 10 AA.
XX AAB61398;
XX
XX 03-APR-2001 (first entry)
DE Multiple mutant VH CDR3 #4.
XX
KW LM609; grafted antibody; alphaVbeta_3 integrin; angiogenesis;
KW inflammatory; cancer; retina; restenosis; osteoporosis.
XX
OS Unidentified.
XX
PN WO200078915-A1.
XX
PD 28-DEC-2000.
XX
XX 23-JUN-2000; 2000WO-US17454.
XX
PR 24-JUN-1999; 99US-0339922.
XX
PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX
PI Huse WD, Wu H;
XX
XX WPI: 2001-050110/06.
XX
XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
PT to alpha(V)beta3 integrin, useful in the diagnosis and treatment of
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
PT osteoporosis -
XX
XX Disclosure: Page 43; 132pp; English.
XX
CC The present invention relates to enhanced LM609 grafted antibodies
CC exhibiting selective binding affinity to alphaVbeta_3 integrin or
CC their functional fragments. The antibodies or their functional
CC fragments can be used in the diagnosis and treatment of
CC alphaVbeta_3-mediated diseases such as angiogenesis, inflammatory
CC diseases (such as psoriasis and chronic articular rheumatism),
CC disorders associated with inappropriate or inopportune invasion of
CC vessels (such as diabetic retinopathy, neovascular glaucoma and
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
CC diseases (such as macular degeneration), restenosis and
CC osteoporosis.
XX
XX Sequence 10 AA;
QY 1 ARHNHGSFYS 10
DB 1 ARHNHGSFYS 10
    |||||:|||||
RESULT 6
AAB61395
ID AAB61395 standard; peptide; 10 AA.
XX
XX AAB61395;
XX
XX 03-APR-2001 (first entry)
XX
XX Multiple mutant VH CDR3 #1.
DE
XX
KW LM609; grafted antibody; alphaVbeta_3 integrin; angiogenesis;
KW inflammatory; cancer; retina; restenosis; osteoporosis.

```

```

AC AAW76037;
XX
DT 02-NOV-1998 (first entry)
XX
DE LM609 grafted antibody V-H region CDR3 protein fragment #13.
XX
XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
XX complementarity determining region.
XX
OS Mus sp.
XX
XX WO9833919-A2.
XX
XX 06-AUG-1998.
XX
XX 30-JAN-1998; 98WO-US01826.
XX
XX 30-JAN-1997; 97US-0791391.
XX
XX (IXSY-) IXSYS INC.
XX
XX Glaser SM, Huse WD;
XX
XX WPI: 1998-437472/37.
XX
XX N-PSDB; AAV49874.
XX
XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
XX Claim. 62; Page 43; 129pp; English.
XX
XX AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphaVbeta3 and can be used to
CC inhibit binding of alphaVbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphaVbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
CC antibodies contain non-murine framework regions so are suitable for use
CC in humans. Enhanced types of LM609 have affinity more than 90 times
CC greater than that of parent the parent antibody.
XX
XX Sequence 10 AA;
QY 1 ARHNHGSFYS 10
DB 1 ARHNHGSFYS 10
    |||||:|||||
Query Match      84.5%; Score 49; DB 19; Length 10;
Best Local Similarity 90.0%; Pred. NO. 0.022;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNHGSFYS 10
DB 1 ARHNHGSFYS 10
    |||||:|||||
RESULT 6
AAB61395
ID AAB61395 standard; peptide; 10 AA.
XX
XX AAB61395;
XX
XX 03-APR-2001 (first entry)
XX
XX Multiple mutant VH CDR3 #1.
DE
XX
KW LM609; grafted antibody; alphaVbeta_3 integrin; angiogenesis;
KW inflammatory; cancer; retina; restenosis; osteoporosis.

```

```

XX OS Unidentified.
XX PN WO200078815-A1.
XX PD 28-DEC-2000.
XX PF 23-JUN-2000; 2000WO-US17454.
XX PR 24-JUN-1999; 99US-0339922.
XX PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX PI Huse WD, Wu H;
XX XX
XX DR WPI; 2001-050110/06.
XX XX
XX PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity
XX PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
XX PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
XX PT osteoporosis.
XX PS Disclosure; Page 42; 132pp; English.
XX CC The present invention relates to enhanced LM609 grafted antibodies
XX CC exhibiting selective binding affinity to alphaVbeta3 integrin or
XX CC their functional fragments. The antibodies or their functional
XX CC fragments can be used in the diagnosis and treatment of
XX CC alphaVbeta3-mediated diseases such as angiogenesis, inflammatory
XX CC diseases (such as psoriasis and chronic articular rheumatism),
XX CC disorders associated with inappropriate or inopportune invasion of
XX CC vessels (such as diabetic retinopathy, neovascular glaucoma and
XX CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
XX CC diseases (such as macular degeneration), restenosis and
XX CC osteoporosis.
XX SQ Sequence 10 AA;

Query Match 84.5%; Score 49; DB 22; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.022;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNHGSFYS 10
   | | | | | | | |
Db 1 ARHNHGSFAS 10

RESULT 7
AAW76039
ID AAW76039 standard; Protein; 10 AA.
XX AC AAW76039;
XX AC AAW76039;
XX DT 02-NOV-1998 (first entry)
XX DE LM609 grafted antibody V-H region CDR3 protein fragment #15.
XX KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
XX KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
XX KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
XX KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
XX KW macular degeneration; osteoporosis; primer; V-H region; CDR;
XX KW complementarity determining region.
XX OS Mus sp.
XX PN WO9833919-A2.
XX PD 06-AUG-1998.
XX PF 30-JAN-1998; 98WO-US01826.
XX PR 30-JAN-1997; 97US-0791391.
XX PA (IXSY-) IXXSYS INC.
XX PI Glaser SM, Huse WD;
XX XX
XX DR WPI; 1998-437472/37.
XX DR N-PSDB; AAW49860.

XX PA (IXSY-) IXXSYS INC.
XX PI Glaser SM, Huse WD;
XX XX
XX DR WPI; 1998-437472/37.
XX DR N-PSDB; AAW49860.

AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
LM609 heavy and light chain variable region. LM609 and the antibody
vitaxin bind selectively to integrin alphavbeta3 and can be used to
inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
CC antibodies contain non-murine framework regions so are suitable for use
CC in humans. Enhanced types of LM609 have affinity more than 90 times
CC greater than that of parent the parent antibody.
XX SQ Sequence 10 AA;

Query Match 82.8%; Score 48; DB 19; Length 10;
Best Local Similarity 88.9%; Pred. No. 0.033;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNHGSFY 9
   | | | | | | | |
Db 1 ARHNHGSFY 9

RESULT 8
AAW76023
ID AAW76023 standard; Protein; 10 AA.
XX AC AAW76023;
XX DT 02-NOV-1998 (first entry)
XX DE LM609 grafted antibody V-H region CDR3 protein fragment #5.
XX KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
XX KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
XX KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
XX KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
XX KW macular degeneration; osteoporosis; primer; V-H region; CDR;
XX KW complementarity determining region.
XX OS Mus sp.
XX PN WO9833919-A2.
XX PD 06-AUG-1998.
XX PF 30-JAN-1998; 98WO-US01826.
XX PR 30-JAN-1997; 97US-0791391.
XX PA (IXSY-) IXXSYS INC.
XX PI Glaser SM, Huse WD;
XX XX
XX DR WPI; 1998-437472/37.
XX DR N-PSDB; AAW49860.

```

PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
XX
PS Claim 62; Page 41; 129pp; English.
XX
XX AA76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
CC antibodies contain non-murine framework regions so are suitable for use
CC in humans. Enhanced types of LM609 have affinity more than 90 times
CC greater than that of parent the parent antibody.
XX
SQ Sequence 10 AA;
Query Match 82.8%; Score 48; DB 19; Length 10;
Best Local Similarity 88.9%; Pred. No. 0.033;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 ARHNHGSFY 9
DB 1 ARHNHGSFY 9
||||:||||
RESULT 9
AAB61381
ID AAB61381 standard; peptide; 10 AA.
XX
AC AAB61381;
XX
DT 03-APR-2001 (first entry)
XX
DE Mutant VH CDR3 peptide #4.
XX
KW LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
KW inflammatory; cancer; retina; restenosis; osteoporosis.
XX
OS Unidentified.
XX
XX WO200078815-A1.
XX
PD 28-DEC-2000.
XX
PF 23-JUN-2000; 2000WO-US17454.
XX
PR 24-JUN-1999; 99US-0339922.
XX
PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX
PI Huse WD, Wu H;
XX
DR WPI; 2001-050110/06.
XX
PN WO200078815-A1.
XX
PD 28-DEC-2000.
XX
PF 23-JUN-2000; 2000WO-US17454.
XX
PR 24-JUN-1999; 99US-0339922.
XX
PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX
PI Huse WD, Wu H;
XX
DR WPI; 2001-050110/06.
XX
PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity
PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
PT osteoporosis -
XX
PS Disclosure; Page 41; 132pp; English.
XX
CC The present invention relates to enhanced LM609 grafted antibodies
CC exhibiting selective binding affinity to alphavbeta_3 integrin or
CC their functional fragments. The antibodies or their functional
CC fragments can be used in the diagnosis and treatment of
CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
CC diseases (such as psoriasis and chronic articular rheumatism),
XX
PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity
PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
PT osteoporosis -
XX
PS Disclosure; Page 41; 132pp; English.

CC disorders associated with inappropriate or inopportune invasion of
CC vessels (such as diabetic retinopathy, neovascular glaucoma and
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
CC diseases (such as macular degeneration), restenosis and
CC osteoporosis.
XX
SQ Sequence 10 AA;
Query Match 82.8%; Score 48; DB 22; Length 10;
Best Local Similarity 88.9%; Pred. No. 0.033;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 ARHNHGSFY 9
DB 1 ARHNHGSFY 9
||||:||||
RESULT 10
AAB61397
ID AAB61397 standard; peptide; 10 AA.
XX
AC AAB61397;
XX
DT 03-APR-2001 (first entry)
XX
DE Multiple mutant VH CDR3 #3.
XX
KW LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
KW inflammatory; cancer; retina; restenosis; osteoporosis.
XX
OS Unidentified.
XX
XX WO200078815-A1.
XX
PD 28-DEC-2000.
XX
PF 23-JUN-2000; 2000WO-US17454.
XX
PR 24-JUN-1999; 99US-0339922.
XX
PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX
PI Huse WD, Wu H;
XX
DR WPI; 2001-050110/06.
XX
PN Enhanced LM609 grafted antibodies exhibiting selective binding affinity
PN to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
PN angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
PN osteoporosis -
XX
PS Disclosure; Page 43; 132pp; English.
XX
CC The present invention relates to enhanced LM609 grafted antibodies
CC exhibiting selective binding affinity to alphavbeta_3 integrin or
CC their functional fragments. The antibodies or their functional
CC fragments can be used in the diagnosis and treatment of
CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
CC diseases (such as psoriasis and chronic articular rheumatism),
CC disorders associated with inappropriate or inopportune invasion of
CC vessels (such as diabetic retinopathy, neovascular glaucoma and
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
CC diseases (such as macular degeneration), restenosis and
CC osteoporosis.
XX
SQ Sequence 10 AA;
Query Match 82.8%; Score 48; DB 22; Length 10;
Best Local Similarity 88.9%; Pred. No. 0.033;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 ARHNHGSFY 9
||||:||||

```

Db      1 ARHNHGSFY 9

RESULT 11
AAW76020
ID      AAW76020 standard; Protein; 10 AA.
XX
AC      AAW76020;
XX
DT      02-NOV-1998 (first entry)
XX
XX      LM609 grafted antibody V-H region CDR3 protein fragment #2.
XX
XX      Vitaxin; antibody; variable region; heavy chain; integrin;
KW      LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW      diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW      neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW      macular degeneration; osteoporosis; primer; V-H region; CDR;
KW      complementarity determining region.
XX
OS      Mus sp.
XX
PN      WO9833919-A2.
XX
PD      06-AUG-1998.
XX
PF      30-JAN-1998; 98WO-US01826.
XX
PR      30-JAN-1997; 97US-0791391.
XX
PA      (IXSY-) IXSYS INC.
XX
PI      Glaser SM, Huse WD;
XX
XX      WPI; 1998-437472/37.
DR      N-PSDB; AAV49857.
XX
XX      Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT      integrin - and related grafted antibodies based on murine monoclonal
PT      LM609, also related nucleic acid, used to treat, prevent or diagnose
PT      angiogenesis or restenosis
XX
PS      Claim 62; Page 41; 129pp; English.
XX
CC      AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
CC      LM609 heavy and light chain variable region. LM609 and the antibody
CC      vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC      inhibit binding of alphavbeta3 to a ligand and thus block
CC      prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC      angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC      diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
CC      rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
CC      antibodies contain non-murine framework regions so are suitable for use
CC      in humans. Enhanced types of LM609 have affinity more than 90 times
CC      greater than that of parent the parent antibody.
XX
SQ      Sequence 10 AA;

Query Match      81.0%; Score 47; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ARHNHGSF 8
        |||||
Db      1 ARHNHGSF 8

RESULT 12
AAB61378
ID      AAB61378 standard; peptide; 10 AA.
XX
AC      AAB61378;

Query Match      81.0%; Score 47; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ARHNHGSF 8
        |||||
Db      1 ARHNHGSF 8

RESULT 13
AAW76024
ID      AAW76024 standard; Protein; 10 AA.
XX
AC      AAW76024;
XX
DT      02-NOV-1998 (first entry)
XX
XX      LM609 grafted antibody V-H region CDR3 protein fragment #6.
XX
XX      Vitaxin; antibody; variable region; heavy chain; integrin;
KW      LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW      diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW      neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW      macular degeneration; osteoporosis; primer; V-H region; CDR;
KW      complementarity determining region.
XX
OS      Mus sp.
XX

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```

XX      03-APR-2001 (first entry)
DT
XX      Mutant VH CDR3 peptide #1.
DE
XX      LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
KW      inflammatory; cancer; retina; restenosis; osteoporosis.
KW
XX      Unidentified.
OS
XX      WO200078815-A1.
PN
XX      28-DEC-2000.
PD
XX      23-JUN-2000; 2000WO-US17454.
PF
XX      24-JUN-1999; 99US-0339922.
PR
XX      (MOLE-) APPLIED MOLECULAR EVOLUTION.
PA
XX      Huse WD, Wu H;
PI
XX      WPI; 2001-050110/06.
DR
XX      Enhanced LM609 grafted antibodies exhibiting selective binding affinity
PT      to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
PT      angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
PT      osteoporosis -
XX
PS      Disclosure; Page 41; 132pp; English.
XX
CC      The present invention relates to enhanced LM609 grafted antibodies
CC      exhibiting selective binding affinity to alphavbeta_3 integrin or
CC      their functional fragments. The antibodies or their functional
CC      fragments can be used in the diagnosis and treatment of
CC      alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
CC      diseases (such as psoriasis and chronic articular rheumatism),
CC      disorders associated with inappropriate or inopportune invasion of
CC      vessels (such as diabetic retinopathy, neovascular glaucoma and
CC      cancer disorders such as tumours and Kaposi's sarcoma), retinal
CC      diseases (such as macular degeneration), restenosis and
CC      osteoporosis.
XX
SQ      Sequence 10 AA;

Query Match      81.0%; Score 47; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ARHNHGSF 8
        |||||
Db      1 ARHNHGSF 8

RESULT 13
AAW76024
ID      AAW76024 standard; Protein; 10 AA.
XX
AC      AAW76024;
XX
DT      02-NOV-1998 (first entry)
XX
XX      LM609 grafted antibody V-H region CDR3 protein fragment #6.
XX
XX      Vitaxin; antibody; variable region; heavy chain; integrin;
KW      LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW      diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW      neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW      macular degeneration; osteoporosis; primer; V-H region; CDR;
KW      complementarity determining region.
XX
OS      Mus sp.
XX

```

PN WO9833919-A2.
 XX
 PD 06-AUG-1998.
 XX
 PF 30-JAN-1998; 98WO-US01826.
 XX
 PR 30-JAN-1997; 97US-0791391.
 XX
 PA (IXSY-) IXSYS INC.
 XX
 XX Glaser SM, Huse WD;
 PI
 XX WPI: 1998-437472/37.
 DR N-PSDB; AAV49861.
 DR
 XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 XX Claim 62; Page 41; 129pp; English.
 PS
 XX AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, the
 CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
 CC antibodies contain non-murine framework regions so are suitable for use
 CC in humans. Enhanced types of LM609 have affinity more than 90 times
 CC greater than that of parent the parent antibody.
 XX
 XX Sequence 10 AA;
 SQ
 Query Match 74.1%; Score 43; DB 19; Length 10;
 Best Local Similarity 80.0%; Pred. NO. 0.25;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ARNHGGSFYS 10
 Db | | | | : | | | | |
 1 ARHNYGSFAS 10
 RESULT 14
 AAB61382
 ID AAB61382 standard; peptide; 10 AA.
 XX
 AC AAB61382;
 AC
 DT 03-APR-2001 (first entry)
 XX
 XX Mutant VH CDR3 peptide #5.
 DE
 DE LM609; grafted antibody; alphavbeta3 integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis.
 KW
 XX Unidentified.
 OS
 XX WO200078815-A1.
 PN
 XX 28-DEC-2000.
 PD
 XX 23-JUN-2000; 2000WO-US17454.
 PF
 XX 24-JUN-1999; 99US-0339922.
 PR
 XX (MOLE-) APPLIED MOLECULAR EVOLUTION.
 PA
 XX Huse WD, Wu H;
 PI
 XX

DR WPI: 2001-050110/06.
 XX
 PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis
 XX
 PS Disclosure; Page 41; 132pp; English.
 XX
 XX The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphavbeta3 integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphavbeta3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.
 XX
 XX Sequence 10 AA;
 SQ
 Query Match 74.1%; Score 43; DB 22; Length 10;
 Best Local Similarity 80.0%; Pred. NO. 0.25;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ARNHGGSFYS 10
 Db | | | | : | | | | |
 1 ARHNYGSFAS 10
 RESULT 15
 AAW76022
 ID AAW76022 standard; Protein; 10 AA.
 XX
 AC AAW76022;
 AC
 DT 02-NOV-1998 (first entry)
 XX
 XX LM609 grafted antibody V-H region CDR3 protein fragment #4.
 DE
 XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 XX
 OS Mus sp.
 XX
 XX WO9833919-A2.
 PN
 XX 06-AUG-1998.
 PD
 XX 30-JAN-1998; 98WO-US01826.
 PF
 XX 30-JAN-1997; 97US-0791391.
 PR
 XX (IXSY-) IXSYS INC.
 PA
 XX Glaser SM, Huse WD;
 PI
 XX WPI: 1998-437472/37.
 DR N-PSDB; AAV49859.
 DR
 XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 XX Claim 62; Page 41; 129pp; English.
 PS
 XX

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OM protein - protein search, using sw model

Run on: November 18, 2002, 18:45:22 : Search time 4.60526 Seconds
(without alignments)
32.704 Million cell updates/sec

Title: US-09-016-061-96

Perfect score: 58

Sequence: 1 ARNHGSFYS 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 97044 seqs, 15060890 residues

Total number of hits satisfying chosen parameters: 97044

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
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12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	41	70.7	117	8	US-08-790-540A-2
2	41	70.7	117	8	US-08-790-540A-6
3	41	70.7	117	8	US-08-791-391A-2
4	41	70.7	117	8	US-08-791-391A-6
5	38	65.5	196	10	US-09-741-669-368
6	38	65.5	196	10	US-09-912-020-376
7	36	62.1	627	9	US-10-041-007-26
8	36	62.1	627	10	US-09-887-586A-30
9	36	62.1	627	10	US-09-903-012-30
10	34	58.6	81	10	US-09-864-761-36626
11	34	58.6	466	10	US-09-944-807-12
12	34	58.6	462	10	US-09-815-242-4953
13	34	58.6	491	10	US-09-815-242-10940
14	33	56.9	18	9	US-10-038-612-86
15	33	56.9	19	9	US-10-038-612-96
16	33	56.9	19	9	US-10-032-330-2
17	33	56.9	21	9	US-10-032-330-45
18	33	56.9	40	10	US-09-864-761-34899
19	33	56.9	101	10	US-09-764-853-432

Query Match 70.7%; Score 41; DB 8; Length 117;
Best Local Similarity 87.5%; Pred. No. 0.95;

ALIGNMENTS

RESULT 1

US-08-790-540A-2
; Sequence 2, Application US/08790540A
; Patent No. US20010011125A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,540A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-790-540A-2

Query Match 70.7%; Score 41; DB 8; Length 117;
Best Local Similarity 87.5%; Pred. No. 0.95;

20	33	56.9	318	10	US-09-334-477-6	Sequence 6, Appl1
21	33	56.9	326	10	US-09-334-477-25	Sequence 25, Appl
22	33	56.9	329	10	US-09-334-477-39	Sequence 39, Appl
23	33	56.9	432	10	US-09-817-774-39	Sequence 39, Appl
24	33	56.9	480	10	US-09-815-242-10999	Sequence 10999, A
25	33	56.9	502	10	US-09-903-068-12	Sequence 12, Appl
26	33	56.9	503	9	US-09-982-543A-2	Sequence 2, Appl1
27	33	56.9	503	10	US-09-903-068-2	Sequence 2, Appl1
28	33	56.9	597	10	US-09-815-242-11455	Sequence 11455, A
29	33	56.9	597	10	US-09-815-242-11617	Sequence 11617, A
30	33	56.9	711	10	US-09-334-477-35	Sequence 35, Appl
31	33	56.9	915	10	US-09-817-514A-6	Sequence 6, Appl1
32	33	56.9	2586	10	US-09-905-129-11	Sequence 11, Appl
33	33	56.9	2586	10	US-09-905-129-14	Sequence 14, Appl
34	33	56.9	2586	10	US-09-991-630-11	Sequence 11, Appl
35	33	56.9	2586	10	US-09-991-630-14	Sequence 14, Appl
36	33	56.9	2587	10	US-09-905-129-16	Sequence 16, Appl
37	33	56.9	2587	10	US-09-991-630-16	Sequence 16, Appl
38	33	56.9	2589	10	US-09-991-630-24	Sequence 24, Appl
39	32	55.2	29	10	US-09-864-761-34610	Sequence 34610, A
40	32	55.2	81	10	US-09-759-143-556	Sequence 556, App
41	32	55.2	81	10	US-09-780-669-556	Sequence 556, App
42	32	55.2	81	10	US-09-822-827-556	Sequence 556, App
43	32	55.2	100	10	US-09-864-761-35983	Sequence 35983, A
44	32	55.2	189	9	US-09-992-738-1	Sequence 1, Appl1
45	32	55.2	299	9	US-09-992-598-213	Sequence 213, App

Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARNHGSF 8
||||:||||
Db 97 ARNYGSF 104

RESULT 2
US-08-790-540A-6
; Sequence 6, Application US/08790540A
; Patent No. US20010011125A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,540A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-790-540A-6

Query Match 70.7%; Score 41; DB 8; Length 117;
Best Local Similarity 87.5%; Pred. No. 0.95;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARNHGSF 8
||||:||||
Db 97 ARNYGSF 104

RESULT 3
US-08-791-391A-2
; Sequence 2, Application US/08791391A
; Patent No. US20010016645A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,391A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-391A-2

Query Match 70.7%; Score 41; DB 8; Length 117;
Best Local Similarity 87.5%; Pred. No. 0.95;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARNHGSF 8
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Db 97 ARNYGSF 104

RESULT 4
US-08-791-391A-6
; Sequence 6, Application US/08791391A
; Patent No. US20010016645A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,391A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-391A-6

Query Match 70.7%; Score 41; DB 8; Length 117;
Best Local Similarity 87.5%; Pred. No. 0.95;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARNHGSF 8
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Db 97 ARHNGSF 104

RESULT 5

US-09-741-669-368

; Sequence 368, Application US/09741669

; Patent No. US2002022718A1

; GENERAL INFORMATION:

; APPLICANT: Forsyth, R. Allyn

; APPLICANT: Ohlsen, Karl L.

; APPLICANT: Zyskind, Judith W.

; TITLE OF INVENTION: Genes identified as required for

; TITLE OF INVENTION: proliferation of E. coli

; FILE REFERENCE: ELITRA.009A

; CURRENT APPLICATION NUMBER: US/09/741.669

; CURRENT FILING DATE: 2000-12-19

; PRIOR APPLICATION NUMBER: US 60/173005

; PRIOR FILING DATE: 1999-12-23

; NUMBER OF SEQ ID NOS: 481

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 368

; LENGTH: 196

; TYPE: PRT

; ORGANISM: Escherichia coli

US-09-741-669-368

Query Match 65.5%; Score 38; DB 10; Length 196;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNHGSF 8

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Db 105 HNHGSF 110

RESULT 6

US-09-912-020-376

; Sequence 376, Application US/09912020

; Patent No. US20020045592A1

; GENERAL INFORMATION:

; APPLICANT: Zyskind, Judith

; APPLICANT: Ohlsen, Karl L.

; APPLICANT: Trawick, John

; APPLICANT: Forsyth, R. Allyn

; APPLICANT: Froelich, Jamie M.

; APPLICANT: Carr, Grant J.

; APPLICANT: Yamamoto, Robert T.

; APPLICANT: Xu, H. Howard

; TITLE OF INVENTION: GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION IN

; TITLE OF INVENTION: ESCHERICHIA COLI

; FILE REFERENCE: ELITRA.001DV1

; CURRENT APPLICATION NUMBER: US/09/912.020

; CURRENT FILING DATE: 2001-07-23

; PRIOR APPLICATION NUMBER: 09/492,709

; PRIOR FILING DATE: 2000-01-27

; PRIOR APPLICATION NUMBER: 60/117,405

; PRIOR FILING DATE: 1999-01-27

; NUMBER OF SEQ ID NOS: 485

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 376

; LENGTH: 196

; TYPE: PRT

; ORGANISM: E. Coli

US-09-912-020-376

Query Match 65.5%; Score 38; DB 10; Length 196;

Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNHGSF 8

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Db 105 HNHGSF 110

RESULT 7

US-10-041-007-26

; Sequence 26, Application US/10041007

; Patent No. US20020164736A1

; GENERAL INFORMATION:

; APPLICANT: Matsuda, Seichi P.T.

; APPLICANT: Schepmann, Hala G

; TITLE OF INVENTION: Ginkgo Biloba Levopimaradiene Synthase

; FILE REFERENCE: P02081US1

; CURRENT APPLICATION NUMBER: US/10/041,007

; CURRENT FILING DATE: 2002-01-07

; PRIOR APPLICATION NUMBER: US 60/259,881

; PRIOR FILING DATE: 2001-01-05

; NUMBER OF SEQ ID NOS: 41

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 26

; LENGTH: 627

; TYPE: PRT

; ORGANISM: Abies grandis

US-10-041-007-26

Query Match 62.1%; Score 36; DB 9; Length 627;
Best Local Similarity 60.0%; Pred. No. 41;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARHNGSFYS 10

 |||||

Db 340 ARHRHVEFYT 349

RESULT 8

US-09-887-586A-30

; Sequence 30, Application US/09887586A

; Patent No. US20020094556A1

; GENERAL INFORMATION:

; APPLICANT: Chappell, Joseph

; APPLICANT: No. US20020094556A11, Joseph P.

; APPLICANT: Starks, Courtney M.

; APPLICANT: Manna, Kathleen R.

; TITLE OF INVENTION: SYNTHASES

; FILE REFERENCE: 07678-025001

; CURRENT APPLICATION NUMBER: US/09/887,586A

; CURRENT FILING DATE: 2001-06-22

; PRIOR APPLICATION NUMBER: 09/398,395

; PRIOR FILING DATE: 1999-09-17

; PRIOR APPLICATION NUMBER: 60/130,628

; PRIOR FILING DATE: 1999-04-22

; PRIOR APPLICATION NUMBER: 60/150,262

; PRIOR FILING DATE: 1999-08-23

; NUMBER OF SEQ ID NOS: 58

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 30

; LENGTH: 627

; TYPE: PRT

; ORGANISM: Abies grandis

US-09-887-586A-30

Query Match 62.1%; Score 36; DB 10; Length 627;
Best Local Similarity 60.0%; Pred. No. 41;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARHNGSFYS 10

 |||||

Db 340 ARHRHVEFYT 349

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RESULT 9
US-09-903-012-30
; Sequence 30, Application US/09903012
; Patent No. US20020094557A1
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: NO. US20020094557A1, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/903,012
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 627
; TYPE: PRT
; ORGANISM: Abies grandis
US-09-903-012-30

Query Match      62.1%; Score 36; DB 10; Length 627;
Best Local Similarity 60.0%; Pred. No. 41;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARNHGSPYS 10
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Db 340 ARHRHVEFYT 349

RESULT 10
US-09-864-761-36626
; Sequence 36626, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aesomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
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; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 36626
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC009892.2
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5.4
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.8
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2.1
; OTHER INFORMATION: EST HUMAN HIT: AW503927.1, EVALUE 2.00e-08
; OTHER INFORMATION: SWISSPROT HIT: Q64281, EVALUE 9.00e-11
US-09-864-761-36626

Query Match      58.6%; Score 34; DB 10; Length 81;
Best Local Similarity 75.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 HNHGSPYS 10
   ||| | ||
Db 66 HNHSSSEYS 73

RESULT 11
US-09-944-807-12
; Sequence 12, Application US/09944807
; Patent No. US20020119494A1
; GENERAL INFORMATION:
; APPLICANT: Boehringer Ingelheim Pharma KG
; TITLE OF INVENTION: Method for identifying substances which positively
; TITLE OF INVENTION: Influence inflammatory conditions of chronic
; TITLE OF INVENTION: Inflammatory airway diseases
; FILE REFERENCE: 082.00n
; CURRENT APPLICATION NUMBER: US/09/944,807
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: UK 0021484.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 466
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-944-807-12

Query Match      58.6%; Score 34; DB 10; Length 466;
Best Local Similarity 75.0%; Pred. No. 68;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 3 HNHGSFYS 10
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 Db 102 HNHSEYS 109

RESULT 12

US-09-815-242-4953
 ; Sequence 4953, Application US/09815242
 ; Patent No. US20020061569A1

GENERAL INFORMATION:

; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Ohlsen, Karl L.
 ; APPLICANT: Zyskind, Judith W.
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John D.
 ; APPLICANT: Carr, Grant J.
 ; APPLICANT: Yamamoto, Robert T.
 ; APPLICANT: Xu, H. Howard
 ; TITLE OF INVENTION: Identification of Essential Genes in
 ; TITLE OF INVENTION: Prokaryotes
 ; FILE REFERENCE: ELITRA.011A

; CURRENT APPLICATION NUMBER: US/09/815,242

; CURRENT FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,727

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/242,578

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/253,625

; PRIOR FILING DATE: 2000-11-27

; PRIOR APPLICATION NUMBER: 60/257,931

; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; NUMBER OF SEQ ID NOS: 14110

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 4953

; LENGTH: 482

; TYPE: PRT

; ORGANISM: Enterococcus faecalis

US-09-815-242-4953

Query Match 58.6%; Score 34; DB 10; Length 482;
 Best Local Similarity 75.0%; Pred. No. 70;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNHGSF 8
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 Db 29 ARHNDGEF 36

RESULT 13

US-09-815-242-10940

; Sequence 10940, Application US/09815242

; Patent No. US20020061569A1

GENERAL INFORMATION:

; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Ohlsen, Karl L.
 ; APPLICANT: Zyskind, Judith W.
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John D.
 ; APPLICANT: Carr, Grant J.
 ; APPLICANT: Yamamoto, Robert T.
 ; APPLICANT: Xu, H. Howard
 ; TITLE OF INVENTION: Identification of Essential Genes in
 ; TITLE OF INVENTION: Prokaryotes
 ; FILE REFERENCE: ELITRA.011A
 ; CURRENT APPLICATION NUMBER: US/09/815,242
 ; CURRENT FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: 60/206,848
 ; PRIOR FILING DATE: 2000-05-23
 ; PRIOR APPLICATION NUMBER: 60/207,727
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: 60/242,578
 ; PRIOR FILING DATE: 2000-10-23
 ; PRIOR APPLICATION NUMBER: 60/253,625
 ; PRIOR FILING DATE: 2000-11-27
 ; PRIOR APPLICATION NUMBER: 60/257,931
 ; PRIOR FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: 60/269,308
 ; PRIOR FILING DATE: 2001-02-16
 ; NUMBER OF SEQ ID NOS: 14110
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 10940

; LENGTH: 491

; TYPE: PRT

; ORGANISM: Enterococcus faecalis

US-09-815-242-10940

Query Match 58.6%; Score 34; DB 10; Length 491;
 Best Local Similarity 75.0%; Pred. No. 72;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNHGSF 8
 ||| | |
 Db 37 ARHNDGEF 44

RESULT 14

US-10-038-612-86

; Sequence 86, Application US/10038612

; Patent No. US20020160478A1

GENERAL INFORMATION:

; APPLICANT: Ben-Sasson, Shmuel A.
 ; TITLE OF INVENTION: Short Peptides Which Selectively
 ; TITLE OF INVENTION: Modulate the Activity of Protein Kinases
 ; FILE REFERENCE: 1242.1029-000 (CMCC-679)
 ; CURRENT APPLICATION NUMBER: US/10/038,612
 ; CURRENT FILING DATE: 2002-01-08
 ; PRIOR APPLICATION NUMBER: US 09/161,094
 ; PRIOR FILING DATE: 1998-09-25
 ; NUMBER OF SEQ ID NOS: 172
 ; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 86

; LENGTH: 18

; TYPE: PRT

; ORGANISM: unknown

; FEATURE:

; OTHER INFORMATION: ALK1

US-10-038-612-86

Query Match 56.9%; Score 33; DB 9; Length 18;
 Best Local Similarity 71.4%; Pred. No. 3.5;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 HNHGSFY 9
 | | | | |
 Db 4 HEHGSFY 10

RESULT 15

US-10-038-612-96

; Sequence 96, Application US/10038612

; Patent No. US20020160478A1

GENERAL INFORMATION:

; APPLICANT: Ben-Sasson, Shmuel A.
 ; TITLE OF INVENTION: Short Peptides Which Selectively
 ; TITLE OF INVENTION: Modulate the Activity of Protein Kinases
 ; FILE REFERENCE: 1242.1029-000 (CMCC-679)
 ; CURRENT APPLICATION NUMBER: US/10/038,612
 ; CURRENT FILING DATE: 2002-01-08

; PRIOR APPLICATION NUMBER: US 09/161,094
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 96
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MYRISTATE
; LOCATION: (1)...(0)
; NAME/KEY: AMIDATION
; LOCATION: (0)...(19)
; OTHER INFORMATION: Alk1
US-10-038-612-96

Query Match 56.9%; Score 33; DB 9; Length 19;
Best Local Similarity 71.4%; Pred. No. 3.7;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 HNHGSFY 9
| | | | |
Db 5 HEHGSly 11

Search completed: November 18, 2002, 19:04:23
Job time : 4.60526 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:43:42 ; Search time 9.47368 Seconds
(without alignments)
31.058 Million cell updates/sec

Title: US-09-016-061-96
Perfect score: 58
Sequence: 1 ARHNHGSFYS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database :
- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
 - 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
 - 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
 - 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
 - 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
 - 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	62.1	627	4	US-09-360-545-2
2	36	62.1	627	4	US-09-360-545-32
3	36	62.1	627	4	US-09-398-395A-30
4	35	60.3	215	4	US-09-134-001C-5483
5	35	60.3	659	1	US-08-198-446B-13
6	35	60.3	659	2	US-08-870-693-13
7	35	60.3	659	4	US-09-292-858B-21
8	34	58.6	99	4	US-09-199-637A-75
9	34	58.6	204	1	US-08-591-989-4
10	34	58.6	483	4	US-09-310-463-16
11	34	58.6	483	4	US-08-842-248A-16
12	33	56.9	94	3	US-09-147-550-14
13	33	56.9	94	3	US-09-147-550-45
14	33	56.9	94	3	US-09-147-550-48
15	33	56.9	94	3	US-09-147-550-77
16	33	56.9	94	3	US-09-147-550-84
17	33	56.9	94	3	US-09-147-550-90
18	33	56.9	94	3	US-09-147-550-101
19	33	56.9	94	4	US-09-557-917-14
20	33	56.9	94	4	US-09-557-917-45
21	33	56.9	94	4	US-09-557-917-48
22	33	56.9	94	4	US-09-557-917-77
23	33	56.9	94	4	US-09-557-917-84
24	33	56.9	94	4	US-09-557-917-90
25	33	56.9	94	4	US-09-557-917-101
26	33	56.9	303	4	US-08-158-735A-15
27	33	56.9	318	3	US-08-816-977-6

28	33	56.9	326	3	US-08-816-977-25	Sequence 25, Appl
29	33	56.9	329	3	US-08-816-977-39	Sequence 39, Appl
30	33	56.9	502	4	US-09-382-256-12	Sequence 12, Appl
31	33	56.9	502	4	US-09-395-115-12	Sequence 12, Appl
32	33	56.9	502	4	US-08-436-265-12	Sequence 12, Appl
33	33	56.9	502	4	US-09-679-187-12	Sequence 12, Appl
34	33	56.9	503	2	US-08-481-337A-2	Sequence 2, Appl
35	33	56.9	503	2	US-08-696-268B-2	Sequence 2, Appl
36	33	56.9	503	4	US-09-382-256-2	Sequence 2, Appl
37	33	56.9	503	4	US-09-393-115-2	Sequence 2, Appl
38	33	56.9	503	4	US-08-436-265-2	Sequence 2, Appl
39	33	56.9	503	4	US-09-679-187-2	Sequence 2, Appl
40	33	56.9	503	5	PCT-US94-11328A-4	Sequence 4, Appl
41	33	56.9	503	5	PCT-US95-05467-2	Sequence 2, Appl
42	33	56.9	505	1	US-08-149-105-16	Sequence 16, Appl
43	33	56.9	505	1	US-08-317-847-16	Sequence 16, Appl
44	33	56.9	630	4	US-09-360-545-78	Sequence 78, Appl
45	33	56.9	711	3	US-08-816-977-35	Sequence 35, Appl

ALIGNMENTS

RESULT 1
US-09-360-545-2
; Sequence 2, Application US/09360545
; Patent No. 6429014
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney B
; APPLICANT: Bohlmann, Jorg
; APPLICANT: Steele, Christopher L
; APPLICANT: Phillips, Michael A
; TITLE OF INVENTION: MONOTERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS)
; FILE REFERENCE: wsur13885
; CURRENT APPLICATION NUMBER: US/09/360,545
; CURRENT FILING DATE: 1999-07-26
; EARLIER APPLICATION NUMBER: 60/052,249
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: PCT/US98/14528
; EARLIER FILING DATE: 1998-07-10
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 627
; TYPE: PRT
; ORGANISM: Abies grandis
US-09-360-545-2

Query Match	62.1%	Score 36;	DB 4;	Length 627;
Best Local Similarity	60.0%	Pred. No. 1.4e+02;		
Matches	6;	Conservative	1;	Mismatches 3;
				Indels 0;
				Gaps 0;
Qy	1	ARHNHGSFYS 10		
Db	340	ARRHRVFT 349		
RESULT 2				
US-09-360-545-32				
; Sequence 32, Application US/09360545				
; Patent No. 6429014				
; GENERAL INFORMATION:				
; APPLICANT: Croteau, Rodney B				
; APPLICANT: Bohlmann, Jorg				
; APPLICANT: Steele, Christopher L				
; APPLICANT: Phillips, Michael A				
; TITLE OF INVENTION: MONOTERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS)				
; FILE REFERENCE: wsur13885				
; CURRENT APPLICATION NUMBER: US/09/360,545				
; CURRENT FILING DATE: 1999-07-26				
; EARLIER APPLICATION NUMBER: 60/052,249				
; EARLIER FILING DATE: 1997-11-07				
; EARLIER APPLICATION NUMBER: PCT/US98/14528				

; EARLIER FILING DATE: 1998-07-10
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 627
; TYPE: PRT
; ORGANISM: Abies grandis
US-09-360-545-32

Query Match 62.1%; Score 36; DB 4; Length 627;
Best Local Similarity 60.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARNHGSEFYS 10
||| | |||
Db 340 ARHRHVEFYT 349

RESULT 3
US-09-398-395A-30
; Sequence 30, Application US/09398395A
; Patent No. 6468772
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 64687721, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/398,395A
; PRIORITY FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 627
; TYPE: PRT
; ORGANISM: Abies grandis
US-09-398-395A-30

Query Match 62.1%; Score 36; DB 4; Length 627;
Best Local Similarity 60.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARNHGSEFYS 10
||| | |||
Db 340 ARHRHVEFYT 349

RESULT 4
US-09-134-001C-5483
; Sequence 5483, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; PRIORITY FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO: 5483
; LENGTH: 215
; TYPE: PRT

; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5483

Query Match 60.3%; Score 35; DB 4; Length 215;
Best Local Similarity 85.7%; Pred. No. 70;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 NHGSEFYS 10
||| ||| |||
Db 205 NHSSEFYS 211

RESULT 5
US-08-198-446B-13
; Sequence 13, Application US/08198446B
; Patent No. 5674996
; GENERAL INFORMATION:
; APPLICANT: Hartwell, Leland H.
; APPLICANT: Weinert, Ted A.
; APPLICANT: Plon, Sharon E.
; APPLICANT: Groudine, Mark T.
; TITLE OF INVENTION: Cell Cycle Checkpoint Genes
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Christensen O'Connor Johnson Kindness PLLC
; STREET: 1420 Fifth Ave., Suite 2800
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101-2347
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/198,446B
; FILING DATE: 18-FEB-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Sheiness, Diana K.
; REGISTRATION NUMBER: 35,356
; REFERENCE/DOCKET NUMBER: FHCRI7537
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-682-8100
; TELEFAX: 206-224-0779
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 659 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: yeast RAD24 protein
US-08-198-446B-13

Query Match 60.3%; Score 35; DB 1; Length 659;
Best Local Similarity 71.4%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNHGSFY 9
||| | |
Db 436 HNHGTIV 442

RESULT 6
US-08-870-693-13
; Sequence 13, Application US/08870693
; Patent No. 5866338
; GENERAL INFORMATION:
; APPLICANT: Hartwell, Leland H.
; APPLICANT: Weinert, Ted A.
; APPLICANT: Plon, Sharon E.
; APPLICANT: Groudine, Mark T.

;/ TITLE OF INVENTION: Cell Cycle Checkpoint Genes
;/ NUMBER OF SEQUENCES: 19
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Christensen O'Connor Johnson Kindness PLLC
;/ STREET: 1420 Fifth Ave., Suite 2800
;/ CITY: Seattle
;/ STATE: WA
;/ COUNTRY: USA
;/ ZIP: 98101-2347
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.25
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/870,693
;/ FILING DATE:
;/ CLASSIFICATION: 536
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 08/198,446
;/ FILING DATE: February 18, 1994
;/ APPLICATION NUMBER: PCT/US93/04458
;/ FILING DATE: May 12, 1993
;/ APPLICATION NUMBER: US 07/884,426
;/ FILING DATE: May 14, 1992
;/ APPLICATION NUMBER: US 07/882,051
;/ FILING DATE: May 12, 1992
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Sheiness, Diana K.
;/ REGISTRATION NUMBER: 35,356
;/ REFERENCE/DOCKET NUMBER: FHCRI10798
;/ TELEPHONE: 206-682-8100
;/ TELEFAX: 206-224-0779
;/ INFORMATION FOR SEQ ID NO: 13:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 659 amino acids
;/ TYPE: amino acid
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: protein
;/ DESCRIPTION: Yeast RAD24 protein
;/ US-08-870-693-13

Query Match 60.3%; Score 35; DB 2; Length 659;
Best Local Similarity 71.4%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNHGSFY 9
Db 436 HNHGTIVY 442

RESULT 7
US-09-292-858B-21
; Sequence 21, Application US/09292858B
; Patent No. 6455681
; GENERAL INFORMATION:
; APPLICANT: Dean, Frank
; APPLICANT: O'Donnell, Michael E.
; TITLE OF INVENTION: DNA MOLECULES ENCODING SINGLE STRAND GAP RESPONSE
; TITLE OF INVENTION: PROTEINS INVOLVED IN ACTIVATION OF A DNA REPAIR/CELL
; FILE REFERENCE: CYCLE CHECKPOINT PATHWAY
; FILE REFERENCE: 2221/1011
; CURRENT APPLICATION NUMBER: US/09/292,858B
; CURRENT FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 60/082,020
; PRIOR FILING DATE: 1998-04-16
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 659
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae

US-09-292-858B-21

Query Match 60.3%; Score 35; DB 4; Length 659;
Best Local Similarity 71.4%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNHGSFY 9
Db 436 HNHGTIVY 442

RESULT 8
US-09-199-637A-75
; Sequence 75, Application US/09199637A
; Patent No. 6355411
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Frederick
; APPLICANT: Goodman, Howard M.
; APPLICANT: Rahme, Laurence G.
; APPLICANT: Mahajan-Miklos, Shalina
; APPLICANT: Tan, Man-Wah
; APPLICANT: Cao, Hui
; APPLICANT: Drenkard, Eliana
; APPLICANT: Tsongalis, John
; TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID
; TITLE OF INVENTION: SEQUENCES AND USES THEREOF
; FILE REFERENCE: 00786/361002
; CURRENT APPLICATION NUMBER: US/09/199,637A
; CURRENT FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 60/066,517
; PRIOR FILING DATE: 1997-11-25
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 75
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-199-637A-75

Query Match 58.6%; Score 34; DB 4; Length 99;
Best Local Similarity 71.4%; Pred. No. 48;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNHGSF 8
Db 15 RHRHGNF 21

RESULT 9
US-08-591-989-4
; Sequence 4, Application US/08591989
; Patent No. 5795721
; GENERAL INFORMATION:
; APPLICANT: Ross S. Rabin, Sumedha Jayasena
; APPLICANT: and Larry Gold
; TITLE OF INVENTION: HIGH AFFINITY NUCLEIC
; TITLE OF INVENTION: ACID LIGANDS OF ICP4
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 East Prentice Avenue, Suite #200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.40 MB
; MEDIUM TYPE: storage
; COMPUTER: IBM COMPATIBLE
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/591,989

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; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX 49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 204
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-591-989-4

Query Match 58.6%; Score 34; DB 1; Length 204;
Best Local Similarity 75.0%; Pred. No. 98;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARNHGSF 8
Db 137 APHGHGSF 144

RESULT 10
US-09-310-463-16
; Sequence 16, Application US/09310463A
; Patent No. 6384203
; GENERAL INFORMATION:
; APPLICANT: Cosman, David J.
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Borges, Luis
; TITLE OF INVENTION: Family of Immunoregulators Designated Leukocyte Immunoglobulin-
; TITLE OF INVENTION: Like Receptors (LIR)
; FILE REFERENCE: 2624-A
; CURRENT APPLICATION NUMBER: US/09/310,463A
; CURRENT FILING DATE: 1999-05-12
; EARLIER APPLICATION NUMBER: 08/842,248
; EARLIER FILING DATE: 1997-04-24
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 16
; LENGTH: 483
; TYPE: PRT
; ORGANISM: human
; US-09-310-463-16

Query Match 58.6%; Score 34; DB 4; Length 483;
Best Local Similarity 75.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 HNHGSFYS 10
Db 102 HNHSEYS 109

RESULT 11
US-08-842-248A-16
; Sequence 16, Application US/08842248A
; Patent No. 6448035
; GENERAL INFORMATION:
; APPLICANT: Cosman, David J.
; TITLE OF INVENTION: Family of Immunoregulators Designated
; TITLE OF INVENTION: Leukocyte Immunoglobulin-Like Receptors (LIR)
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janis C. Henry, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: US

Query Match 58.6%; Score 34; DB 4; Length 483;
Best Local Similarity 75.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 HNHGSFYS 10
Db 102 HNHSEYS 109

RESULT 12
US-09-147-550-14
; Sequence 14, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 14
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
; US-09-147-550-14

Query Match 56.9%; Score 33; DB 3; Length 94;
Best Local Similarity 66.7%; Pred. No. 67;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNGSFYS 10
Db 80 RHNYGVFS 88

RESULT 13
US-09-147-550-45
; Sequence 45, Application US/09147550
; Patent No. 6090540
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; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM/PC Compatible
; OPERATING SYSTEM: Microsoft Word 7.0
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/842,248A
; FILING DATE: April 24, 1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Henry, Janis C.
; REGISTRATION NUMBER: 34,347
; REFERENCE/DOCKET NUMBER: 2624
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 483 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-842-248A-16

Query Match 58.6%; Score 34; DB 4; Length 483;
Best Local Similarity 75.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 HNHGSFYS 10
Db 102 HNHSEYS 109

RESULT 12
US-09-147-550-14
; Sequence 14, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 14
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
; US-09-147-550-14

Query Match 56.9%; Score 33; DB 3; Length 94;
Best Local Similarity 66.7%; Pred. No. 67;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNGSFYS 10
Db 80 RHNYGVFS 88

RESULT 13
US-09-147-550-45
; Sequence 45, Application US/09147550
; Patent No. 6090540
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GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-45

Query Match 56.9%; Score 33; DB 3; Length 94;
Best Local Similarity 66.7%; Pred. No. 67;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 2 RHNGSFYS 10
Db 80 RHNYGVFES 88

RESULT 14
US-09-147-550-48
; Sequence 48, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-48

Query Match 56.9%; Score 33; DB 3; Length 94;
Best Local Similarity 66.7%; Pred. No. 67;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 2 RHNGSFYS 10
Db 80 RHNYGVFES 88

RESULT 15
US-09-147-550-77
; Sequence 77, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550

; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 77
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-77

Query Match 56.9%; Score 33; DB 3; Length 94;
Best Local Similarity 66.7%; Pred. No. 67;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 2 RHNGSFYS 10
Db 80 RHNYGVFES 88

Search completed: November 18, 2002, 17:55:53
Job time : 10.4737 secs

GenCore version 5.1.1.3
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OM protein - protein search, using sw model
Run On: November 18, 2002, 17:47:14 : Search time 10,6579 Seconds
(without alignments)
90.200 Million cell updates/sec

Title: US-09-016-061-98
Perfect score: 58
Sequence: 1 ARHNYGSFY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	72.4	195	2 G86742	conserved hypothetical
2	39	67.2	113	2 S26468	Ig heavy chain V r
3	38	65.5	275	2 G75130	translation initia
4	38	65.5	275	2 D71087	probable translati
5	38	65.5	402	2 T25001	hypothetical prote
6	37	63.8	62	2 H95154	hypothetical prote
7	37	63.8	92	2 F95156	hypothetical prote
8	37	63.8	92	2 G98022	hypothetical prote
9	37	63.8	134	2 B72651	hypothetical prote
10	37	63.8	386	2 S51436	probable membrane
11	37	63.8	388	1 JC5461	cellulase (EC 3.2.
12	37	63.8	388	1 S43920	cellulase (EC 3.2.
13	37	63.8	405	2 F81273	hypothetical prote
14	37	63.8	483	2 E84866	hypothetical prote
15	37	63.8	2288	2 T29999	hypothetical prote
16	36.5	62.9	1052	2 AF2959	conserved hypothet
17	36.5	62.9	1341	2 H98323	hypothetical prote
18	36	62.1	82	2 I51106	Major histocompati
19	36	62.1	89	2 S38688	MHC class II histo
20	36	62.1	89	2 S38683	MHC class II histo
21	36	62.1	89	2 S38684	MHC class II histo
22	36	62.1	177	2 C84952	aminocacyl-tRNA hyd
23	36	62.1	225	2 I47095	MHC class II OVAR-
24	36	62.1	233	2 H82163	arginyl-tRNA-prote
25	36	62.1	244	2 AH1342	transcription regu
26	36	62.1	446	2 T19625	hypothetical prote
27	36	62.1	470	2 H71667	glutamate-tRNA lig
28	36	62.1	723	2 F83173	outer membrane pro
29	36	62.1	786	2 S37031	probable succinogl

30	36	62.1	786	2 F95977	protein tyrosine k
31	35	60.3	9	2 S36850	Ig heavy chain V r
32	35	60.3	167	2 T16454	hypothetical prote
33	35	60.3	190	2 H84403	isochorismatase I1
34	35	60.3	210	1 B69265	conserved hypothet
35	35	60.3	230	2 S46332	homeotic protein G
36	35	60.3	255	2 B71273	probable methionin
37	35	60.3	296	2 H65118	hypothetical adeni
38	35	60.3	296	2 F91145	probable methyltra
39	35	60.3	296	2 B85991	probable methyltra
40	35	60.3	326	2 S47248	site-specific DNA-
41	35	60.3	378	2 T11713	probable alpha-1,2
42	35	60.3	555	2 T47604	oligopeptide trans
43	35	60.3	555	2 T21028	hypothetical prote
44	35	60.3	575	2 T12094	beta-fructofuranos
45	35	60.3	583	2 S56680	beta-fructofuranos

ALIGNMENTS

RESULT 1
G86742
conserved hypothetical protein yjgF [imported] - Lactococcus lactis subsp. lactis (st
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 17-May-2002
C;Accession: G86742
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Eh
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis
A;Reference number: A86825; MUID:21235186; PMID:11337471
A;Accession: G86742
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-195 <SPO>
A;Cross-references: GB:AE005176; PID:gl2723879; PIDN:AAK05041.1; GSPDB:GN00146
A;Experimental source: strain ILL403
C;Genetics:
A;Gene: yjgF
C;Superfamily: hypothetical protein bi011

Query Match 72.4%; Score 42; DB 2; Length 195;
Best Local Similarity 66.7%; Pred. No. 2.6;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY	1	ARHNYGSFY	9
DB	103	AKHNWGAFY	111
		: : : :	

RESULT 2
S26468
Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S26468
R;Kavaler, J.
submitted to the EMBL Data Library, April 1991
A;Reference number: S26459
A;Accession: S26468
A;Status: preliminary
A;Major histocompati
A;Molecule type: mRNA
A;Residues: 1-113 <KAV>
A;Cross-references: EMBL:X59107; NID:g51944; PIDN:CAA41833.1; PTD:g51945
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;I1-94/Domain: immunoglobulin homology <IMM>

Query Match 67.2%; Score 39; DB 2; Length 113;
Best Local Similarity 66.7%; Pred. No. 5.4;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY	1	ARHNYGSFY	9
----	---	-----------	---

Db 93 ARHPYGNYY 101
||| ||::|
RESULT 3
G75130
translation initiation factor aif-2, subunit alpha (aif2a) PAB0568 - Pyrococcus abyssi
C:Species: Pyrococcus abyssi
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C:Accession: G75130
R:anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure
A:Reference number: A75001
A:Accession: G75130
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-275 <KAW>
A:Cross-references: GB:AJ248285; GB:AL096836; NID:g5458067; PIDN:CAB49760.1; PID:g545827
A:Experimental source: strain Orsay
C:Genetics:
C:Superfamily: translation initiation factor eIF-2 alpha chain
Query Match 65.5%; Score 38; DB 2; Length 275;
Best Local Similarity 75.0%; Pred. No. 20;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 3 HNYGSFYE 10
||||:|
Db 23 HNYGAFLE 30
RESULT 4
D71087
probable translation initiation factor eIF-2 alpha chain - Pyrococcus horikoshii
C:Species: Pyrococcus horikoshii
C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000
C:Accession: D71087
R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekita
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
DNA Res. 5, 55-76, 1998
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A:Reference number: A71000; MUID:98344137; PMID:9679194
A:Accession: D71087
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-275 <KAW>
A:Cross-references: GB:AP000004; NID:g3236131; PIDN:BAA30058.1; PID:g3257375
A:Experimental source: strain OT3
A:Note: this accession replaces an interim accession for a sequence replaced by GenBank
C:Genetics:
A:Gene: PH0961
C:Superfamily: translation initiation factor eIF-2 alpha chain
Query Match 65.5%; Score 38; DB 2; Length 275;
Best Local Similarity 75.0%; Pred. No. 20;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 3 HNYGSFYE 10
||||:|
Db 23 HNYGAFLE 30
RESULT 5
T25001
hypothetical protein T19C9.8 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T25001
R:Matthews, L.
submitted to the EMBL Data Library, March 1997
A:Reference number: Z19967

A:Accession: T25001
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-402 <WIL>
A:Cross-references: EMBL:Z92972; PIDN:CAB07486.1; GSPDB:GN00023; CESP:T19C9.8
A:Experimental source: clone T19C9
C:Genetics:
A:Gene: CESP:T19C9.8
A:Map position: 5
A:Introns: 54/1; 229/2; 337/2
Query Match 65.5%; Score 38; DB 2; Length 402;
Best Local Similarity 75.0%; Pred. No. 29;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 3 HNYGSFYE 10
||||:|
Db 261 HDYNSFYE 268
RESULT 6
H95154
hypothetical protein SPI335 [imported] - Streptococcus pneumoniae (strain TIGR4)
C:Species: Streptococcus pneumoniae
C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
C:Accession: H95154
R:Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; H
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzappel
son, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morris
A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: H95154
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-62 <KUR>
A:Cross-references: GB:AE005672; PIDN:AAK75433.1; PID:g14972817; GSPDB:GN00164; TIGR:
A:Experimental source: strain TIGR4
C:Genetics:
A:Gene: SPI335
Query Match 63.8%; Score 37; DB 2; Length 62;
Best Local Similarity 66.7%; Pred. No. 6.9;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 2 RHNYGSFYE 10
||||:|
Db 20 KHNYPLEFYE 28
RESULT 7
F95156
hypothetical protein SPI349 [imported] - Streptococcus pneumoniae (strain TIGR4)
C:Species: Streptococcus pneumoniae
C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
C:Accession: F95156
R:Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; H
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzappel
son, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morris
A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: F95156
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-92 <KUR>
A:Cross-references: GB:AE005672; PIDN:AAK75447.1; PID:g14972833; GSPDB:GN00164; TIGR:
A:Experimental source: strain TIGR4
C:Genetics:
A:Gene: SPI349

Query Match 63.8%; Score 37; DB 2; Length 92;
 Best Local Similarity 66.7%; Pred. No. 10;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFYE 10
 :||| |||
 DB 10 KHNYPLEFYE 18

RESULT 8
 G98022
 hypothetical protein spr1208 [Imported] - Streptococcus pneumoniae (strain R6)
 C:Species: Streptococcus pneumoniae
 C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 22-Oct-2001
 C:Accession: G98022
 R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; E
 e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
 Y, P.; Sun, P.M.; Winkler, M.E.
 J. Bacteriol. 183, 5709-5717, 2001
 A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
 A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
 A:Reference number: A97872; MUID:21429245; PMID:11544234
 A:Accession: G98022
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-92 <KUR>
 A:Cross-references: GB:AE007317; PIDN:AAL00012.1; PID:g15458843; GSPDB:GN00174
 C:Genetics:
 A:Gene: spr1208

Query Match 63.8%; Score 37; DB 2; Length 92;
 Best Local Similarity 66.7%; Pred. No. 10;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFYE 10
 :||| |||
 DB 10 KHNYPLEFYE 18

RESULT 9
 B72651
 hypothetical protein APE0639 - Aeropyrum pernix (strain K1)
 C:Species: Aeropyrum pernix
 C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 24-Aug-2001
 C:Accession: B72651
 R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
 awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
 DNA Res. 6, 83-101, 1999
 A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
 A:Reference number: A72450; MUID:99310339; PMID:10382966
 A:Accession: B72651
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-134 <KAN>
 A:Cross-references: DBJ:AP0000050; NID:g5104188; PIDN:BA79610.1; PID:d1043396; PID:g510
 A:Experimental source: strain K1
 C:Genetics:
 A:Gene: APE0639
 C:Superfamily: conserved hypothetical protein MJ0315

Query Match 63.8%; Score 37; DB 2; Length 134;
 Best Local Similarity 75.0%; Pred. No. 15;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFYE 10
 :||: |||
 DB 26 HVYGNFYE 33

RESULT 10
 S51436
 probable membrane protein YLR191w - yeast (Saccharomyces cerevisiae)
 N:Alternate names: hypothetical protein L9470.1

C:Species: Saccharomyces cerevisiae
 C:Date: 23-Feb-1995 #sequence_revision 12-May-1995 #text_change 06-Feb-1998
 C:Accession: S51436
 R:Wohldmann, P.
 submitted to the EMBL Data Library, November 1994
 A:Description: The sequence of S. cerevisiae cosmid 9470.
 A:Reference number: S51414
 A:Accession: S51436
 A:Molecule type: DNA
 A:Residues: 1-386 <WOH>
 A:Cross-references: EMBL:U17246; NID:g577192; PID:g577193; MIPS:YLR191w
 C:Genetics:
 A:Gene: SGD:PEX13
 A:Cross-references: SGD:S0004181; MIPS:YLR191w
 A:Map position: 12R
 C:Superfamily: SH3 homology
 C:Keywords: transmembrane protein
 F:264-280/Domain: transmembrane #status predicted <TMM>
 F:313-367/Domain: SH3 homology <SH3>

Query Match 63.8%; Score 37; DB 2; Length 386;
 Best Local Similarity 85.7%; Pred. No. 42;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSFY 9
 :||| |||
 DB 117 NNYGSFY 123

RESULT 11
 JC5461
 cellulase (EC 3.2.1.4) precursor - imperfect fungus (Humicola grisea)
 N:Alternate names: endo-1,4-beta-glucanase; endoglucanase
 C:Species: Humicola grisea var. thermolidea
 C:Date: 11-Sep-1998 #sequence_revision 11-Sep-1998 #text_change 16-Jun-2000
 C:Accession: JC5461
 R:Takashima, S.; Nakamura, A.; Masaki, H.; Uozumi, T.
 Biosci. Biotechnol. Biochem. 61, 245-250, 1997
 A:Title: Cloning, sequencing, and expression of a thermostable cellulase gene of Humi
 A:Reference number: JC5461; MUID:97212020; PMID:9058960
 A:Accession: JC5461
 A:Molecule type: DNA
 A:Residues: 1-388 <TAK>
 A:Cross-references: DBJ:D84470; NID:g1304101; PIDN:BAAL2676.1; PID:g1304102
 A:Experimental source: strain IF09854
 C:Genetics:
 A:Gene: egl2
 A:Introns: 120/3; 369/1
 C:Function:
 A:Description: hydrolysis of 1,4-beta-D-glucosidic linkages in beta-D-glucans such as
 A:Pathway: cellulose degradation
 C:Superfamily: Trichoderma cellulase III; fungal cellulose-binding domain homology
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation
 F:1-16/Domain: signal sequence #status predicted <Sig>
 F:17-388/Product: cellulase #status predicted <MAT>
 F:21-52/Domain: fungal cellulose-binding domain homology <FCB>

Query Match 63.8%; Score 37; DB 1; Length 388;
 Best Local Similarity 62.5%; Pred. No. 43;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFYE 10
 :||: |||
 DB 175 HNFGRFYE 182

RESULT 12
 S43920
 cellulase (EC 3.2.1.4) precursor - imperfect fungus (Humicola insolens)
 N:Alternate names: endo-1,4-beta-glucanase; endoglucanase
 C:Species: Humicola insolens
 C:Date: 11-Sep-1998 #sequence_revision 11-Sep-1998 #text_change 18-Jun-1999
 C:Accession: S43920

R;Dalboge, H.; Helldt-Hansen, H.P.
Mol. Gen. Genet. 243, 253-260, 1994
A;Title: A novel method for efficient expression cloning of fungal enzyme genes.
A;Reference number: S43919; MUID:94247364; PMID:8190078
A;Accession: S43920
A;Molecule type: mRNA
A;Residues: 1-388 <DAL>
A;Cross-references: EMBL:X76046; NID:g505194; PIDN:CAA53631.1; PID:g505195
C;Genetics:
A;Gene: CMC3
C;Function:
A;Description: hydrolysis of 1,4-beta-D-glucosidic linkages in beta-D-glucans such as cel-
A;Pathway: cellulose degradation
C;Superfamily: Trichoderma cellulase III; fungal cellulose-binding domain homology
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
F;1-16/Domain: signal sequence #status predicted <SIG>
F;17-388/Product: cellulase #status predicted <MAT>
F;21-52/Domain: fungal cellulose-binding domain homology <FCB>

Query Match 63.8%; Score 37; DB 1; Length 388;
Best Local Similarity 62.5%; Pred. No. 43;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFYE 10
| | | : | |
DB 175 HNFGRYE 182

RESULT 13
F81273
hypothetical protein Cj1305c [imported] - Campylobacter jejuni (strain NCTC 11168)
C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
C;Accession: F81273
R;Parkhill, J.; Wren, B.W.; Mungall, K.; Kettle, J.M.; Churcher, C.; Basham, D.; Chilling-
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrell
Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp
A;Reference number: A81250; MUID:20150912; PMID:10668204
A;Accession: F81273
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-405 <PAR>
A;Cross-references: GB:AL139078; GB:AL111168; NID:g6968723; PIDN:CAB73732.1; PID:g696873
A;Experimental source: serotype O2, strain NCTC 11168
C;Genetics:
A;Gene: Cj1305c
C;Superfamily: Campylobacter jejuni hypothetical protein Cj1306c

Query Match 63.8%; Score 37; DB 2; Length 405;
Best Local Similarity 62.5%; Pred. No. 45;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFYE 10
| | | : | |
DB 238 HSYGDYE 245

RESULT 14
E84866
hypothetical protein At2g43470 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: E84866
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: E84866
A;Status: preliminary
A;Molecule type: DNA

A;Residues: 1-483 <STO>
A;Cross-references: GB:AE002093; NID:g2289012; PIDN:AAB64341.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2g43470
A;Map position: 2

Query Match 63.8%; Score 37; DB 2; Length 483;
Best Local Similarity 75.0%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 HNYGSFYE 10
| | | | | |
DB 288 HQYASFYE 295

RESULT 15

T29999

hypothetical protein ZC8.4 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000

C;Accession: T29999

R;Latreille, P.; Bradshaw, H.

submitted to the EMBL Data Library, July 1996

A;Description: The sequence of C. elegans cosmid ZC8.

A;Reference number: Z20719

A;Accession: T29999

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-2288 <LAT>

A;Cross-references: EMBL:U64862; PIDN:AAB52624.1; GSPDB:GN00028; CBSP:ZC8.4

A;Experimental source: strain Bristol N2; clone ZC8

C;Genetics:

A;Gene: CBSP:ZC8.4

A;Map position: X

A;Introns: 43/2; 80/3; 110/3; 153/2; 274/3; 738/2; 1249/1; 1392/3; 1454/1; 1602/1; 16

Query Match 63.8%; Score 37; DB 2; Length 2288;
Best Local Similarity 66.7%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSFY 9
: | | | | |
DB 34 SRSNYGEFY 42

Search completed: November 18, 2002, 17:57:24
Job time : 11.6579 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 18, 2002, 17:33:36 : Search time 5.39474 Seconds
(without alignments)
76.883 Million cell updates/sec

Title: US-09-016-061-98
Perfect score: 58
Sequence: 1 ARNYGSFYE 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	65.5	275	1	IF2A_PYRAB
2	38	65.5	275	1	IF2A_PYRHO
3	37	63.8	134	1	SPHL_AERPE
4	37	63.8	323	1	CCSA_LOTUA
5	37	63.8	386	1	PEXD_YEAST
6	37	63.8	388	1	GUN3_HUMIN
7	36	62.1	177	1	PTH_BUCAI
8	36	62.1	470	1	SVZ2_RICPR
9	36	62.1	786	1	EXOP_RHIME
10	35	60.3	255	1	AMPX_TREPA
11	35	60.3	294	1	YHDJ_ECOLI
12	35	60.3	367	1	LHX4_HUMAN
13	35	60.3	367	1	LHX4_MOUSE
14	35	60.3	583	1	INV3_DAUCA
15	35	60.3	592	1	INV1_DAUCA
16	35	60.3	592	1	INV2_DAUCA
17	35	60.3	686	1	RECG_TREPA
18	34	58.6	108	1	Y019_NPVAC
19	34	58.6	196	1	FLC_ARATH
20	34	58.6	226	1	GPH_VIBCH
21	34	58.6	284	1	IPYR_PICPA
22	34	58.6	286	1	IPYR_KLULA
23	34	58.6	286	1	IPYR_YEAST
24	34	58.6	564	1	LDHD_HAEIN
25	34	58.6	586	1	SYD_BUCAI
26	34	58.6	718	1	LSP2_DROME
27	34	58.6	887	1	QUAI_DROME
28	33	56.9	89	1	CFA_CITFR
29	33	56.9	347	1	UL33_HSV6U
30	33	56.9	364	1	SUCC_METJA
31	33	56.9	448	1	NCAP_CVHOC
32	33	56.9	473	1	SYE_AQUAE
33	33	56.9	494	1	RNHI_CRIFA

34	33	56.9	512	1	PNTA_HAEIN	P43842 haemophilus
35	33	56.9	514	1	LIM_HALRO	Q25132 halocynthia
36	33	56.9	572	1	NH25_CAEEL	Q19345 caenorhabdi
37	33	56.9	713	1	HS90_EIMTE	Q44001 elmeria ten
38	33	56.9	715	1	ADSV_BOVIN	Q28046 bos taurus
39	33	56.9	725	1	SPEI_DIACA	Q96412 dianthus ca
40	33	56.9	738	1	GCP4_ARATH	Q9m350 arabidopsis
41	33	56.9	826	1	VILI_CHICK	P02640 gallus gall
42	33	56.9	1386	1	RPOD_MARPO	P06274 marchantia
43	33	56.9	1396	1	ITA2_DROME	P12080 drosophila
44	33	56.9	2184	1	RRPL_CDOVO	P24658 canine dist
45	32.5	56.0	2148	1	VITL_AEDAE	Q16927 aedes aegypt

ALIGNMENTS

RESULT 1
ID IF2A_PYRAB STANDARD; PRT; 275 AA.
AC Q9V0E4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable translation initiation factor 2 alpha subunit (eIF-2-alpha).
GN EIF2A OR PAB0568.
OS Pyrococcus abyssi.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=29292;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GE5 / Orsay;
RA Heilig R.;
RT "Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure and evolution".
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: EIF-2 FUNCTIONS IN THE EARLY STEPS OF PROTEIN SYNTHESIS BY FORMING A TERNARY COMPLEX WITH GTP AND INITIATOR TRNA (BY SIMILARITY).
CC -!- SUBUNIT: HETEROTRIMER COMPOSED OF AN ALPHA, A BETA, AND A GAMMA CHAIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE EIF-2-ALPHA FAMILY.
CC -!- SIMILARITY: CONTAINS 1 SI MOTIF DOMAIN.
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CC -----
CC EMBL; AJ248285; CAB49760.1; -.
CC HSSP; P05055; ISRO.
CC InterPro; IPR003029; SI.
CC Pfam; PF00575; SI; 1.
CC SMART; SM00316; SI; 1.
CC PROSITE; PS0126; SI; 1.
CC Initiation factor; Protein biosynthesis; RNA-binding;
CC Complete proteome.
CC DOMAIN 12 83 SI MOTIF.
SQ SEQUENCE 275 AA; 31912 MW; B2659F3A49879B4F CRC64;

Query Match 65.5%; Score 38; DB 1; Length 275;
Best Local Similarity 75.0%; Pred. NO. 4.7;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 3 HNYGSFYE 10
|||||
DB 23 HNYGAFLE 30


```
RESULT 2
IF2A_PYRHO          STANDARD;          PRT;   275 AA.
AC   OS8655;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Probable translation Initiation factor 2 alpha subunit (eIF-2-alpha).
GN   IF2A OR PH0961.
OS   Pyrococcus horikoshii.
OC   Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC   Pyrococcus.
OX   NCBI_TaxID=53953;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98344137; PubMed=9679194;
RA   Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
RA   Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
RA   Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
RA   Funahashi T., Tanaka T., Kudo Y., Yamazaki J., Kishida N., Oguchi A.,
RA   Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RA   Masuchi Y., Shizuwa H., Kikuchi H.;
RT   "Complete sequence and gene organization of the genome of a hyper-
RT   thermophilic archaeobacterium, Pyrococcus horikoshii OT3."
RL   DNA Res. 5:55-76(1998).
CC   -1- FUNCTION: EIF-2 FUNCTIONS IN THE EARLY STEPS OF PROTEIN SYNTHESIS
CC   BY FORMING A TERNARY COMPLEX WITH GTP AND INITIATOR TRNA.
CC   (BY SIMILARITY).
CC   -1- SUBUNIT: HETEROTRIMER COMPOSED OF AN ALPHA, A BETA, AND A GAMMA
CC   CHAIN (BY SIMILARITY).
CC   -1- SIMILARITY: BELONGS TO THE EIF-2-ALPHA FAMILY.
CC   -1- SIMILARITY: CONTAINS 1 S1 MOTIF DOMAIN.
CC   -----
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CC   or send an email to license@isb-sib.ch).
CC   -----
DR   EMBL; AP000004; BAA30058.1; -.
DR   HSP; P05055; ISRO.
DR   InterPro; IPR003029; S1.
DR   Pfam; PF00575; S1; 1.
DR   SMART; SM00316; S1; 1.
DR   PROSITE; PS0126; S1; 1.
KW   Initiation factor; Protein biosynthesis; RNA-binding;
KW   Complete proteome.
FT   DOMAIN          12      83
FT   SEQUENCE        275 AA; 31980 MW; 6AAAD15F10FFB436 CRC64;
Query Match          65.5%; Score 38; DB 1; Length 275;
Best Local Similarity 75.0%; Pred. No. 4.7;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY   3 HNYGSFYE 10
DB   23 HNYGAFLE 30
|||||
RESULT 3
SPHL_AERPE
AC   QYED6;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   S-adenosylmethionine decarboxylase proenzyme 1 (EC 4.1.1.50) (AdoMetDC
DE   1) (SamDC 1) [Contains: S-adenosylmethionine decarboxylase 1 beta
DE   chain; S-adenosylmethionine decarboxylase 1 alpha chain].
GN   SPEH1 OR APE0639.
```

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OS   Aeropyrum pernix.
OC   Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
OC   Desulfurococaceae; Aeropyrum.
OX   NCBI_TaxID=56636;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   STRAIN=K1;
RX   MEDLINE=99310339; PubMed=10382966;
RA   Kawarabayashi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
RA   Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankaï A., Kosugi H.,
RA   Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
RA   Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudo Y.,
RA   Yamazaki J., Kishida N., Oguchi A., Aoki K.-I., Kubota K.,
RA   Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
RT   "Complete genome sequence of an aerobic hyper-thermophilic
RT   crenarchaeon, Aeropyrum pernix K1."
RL   DNA Res. 6:83-101(1999).
CC   -1- FUNCTION: DECARBOXYLATION OF S-ADENOSYLMETHIONINE PROVIDES THE
CC   AMINOPROPYL MOIETY REQUIRED FOR SPERMIDINE BIOSYNTHESIS FROM
CC   PUTRESCINE (BY SIMILARITY).
CC   -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine = (5'-deoxy-5'-
CC   adenosyl)(3'-aminopropyl) methylsulfonium salt + CO(2).
CC   -1- COFACTOR: Pyruvoyl group (By similarity).
CC   -1- SIMILARITY: BELONGS TO THE PROKARYOTIC ADOMETDC FAMILY. SUBFAMILY
CC   1.
CC   -----
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CC   or send an email to license@isb-sib.ch).
CC   -----
DR   EMBL; AP000060; BAA79610.1; -.
DR   InterPro; IPR003826; SAMDC.
DR   Pfam; PF02675; DUF206; 1.
KW   Spermidine biosynthesis; Lyase; Decarboxylase; Zymogen; Pyruvate;
KW   Complete proteome.
FT   CHAIN           1      81
FT   SEQUENCE        134 AA; 14845 MW; 57942011F9A404C4 CRC64;
S-ADENOSYLMETHIONINE DECARBOXYLASE 1 BETA
CHAIN (BY SIMILARITY).
FT   CHAIN           82     134
FT   SEQUENCE        52 AA; 5794 AA; 14845 MW; 57942011F9A404C4 CRC64;
S-ADENOSYLMETHIONINE DECARBOXYLASE 1
ALPHA CHAIN (BY SIMILARITY).
FT   SITE            81     82
FT   MOD_RES         82     82
FT   SEQUENCE        134 AA; 14845 MW; 57942011F9A404C4 CRC64;
CLEFTAGE (NONHYDROLYTIC) (BY SIMILARITY).
CONVERTED TO A PYRUVOYL GROUP (BY
SIMILARITY).
Query Match          63.8%; Score 37; DB 1; Length 134;
Best Local Similarity 75.0%; Pred. No. 3.4;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY   3 HNYGSFYE 10
DB   26 HNYGNFYE 33
|||||
RESULT 4
CCSA_LOTJA
ID   CCSA_LOTJA          STANDARD;          PRT;   323 AA.
AC   Q9BBP4;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Cytochrome c biogenesis protein CCSA.
GN   CCSA.
OS   Lotus japonicus.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Chloroplast.
OC   Eukaryota; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   Spermatophyta; Magnoliophyta; Fabaceae; Papilionoideae; Lotaeae; Lotus.
OX   NCBI_TaxID=34305;
RN   [1]
```

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RP SEQUENCE FROM N.A.
RC STRAIN=Accession MG-20;
RX MEDLINE=21082929; PubMed=11214967;
RA Kato T., Kaneko T., Sato S., Nakamura Y., Tabata S.;
RT "Complete structure of the chloroplast genome of a legume, Lotus
RL japonicus.";
RL DNA Res. 7:323-330(2000).
CC -!- FUNCTION: REQUIRED DURING CYTOCHROME BIOGENESIS AT THE STEP OF
CC HEME ATTACHMENT (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CCMF/CYCK/CCL1/NRFE/CCSA FAMILY.
CC -----
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CC -----
DR EMBL: AP002983; BAB33244.1; -.
DR InterPro: IPR002541; CytC_asm.
DR Pfam: PF01578; CytC_asm; 1.
KW Cytochrome c-type biogenesis; Chloroplast.
SQ SEQUENCE 323 AA; 37185 MW; 5A034E3E2829FE35 CRC64;

Query Match 63.8%; Score 37; DB 1; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
Db 315 HNYGSF 320
|||||

RESULT 5
PEXD_YEAST STANDARD; PRT; 386 AA.
ID PEXD_YEAST
AC P80667;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Peroxisomal membrane protein PAS20 (peroxin-13).
GN PEX13 OR PAS20 OR YLR191W OR L9470.1.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97011136; PubMed=8858166;
RA Elgersma Y., Kwaast L., Klein A., Voorn-Brouwer T., van den Berg M.,
RA Tabak H.F., Distel B.;
RT "The SH3 domain of the Saccharomyces cerevisiae peroxisomal membrane
RT protein Pex13p functions as a docking site for Pex5p, a mobile
RT receptor for the import PEX1-containing proteins.";
RL J. Cell Biol. 135:97-109(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,
RA Favell A., Fulton L., Gattung S., Greco T., Kirsten J., Kucaba T.,
RA Hallsworth K., Hawkins J., Hillier L., Jier M., Johnson D.,
RA Johnston L., Langston Y., Latreille P., Le T., Mardis E., Meneses S.,
RA Miller N., Nhan M., Pauley A., Peluso D., Rifken L., Riles L.,
RA Tailch A., Trevasakis E., Vignati D., Wilcox L., Wohlman P., Vaudin M.,
RA Wilson R., Waterston R.;
RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
RN [3]
RP PARTIAL SEQUENCE, AND CHARACTERIZATION.
RC STRAIN=S288C;
RX MEDLINE=97011157; PubMed=8858167;
RA Erdmann R., Blobel G.;
RT "Identification of Pex13p a peroxisomal membrane receptor for the

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RT PTS1 recognition factor.";
RL J. Cell Biol. 135:111-121(1996).
CC -!- FUNCTION: COMPONENT OF THE PEROXISOMAL TRANSLOCATION MACHINERY
CC WITH PEX14 AND PEX17. INTERACTS WITH THE PTS1 RECEPTOR
CC (PAS10/PEX5).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Peroxisomal.
CC -!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
CC -----
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CC -----
DR EMBL: S82971; AAB46885.1; -.
DR EMBL: U37420; AAB79308.1; -.
DR EMBL: U17246; AAB67453.1; -.
DR EMBL: U14913; AAB67448.1; -.
DR HSSP: Q06187; LAWX.
DR SGD: S0004181; PEX13.
DR InterPro: IPR001452; SH3.
DR Pfam: PF00018; SH3; 1.
DR PRINTS: PR00452; SH3DOMAIN.
DR PRODOM: PD000066; SH3; 1.
DR SMART: SM00326; SH3; 1.
DR PROSITE: PS50002; SH3; 1.
KW Peroxisome; Transport; Protein transport; Transmembrane; SH3 domain.
FT DOMAIN 1 263 POTENTIAL.
FT TRANSMEM 264 280 POTENTIAL.
FT DOMAIN 281 386 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 306 372 SH3.
SQ SEQUENCE 386 AA; 42705 MW; DBEA9A2372185860 CRC64;

Query Match 63.8%; Score 37; DB 1; Length 386;
Best Local Similarity 85.7%; Pred. No. 10;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSFY 9
Db 117 HNYGSFY 123
|||||

RESULT 6
GUN3_HUMIN STANDARD; PRT; 388 AA.
ID GUN3_HUMIN
AC Q12624; Q12620;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Endoglucanase 3 precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase 3)
DE (Cellulase 3).
GN GNC3.
OS Humicola insolens.
OC Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Humicola.
OX NCBI_TaxID=34413;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94247364; PubMed=81900078;
RA Dalboege H., Hansen H.P.H.;
RT "A novel method for efficient expression cloning of fungal enzyme
RT genes.";
RL Mol. Gen. Genet. 243:253-260(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=IFO 9854;
RA Takashima S., Nakamura A., Masaki H., Uozumi T.;
RT "Cloning, sequencing and expression of the thermostable cellulase
RT gene of Humicola grisea.";
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic
CC linkages in cellulose.

```

CC -!- BIOTECHNOLOGY: Used as a detergent cellulase. Sold under the name
 CC Celluzyme by Novozymes. This special enzyme has three effects:
 CC colour brightening, softening and removal of particulate soil. The
 CC overall effect is that it helps to preserve the nice appearance of
 CC new fabric and restores old fabric so that it looks new again.
 CC -!- SIMILARITY: BELONGS TO CELLULASE FAMILY A (FAMILY 5 OF GLYCOSYL
 CC HYDROLASES).
 CC -!- SIMILARITY: CONTAINS 1 FUNGAL-TYPE CELLULOSE-BINDING DOMAIN (CBD).
 CC -----
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 CC -----
 CC EMBL; X76046; CAA53631.1; -;
 CC EMBL; D84470; BAA12676.1; -;
 CC HSP; P00725; IAZ6.
 CC InterPro; IPR000254; CBD_fungal.
 CC Pfam; PF00150; cellulase; 1.
 CC Pfam; PF00734; CBM_1; 1.
 CC ProDom; PD001821; CBD_fungal; 1.
 CC SMART; SM00236; fcbd; 1.
 CC PROSITE; PS00562; CBD_FUNGAL; 1.
 CC PROSITE; PS00659; GLYCOSYL_HYDROL_F5; FALSE_NEG.
 CC Cellulose degradation; Hydrolase; Glycosidase; Glycoprotein; Signal.
 CC FT SIGNAL 1 16
 CC CHAIN 17 388
 CC DOMAIN 18 52
 CC DOMAIN 53 91
 CC DOMAIN 92 388
 CC CATALYTIC
 CC BY SIMILARITY.
 CC DISULFID 24 41
 CC BY SIMILARITY.
 CC CARBOHYD 35 51
 CC N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHYD 155 155
 CC N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHYD 259 259
 CC N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC ACT_SITE 215 215
 CC PROTON DONOR (BY SIMILARITY).
 CC ACT_SITE 322 322
 CC NUCLEOPHILE (BY SIMILARITY).
 CC G -> S (IN REF. 2).
 CC CONFLICT 340 340
 CC T -> N (IN REF. 2).
 CC CONFLICT 340 340
 CC SEQUENCE 388 AA; 42563 MW; C7CF349DACC10690 CRC64;

Query Match 63.8%; Score 37; DB 1; Length 388;
 Best Local Similarity 62.5%; Pred. No. 10;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 HNYGSFYE 10
 ||| :||
 Db 175 HNFGRYE 182

RESULT 7
 PTH_BUCAI
 ID PTH_BUCAI STANDARD; PRT; 177 AA.
 AC P57287;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Peptidyl-trna hydrolase (EC 3.1.1.29) (PTH).
 GN PTH OR BU190.
 OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
 OS symbiotic bacterium).
 OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.
 OX NCBI_TaxID=118099;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Tokyo 1998;
 RX MEDLINE=20445173; PubMed=10993077;
 RA Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
 RT "Genome sequence of the endocellular bacterial symbiont of aphids

RT Buchnera sp. APS. #;
 RL Nature 407:81-86(2000).
 CC -!- FUNCTION: THE NATURAL SUBSTRATE FOR THIS ENZYME MAY BE PEPTIDYL-
 CC TRNAS WHICH DROP OFF THE RIBOSOME DURING PROTEIN SYNTHESIS
 CC (BY SIMILARITY).
 CC -!- CATALYTIC ACTIVITY: N-substituted aminoacyl-tRNA + H(2)O = N-
 CC substituted amino acid + tRNA.
 CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE PTH FAMILY.
 CC -----
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 CC -----
 CC EMBL; AP001118; BAB12907.1; -;
 CC HSP; P23932; 2PTH.
 CC InterPro; IPR001328; Pept_trna_hydro.
 CC Pfam; PF01195; Pept_LRNA_hydro; 1.
 CC ProDom; PD005324; Pept_LRNA_hydro; 1.
 CC TIGRFAMs; TIGR00447; pth; 1.
 CC PROSITE; PS01195; PEPT_TRNA_HYDROL_1; FALSE_NEG.
 CC PROSITE; PS01196; PEPT_TRNA_HYDROL_2; 1.
 CC Hydrolase; Complete proteome.
 CC SQ SEQUENCE 177 AA; 20576 MW; BD18DA8FEF0DFAAF CRC64;

Query Match 62.1%; Score 36; DB 1; Length 177;
 Best Local Similarity 75.0%; Pred. No. 7.1;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSFY 9
 ||||| :||
 Db 16 RHNVGSWY 23

RESULT 8
 SYE2_RICPR
 ID SYE2_RICPR STANDARD; PRT; 470 AA.
 AC Q9ZCT8;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Glutamyl-tRNA synthetase 2 (EC 6.1.1.17) (Glutamate--trna ligase 2).
 DE (GLURS'2).
 GN GLTX2 OR RP623.
 OS Rickettsia prowazekii.
 OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
 OC Rickettsiaceae; Rickettsia;
 OX NCBI_TaxID=782;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Madrid E;
 RX MEDLINE=99039499; PubMed=9823893;
 RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,
 RA Sicheritz-Ponten T., Almark U.C.M., Podowski R.M., Naeslund A.K.,
 RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
 RT "The genome sequence of Rickettsia prowazekii and the origin of
 RT mitochondria".
 RL Nature 396:133-140(1998).
 CC -!- CATALYTIC ACTIVITY: ATP + L-glutamate + tRNA(Glu) = AMP +
 CC diphosphate + L-glutamyl-tRNA(Glu).
 CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
 CC -----
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CC -----
 DR EMBL; AJ235272; CAAL5066.1; -
 DR HSSP; P27000; IGLN.
 DR InterPro; IPR004527; GluLact.bact.
 DR InterPro; IPR000924; GluLact-synt_lc.
 DR InterPro; IPR001412; tRNA-synt_I.
 DR Pfam; PF00749; tRNA-synt_lc; 1.
 DR PRINTS; PR00987; TRNASYNTHGLU.
 DR TIGRFAMS; TIGR00464; gltX.bact.1.
 DR PROSITE; PS00178; AA-TRNA_LIGASE_I; FALSE_NEG.
 KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
 KW Complete proteome.
 FT SITE 10 20 "HIGH" REGION.
 FT SITE 239 243 "KMSKS" REGION.
 FT BINDING 242 242 ATP (BY SIMILARITY).
 FT SEQUENCE 470 AA; 53696 MW; DFLCE50A20B8A9FD CRC64;

Query Match 62.1%; Score 36; DB 1; Length 470;
 Best Local Similarity 66.7%; Pred. No. 20;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSFY 9
 DB 31 ARHNGKFF 39
 ||||| | | | | |

RESULT 9
 ID EXP_RHIME STANDARD; PRT; 786 AA.
 AC P33698;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Succinoglycan biosynthesis transport protein exop.
 GN EXP OR RB1086 OR SMB20961.
 OS Rhizobium meliloti (Sinorhizobium meliloti).
 OC Plasmid pSymb (megaplasmid 2).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Sinorhizobium.
 OX NCBI_TaxID=382;
 [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=1021;
 RX MEDLINE=94042869; PubMed=8226645;
 RA Glucksmann M.A., Reuber T.L., Walker G.C.;
 RT "Family of glycosyl transferases needed for the synthesis of
 RT succinoglycan by Rhizobium meliloti.";
 RL J. Bacteriol. 175:7033-7044(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1021;
 RX MEDLINE=94042870; PubMed=8226646;
 RA Glucksmann M.A., Reuber T.L., Walker G.C.;
 RT "Genes needed for the modification, polymerization, export, and
 RT processing of succinoglycan by Rhizobium meliloti: a model for
 RT succinoglycan biosynthesis.";
 RL J. Bacteriol. 175:7045-7055(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RCR2011 / SU47;
 RX MEDLINE=94067019; PubMed=8246891;
 RA Becker A., Kleickmann A., Keller M., Arnold W., Puehler A.;
 RT "Identification and analysis of the Rhizobium meliloti exoAMONP genes
 RT involved in exopolysaccharide biosynthesis and mapping of promoters
 RT located on the exoHKLAMONP fragment.";
 RL Mol. Gen. Genet. 241:367-379(1993).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1021;
 RX MEDLINE=21396508; PubMed=11481431;

RA Finan T.M., Weidner S., Wong K., Buhrmester J., Chain P.,
 RA Vorhoefer F.J., Hernandez-Lucas I., Becker A., Cowie A., Gouzy J.,
 RA Golding B., Puehler A.;
 RT "The complete sequence of the 1.683-kb pSymb megaplasmid from the N2-
 RT fixing endosymbiont Sinorhizobium meliloti.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).
 CC 1- PATHWAY: Exopolysaccharide biosynthesis.
 CC 1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
 CC 1- SIMILARITY: SOME, TO B.SOLANACEARUM EPSB.
 CC -----
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CC -----
 DR EMBL; L20758; AAA16042.1; -
 DR EMBL; Z22636; CAA80349.1; -
 DR EMBL; AL603645; CAC49486.1; -
 DR PIR; B49349; B49349.
 DR PIR; S37031; S37031.
 DR PIR; S39960; S39960.
 DR InterPro; IPR003856; Wzz.
 DR Pfam; PF02706; wzz; 1.
 DR TIGRFAMS; TIGR01005; eps_transp_fam; 1.
 KW Exopolysaccharide synthesis; Transport; Transmembrane; ATP-binding;
 KW Plasmid; Complete proteome.
 FT DOMAIN 1 42 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 43 66 POTENTIAL.
 FT DOMAIN 67 689 PERIPLASMIC (POTENTIAL).
 FT TRANSMEM 690 711 POTENTIAL.
 FT DOMAIN 712 786 CYTOPLASMIC (POTENTIAL).
 FT NP_BIND 583 590 ATP (POTENTIAL).
 SQ SEQUENCE 786 AA; 86123 MW; E19E771E31F2030C CRC64;

Query Match 62.1%; Score 36; DB 1; Length 786;
 Best Local Similarity 62.5%; Pred. No. 34;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFY 9
 DB 768 RHRYGKYY 775
 ||||| | | | | |

RESULT 10
 ID AMPM_TREPA STANDARD; PRT; 255 AA.
 AC O83814;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Methionine aminopeptidase (EC 3.4.11.18) (MAP) (Peptidase M).
 GN MAP OR TP0842.
 OS Treponema pallidum.
 OC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
 OX NCBI_TaxID=160;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Nichols;
 RX MEDLINE=98332770; PubMed=9665876;
 RA Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
 RA Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,
 RA Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
 RA Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,
 RA McDonald L., Artach P., Bowman C., Cotton M.D., Fujii C., Garland S.,
 RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
 RA Venter J.C.;
 RT "Complete genome sequence of Treponema pallidum, the syphilis
 RT spirochete.";
 RL Science 281:375-388(1998).
 CC 1- FUNCTION: REMOVES THE AMINO-TERMINAL METHIONINE FROM NASCENT

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CC CC PROTEINS.
CC CC -!- CATALYTIC ACTIVITY: Release of N-terminal amino acids,
CC CC preferentially methionine, from peptides and arylamides.
CC CC -!- COFACTOR: COBALT; BINDS 2 IONS PER SUBUNIT (By similarity).
CC CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M24A.
CC CC -----
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CC CC -----
CC DR EMBL; AE001255; AAC65810.1; -.
CC DR HSSP; P07906; 1C24.
CC DR MEROPS; M24.001; -.
CC DR TIGR; TP0842; -.
CC DR InterPro; IPR002467; MAP_1.
CC DR InterPro; IPR001714; Methamino_Ptase.
CC DR Pfam; PF00557; Peptidase_M24.
CC DR PRINTS; PR00599; MAPEPTIDASE.
CC DR TIGRFAMS; TIGR00500; met_ptase_1; 1.
CC DR PROSITE; PS00680; MAP_1; 1.
CC KW Aminopeptidase; Hydrolase; Cobalt; Complete proteome.
CC FT METAL 93 93 COBALT 2 (BY SIMILARITY).
CC FT METAL 104 104 COBALT 1 AND 2 (BY SIMILARITY).
CC FT METAL 174 174 COBALT 1 (BY SIMILARITY).
CC FT METAL 201 201 COBALT 1 (BY SIMILARITY).
CC FT METAL 232 232 COBALT 1 AND 2 (BY SIMILARITY).
CC FT METAL 255 255 AA; 27316 MW; 4DE582C57F3526A CRC64;
CC SQ SEQUENCE 255 AA; 27316 MW; 4DE582C57F3526A CRC64;

Query Match 60.3%; Score 35; DB 1; Length 255;
Best Local Similarity 60.0%; Pred. No. 16;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARHNYGSFYE 10
||| :| :|
DB 154 ARHREGVVYE 163

RESULT 11
YHDJ_ECOLI
ID YHDJ_ECOLI STANDARD; PRT; 294 AA.
AC P28638;
DT 01-DEC-1992 (Rel. 24, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical adenine-specific methylase yhdJ (EC 2.1.1.72).
GN YHDJ OR B3262.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RA "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE OF 1-98 FROM N.A.
RX MEDLINE=93094136; PubMed=1459953;
RA Ball C.A., Osuna R., Ferguson K.C., Johnson R.C.;
RA "Dramatic changes in Fis levels upon nutrient upshift in Escherichia
RA coli.";
RL J. Bacteriol. 174:8043-8056(1992).
RN [3]

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RP SEQUENCE OF 1-11 FROM N.A.
RC STRAIN=K12;
RX MEDLINE=88217925; PubMed=2835774;
RA Johnson R.C., Ball C.A., Pfeffer D., Simon M.I.;
RT "Isolation of the gene encoding the Hin recombinational enhancer
RT binding protein.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:3484-3488(1988).
CC -!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + DNA adenine = S-
CC CC adenosyl-L-homocysteine + DNA 6-methylaminopurine.
CC CC -!- SIMILARITY: BELONGS TO THE N6-METHYLTRANSFERASE FAMILY.
CC CC -----
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CC CC or send an email to license@isb-sib.ch).
CC CC -----
CC DR EMBL; U18997; AAA58066.1; ALT_INIT.
CC DR EMBL; AE000405; AAC76294.1; ALT_INIT.
CC DR EMBL; M95784; AAA23784.1; ALT_INIT.
CC DR EMBL; J03245; AAA83857.1; -.
CC DR PIR; D47043; D47043.
CC DR EcoGene; EGI1498; yhdJ.
CC DR InterPro; IPR001091; CN4_Metransf.
CC DR InterPro; IPR002295; D2IN6_mtfase.
CC DR InterPro; IPR001601; Methyltransf.
CC DR InterPro; IPR002941; N6/N4_Mtase.
CC DR InterPro; IPR002052; N6_Mtase.
CC DR Pfam; PF01555; N6_N4_Mtase; 1.
CC DR PRINTS; PR00506; D2IN6MTFRASE.
CC DR PROSITE; PS00508; S2IN4MTFRASE.
CC DR PROSITE; PS00092; N6_MTASE; 1.
CC KW Hypothetical protein; Transferase; Methyltransferase;
KW Complete proteome.
FT CONFLICT 28 28 K -> N (IN REF. 2).
FT SEQUENCE 294 AA; 33397 MW; 6BCC49D9A571884B CRC64;

Query Match 60.3%; Score 35; DB 1; Length 294;
Best Local Similarity 60.0%; Pred. No. 19;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSFYE 10
|: :||| ||
DB 119 AKKHGSMYE 128

RESULT 12
LHX4_HUMAN
ID LHX4_HUMAN STANDARD; PRT; 367 AA.
AC Q969G2; Q969W2; O8WWX2;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE LIM/homeobox protein Lhx4.
GN LHX4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Liu Y., Zhou Y., Wang J., Yuan J., Qiang B., Fan M.;
RT "Isolation and cloning of a novel cDNA encoding human LIM homeobox 4
RT protein.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A. AND DISEASE.
RX PubMed=11567216;
RA Machinis K., Pantel J., Netchine I., Leger J., Camand O.J.A.,
RA Sobrier M.-L., Dastot-Le Moal F., Duquesnoy P., Abitbol M.,
RA Czernichow P., Anselem S.;

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Syndromic short stature in patients with a germline mutation in the LIM homeobox LHX4.
 Am. J. Hum. Genet. 69:961-968(2001).
 [3]
 SEQUENCE FROM N.A.
 TISSUE=Placenta;
 Muraki T., Nakamura K., Sakai T.;
 Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 [4]
 SEQUENCE FROM N.A.
 Kawamata N., Oshimi K.;
 "A novel chromosomal translocation t(1;14)(q25;q32) in acute lymphoblastic leukemia involves the LIM homeodomain protein gene, Lhx4.*;
 Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 [5]
 SEQUENCE FROM N.A.
 TISSUE=Muscle;
 Strausberg R.;
 Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: MAY PLAY A CRITICAL ROLE IN THE DEVELOPMENT OF
 CC RESPIRATORY CONTROL MECHANISMS AND IN THE NORMAL GROWTH AND
 CC MATURATION OF THE LUNG (By similarity).
 CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
 CC -!- DISEASE: Defects in LHX4 are the cause of a syndrome characterized
 CC by short stature, pituitary and cerebellar defects, and small
 CC sella turcica.
 CC -!- SIMILARITY: CONTAINS 1 HOMEODOMAIN.
 CC -!- SIMILARITY: CONTAINS 2 LIM DOMAINS. THE LIM DOMAIN BINDS 2 ZINC
 CC IONS.
 CC -----
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 CC -----
 DR EMBL; AF179849; AAK70923.1; ALT_INIT.
 DR EMBL; AF282899; AAK69169.1; -.
 DR EMBL; AB055703; BAB62817.1; -.
 DR EMBL; AY053457; AAL07260.1; ALT_INIT.
 DR EMBL; BC011759; AAH11759.1; ALT_INIT.
 DR MIM; 602146; -.
 DR MIM; 606606; -.
 DR InterPro; IPR001356; Homeobox.
 DR InterPro; IPR001781; LIM.
 DR Pfam; PF00046; homeobox; 2.
 DR Pfam; PF00412; LIM; 4.
 DR ProDom; PD000010; Homeobox; 1.
 DR ProDom; PD000094; LIM; 2.
 DR PROSITE; PS00478; LIM_DOMAIN_1; 2.
 DR PROSITE; PS00023; LIM_DOMAIN_2; 2.
 DR PROSITE; PS00027; HOMEODOMAIN_1; 1.
 DR PROSITE; PS00071; HOMEODOMAIN_2; 1.
 KW Homeobox; DNA-binding; Nuclear protein; Repeat; LIM domain;
 KW Metal-binding; zinc; Transcription regulation.
 FT DOMAIN 7
 FT DOMAIN 66
 FT DNA_BIND 134
 FT CONFLICT 312
 SQ SEQUENCE 367 AA; 40828 MW; EB9DA0F25BA1E269 CRC64;

Query Match 60.3%; Score 35; DB 1; Length 367;
 Best Local Similarity 55.6%; Pred. No. 24;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFYE 10
 ||.|||
 Db 198 RHRWGQFYK 206

RESULT 13
 LHX4_MOUSE
 ID LHX4_MOUSE STANDARD; PRT; 367 AA.
 AC P53776; O08916; Q9R280;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE LIM/homeobox protein Lhx4.
 GN LHX4 OR GSH4 OR GSH-4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 [1]
 RP SEQUENCE FROM N.A.
 RA Sakai T., Kawaguchi A., Nagashima M.;
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 7-196 FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Embryo;
 RX MEDLINE=97432832; PubMed=9286712;
 RA Yamashita T., Moriyama K., Sheng H.Z., Westphal H.;
 RT "Lhx4, a LIM homeobox gene";
 RL Genomics 44:144-146(1997).
 RN [3]
 RP SEQUENCE OF 136-367 FROM N.A.
 RX MEDLINE=94298779; PubMed=7913017;
 RA Li H., Witte D.P., Branford W.W., Aronow B.J., Weinstein M., Kaur S.,
 RA Wert S., Singh G., Schreiner C.M., Whitsett J.A., Scott W.J. Jr.,
 RA Potter S.S.;
 RT "Gsh-4 encodes a LIM-type homeodomain, is expressed in the developing
 RT central nervous system and is required for early postnatal
 RT survival";
 RL EMBO J. 13:2876-2885(1994).
 CC -!- FUNCTION: MAY PLAY A CRITICAL ROLE IN THE DEVELOPMENT OF
 CC RESPIRATORY CONTROL MECHANISMS AND IN THE NORMAL GROWTH AND
 CC MATURATION OF THE LUNG.
 CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
 CC -!- TISSUE SPECIFICITY: TRANSIENT EXPRESSION IN VENTROLATERAL REGIONS
 CC OF THE DEVELOPING NEURAL TUBE AND HINDBRAIN.
 CC -!- SIMILARITY: CONTAINS 1 HOMEODOMAIN.
 CC -!- SIMILARITY: CONTAINS 2 LIM DOMAINS. THE LIM DOMAIN BINDS 2 ZINC
 CC IONS.
 CC -----
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 CC -----
 DR EMBL; AF135415; AAD30125.1; -.
 DR EMBL; U89343; AAC53336.1; -.
 DR EMBL; S71659; AAB31260.1; -.
 DR HSSP; P06601; 1FJL.
 DR TRANSFAC; T03542; -.
 DR MGD; MGI:101776; Lhx4.
 DR InterPro; IPR001356; Homeobox.
 DR InterPro; IPR001781; LIM.
 DR Pfam; PF00046; homeobox; 1.
 DR Pfam; PF00412; LIM; 2.
 DR ProDom; PD000010; Homeobox; 1.
 DR ProDom; PD000094; LIM; 2.
 DR SMART; SM00389; HOX; 1.
 DR SMART; SM00132; LIM; 2.
 DR PROSITE; PS00478; LIM_DOMAIN_1; 2.
 DR PROSITE; PS00023; LIM_DOMAIN_2; 2.
 DR PROSITE; PS00027; HOMEODOMAIN_1; 1.
 DR PROSITE; PS00071; HOMEODOMAIN_2; 1.
 KW Homeobox; DNA-binding; Nuclear protein; Repeat; LIM domain;
 KW Metal-binding; zinc; Transcription regulation.
 FT DOMAIN 7
 FT DOMAIN 57

FT DOMAIN 66 120 LIM 2.
 FT DNA_BIND 134 193 HOMEBOX.
 SQ SEQUENCE 367 AA; 40811 MW; 86553C7014A0E27C CRC64;

Query Match 60.3%; Score 35; DB 1; Length 367;
 Best Local Similarity 55.6%; Pred. No. 24;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFY 10
 Db 198 RHRWGQFYK 206

RESULT 14

INV3_DAUCA STANDARD; PRT; 583 AA.
 ID INV3_DAUCA
 AC Q39693;
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DE Beta-fructofuranosidase, insoluble isoenzyme 3 precursor (EC 3.2.1.26)
 DE (Sucrose-6-phosphate hydrolase 3) (Invertase 3) (Cell wall beta-fructosidase 3).
 GN INV3.
 OS Daucus carota (Carrot).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids II; Apiales; Apiaceae; Daucus.
 OX NCBI_TaxID=4039;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Queen Anne's Lace;
 RX MEDLINE=95306787; PubMed=7787183;
 RA Lorenz K., Lienhard S., Sturm A.;
 RT "Structural organization and differential expression of carrot beta-fructofuranosidase genes: identification of a gene coding for a flower bud-specific isozyme".
 RL Plant Mol. Biol. 28:189-194(1995).

CC -!- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN PHLOEM UNLOADING AND IN STRESS RESPONSE.
 CC -!- CATALYTIC ACTIVITY: Hydrolysis of terminal non-reducing beta-D-fructofuranoside residues in beta-D-fructofuranosides.
 CC -!- SUBCELLULAR LOCATION: IONICALLY BOUND TO THE CELL WALL.
 CC -!- SIMILARITY: BELONGS TO FAMILY 32 OF GLYCOSYL HYDROLASES.
 CC
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EMBL; X78423; CAA55188.1; ..
 DR InterPro; IPR001362; GH_32.
 DR Pfam; PF00251; Glyco_hydro_32; 1.
 DR PROSITE; PS00609; GLYCOSYL_HYDROL_F32; 1.
 KW Hydrolase; Glycosidase; Glycoprotein; Cell wall; Zymogen; Signal.
 FT SIGNAL 1 ? POTENTIAL.
 FT PROPEP ? ? POTENTIAL.
 FT CHAIN ? 583
 FT BETA-FRUCTOFURANOSIDASE, INSOLUBLE
 FT ISOENZYME 3.
 FT CARBOHYD 164 164 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 280 280 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 303 303 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 340 340 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 561 561 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 583 AA; 66381 MW; 1DBF591CD94749AF CRC64;

Query Match 60.3%; Score 35; DB 1; Length 583;
 Best Local Similarity 62.5%; Pred. No. 39;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHNYGSFY 9
 Db 313 RYDYGNY 320

RESULT 15

INV1_DAUCA STANDARD; PRT; 592 AA.
 ID INV1_DAUCA
 AC P26792;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Beta-fructofuranosidase, insoluble isoenzyme 1 precursor (EC 3.2.1.26)
 DE (Sucrose-6-phosphate hydrolase 1) (Invertase 1) (Cell wall beta-fructosidase 1).
 GN INV1.
 OS Daucus carota (Carrot).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids II; Apiales; Apiaceae; Daucus.
 OX NCBI_TaxID=4039;
 RN [1]

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC STRAIN=cv. Queen Anne's Lace;
 RX MEDLINE=93005650; PubMed=2152110;
 RA Sturm A., Chrispeels M.J.;
 RT "cDNA cloning of carrot extracellular beta-fructosidase and its expression in response to wounding and bacterial infection".
 RL Plant Cell 2:1107-1119(1990).

CC -!- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN PHLOEM UNLOADING AND IN STRESS RESPONSE.
 CC -!- CATALYTIC ACTIVITY: Hydrolysis of terminal non-reducing beta-D-fructofuranoside residues in beta-D-fructofuranosides.
 CC -!- SUBCELLULAR LOCATION: IONICALLY BOUND TO THE CELL WALL.
 CC -!- TISSUE SPECIFICITY: IN LEAVES AND ROOTS OF YOUNG PLANTS.
 CC -!- INDUCTION: By wounding and bacterial infection.
 CC -!- SIMILARITY: BELONGS TO FAMILY 32 OF GLYCOSYL HYDROLASES.
 CC
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EMBL; M58362; AAA03516.1; ..
 DR EMBL; X69321; CAA49162.1; ..
 DR PIR; JQ0991; JQ0991.
 DR GlycoSuiteDB; P26792; ..
 DR InterPro; IPR001362; GH_32.
 DR Pfam; PF00251; Glyco_hydro_32; 1.
 DR PROSITE; PS00609; GLYCOSYL_HYDROL_F32; 1.
 KW Hydrolase; Glycosidase; Glycoprotein; Cell wall; Zymogen; Signal.
 FT SIGNAL 1 31 OR 39 (POTENTIAL).
 FT PROPEP 32 48 OR 40 (POTENTIAL).
 FT CHAIN 49 592 BETA-FRUCTOFURANOSIDASE, INSOLUBLE
 FT ISOENZYME 1.
 FT ACT_SITE 74 74 BY SIMILARITY.
 FT CARBOHYD 170 170 N-LINKED (GLCNAC. . .) (COMPLEX).
 FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 311 311 N-LINKED (GLCNAC. . .) (COMPLEX).
 FT CARBOHYD 348 348 N-LINKED (GLCNAC. . .) (HIGH MANNOSE).
 FT FTID-CAR_000147.

FT CARBOHYD 570 570 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 133 133 R -> W (IN REF. 2).
FT CONFLICT 487 487 A -> V (IN REF. 2).
SQ SEQUENCE 592 AA; 66813 MW; E3DF85355D277D0C CRC64;

Query Match 60.3%; Score 35; DB 1; Length 592;
Best Local Similarity 62.5%; Pred. No. 40;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RHNYGSPY 9

||:|:|:|

Db 321 RYDYGNEY 328

Search completed: November 18, 2002, 17:51:42
Job time : 6.39474 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:40:56 ; Search time 22.3684 Seconds
(without alignments)
92.115 Million cell updates/sec

Title: US-09-016-061-98
Perfect score: 58
Sequence: 1 ARHNGSFYE 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21.*
1: sp-archaea.*
2: sp-bacteria.*
3: sp-fungi.*
4: sp-human.*
5: sp-invertebrate.*
6: sp-mammal.*
7: sp-mhc.*
8: sp-organelle.*
9: sp-phage.*
10: sp-plant.*
11: sp-rodent.*
12: sp-virus.*
13: sp-vertebrate.*
14: sp-unclassified.*
15: sp-rvirus.*
16: sp-bacteriap.*
17: sp-archeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43	74.1	839	10 Q9LIE5	Q9lie5 arabidopsis
2	42	72.4	195	16 Q9CGZ9	Q9cgz9 lactococcus
3	39	67.2	581	10 Q93X59	Q93x59 cichorium i
4	39	67.2	660	10 Q8RX28	Q8rx28 arabidopsis
5	39	67.2	1108	10 Q9FNQ7	Q9fnq7 arabidopsis
6	38	65.5	89	7 Q19495	Q19495 gallus gall
7	38	65.5	402	5 Q45792	Q45792 caenorhabdi
8	37	63.8	62	16 Q97Q90	Q97q90 streptococc
9	37	63.8	92	16 Q97Q77	Q97q77 streptococc
10	37	63.8	143	16 Q8XYU2	Q8xyu2 ralstonia s
11	37	63.8	149	2 Q9ZBB5	Q9zbb5 streptococc
12	37	63.8	405	16 Q9PMZ4	Q9pmz4 campylobact
13	37	63.8	483	10 Q22861	Q22861 arabidopsis
14	37	63.8	2288	5 Q23081	Q23081 caenorhabdi
15	37	63.8	2315	5 Q95ZK3	Q95zk3 caenorhabdi
16	37	63.8	5317	5 Q8TA74	Q8ta74 hemisentrot

17	36.5	62.9	1341	16 Q8UAU1	Q8uau1 agrobacteri
18	36	62.1	39	7 P79474	P79474 cervus elap
19	36	62.1	39	7 P79477	P79477 cervus elap
20	36	62.1	39	7 P79478	P79478 cervus elap
21	36	62.1	39	7 P79479	P79479 cervus elap
22	36	62.1	67	7 Q8SP02	Q8sp02 hapalemur g
23	36	62.1	74	6 Q9TMM4	Q9ttm4 bos taurus
24	36	62.1	75	7 Q9GIJ5	Q9gij5 bos taurus
25	36	62.1	76	7 Q9TPC2	Q9tpc2 macaca mula
26	36	62.1	77	7 Q9GJ91	Q9gj91 ovis aries
27	36	62.1	77	7 Q9GJ90	Q9gj90 ovis aries
28	36	62.1	77	7 Q9GJ82	Q9gj82 ovis aries
29	36	62.1	78	6 Q97968	Q97968 ovis aries
30	36	62.1	78	6 Q97835	Q97835 ovis aries
31	36	62.1	78	6 Q97839	Q97839 ovis aries
32	36	62.1	78	6 Q97844	Q97844 ovis aries
33	36	62.1	78	7 Q9MWT6	Q9mw6 leopardus p
34	36	62.1	78	7 Q9MWT5	Q9mw5 leopardus p
35	36	62.1	78	7 Q9MWT4	Q9mw4 leopardus p
36	36	62.1	78	7 Q95HDI	Q95hdi ovis aries
37	36	62.1	78	7 Q95HC6	Q95hc6 ovis aries
38	36	62.1	79	7 Q9MX19	Q9mx19 leopardus p
39	36	62.1	79	7 Q9MX13	Q9mx13 leopardus p
40	36	62.1	79	7 Q9MX03	Q9mx03 leopardus p
41	36	62.1	79	7 Q9MX00	Q9mx00 leopardus p
42	36	62.1	79	7 Q9MWZ9	Q9mwz9 leopardus p
43	36	62.1	79	7 Q9MWZ8	Q9mwz8 leopardus p
44	36	62.1	79	7 Q9MWZ7	Q9mwz7 leopardus p
45	36	62.1	79	7 Q9MWY9	Q9mwy9 leopardus p

ALIGNMENTS

RESULT 1

Q9LIE5 ID Q9LIE5 PRELIMINARY; PRT; 839 AA.
AC Q9LIE5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Far-red impaired response protein, mutator-like transposase-like
DE protein, phytochrome A signaling protein-like.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RN SEQUENCE FROM N.A.
RC SPTREMBL_21.*
RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=20363099; PubMed=10907853;
RA Nakamura Y.;
RT 'Structural analysis of Arabidopsis thaliana chromosome 3. II.
RT Sequence features of the regions of 4,251,695 bp covered by ninety pl,
RT TAC and BAC clones';
RL DNA Res. 7:217-221(2000).
DR EMBL: AP001306; BAB03065.1; -
DR InterPro: IPR004330; FARI.
DR InterPro: IPR001000; Glyco_hydro_10.
DR Pfam: PF03101; FARI; 1.
DR PROSITE: PS00591; GLYCOSYL_HYDROL_F10; UNKNOWN.1.
SQ SEQUENCE 839 AA; 95996 MW; CBBF60DF8B6797F8 CRC64;

Query Match 74.1%; Score 43; DB 10; Length 839;
Best Local Similarity 87.5%; Pred. No. 16;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ARHNYGSF 8
Db 274 SRHNYGSF 281

RESULT 2
Q9CGZ9 PRELIMINARY; PRT; 195 AA.
AC Q9CGZ9;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Hypothetical protein Yj9F.
GN Yj9F OR L10943.
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1360;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IL1403;
RX MEDLINE=21235186; PubMed=1137471;
RA Bolotin A., Wincker P., Mauger S., Jaillon O., Malarne K.,
RA Weissenbach J., Ehrlich S.D., Sorokin A.;
RT The complete genome sequence of the lactic acid bacterium Lactococcus
RT lactis ssp. lactis IL1403."
RL Genome Res. 11:731-753(2001).
DR EMBL; AE006328; AAK05041.1; -.
DR InterPro; IPR000868; Isochorismatase.
DR Pfam; PF00857; Isochorismatase; 1.
DR Hypothetical protein; Complete proteome.
SQ SEQUENCE 195 AA; 21535 MW; A408E9F70EC7B43F CRC64;

Query Match 72.4%; Score 42; DB 16; Length 195;
Best Local Similarity 66.7%; Pred. No. 4.8;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSF 9
Db 103 AKHNGAFV 111

RESULT 3
Q93X59 PRELIMINARY; PRT; 581 AA.
AC Q93X59;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Fructan 1-exohydrolase IIB precursor (EC 3.2.1.80).
GN 1-PFH IIB.
OS Cichorium intybus (Chicory).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae; Cichorium.
OX NCBI_TaxID=13427;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. FLASH;
RX MEDLINE=21351405; PubMed=11457968;
RA Van den Ende W., Michiels A., Van Wouterghem D., Clerens S.P.,
RA De Roover J., Van Laere A.;
RT Defoliation induces fructan 1-exohydrolase II in witloof chicory
RT roots. Cloning and purification of two isoforms, fructan 1-
RT exohydrolase Iia and fructan 1-exohydrolase IIB. Mass fingerprint of
RT the fructan 1-exohydrolase II enzymes."
RL Plant Physiol. 126:1186-1195(2001).
CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF TERMINAL NON-REDUCING BETA-D-
CC FRUCTOFURANOSIDE RESIDUES IN BETA-D-FRUCTOFURANOSIDES.
CC -1- SIMILARITY: BELONGS TO FAMILY 32 OF GLYCOSYL HYDROLASES.
DR EMBL; AJ295034; CAC37923.1; -.
DR InterPro; IPR001362; GH_32.
DR Pfam; PF00251; Glyco_hydro_32; 1.

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DR PROSITE; PS00609; GLYCOSYL-HYDROL_F32; UNKNOWN_1.
KW Glycoprotein; Glycosidase; Hydrolase; Signal.
FT SIGNAL 1 38 POTENTIAL.
FT CHAIN 39 581 FRUCTAN 1-EXOHYDROLASE IIB.
SQ SEQUENCE 581 AA; 65269 MW; 978EA139DFDC9C5D CRC64;

Query Match 67.2%; Score 39; DB 10; Length 581;
Best Local Similarity 75.0%; Pred. No. 57;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFY 9
Db 305 RYNGQFY 312

RESULT 4
Q8RX28 PRELIMINARY; PRT; 660 AA.
AC Q8RX28;
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Putative histone deacetylase.
GN AT5G01060.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
RA Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,
RA Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,
RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA Kameya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
RA Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki K.,
RA Davis R.W., Ecker J.R., Theologis A.;
RT "Arabidopsis Full Length cDNA Clones."
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY090936; AAM13986.1; -.
SQ SEQUENCE 660 AA; 72722 MW; A40906BF82B397DE CRC64;

Query Match 67.2%; Score 39; DB 10; Length 660;
Best Local Similarity 75.0%; Pred. No. 66;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFY 9
Db 222 RHEYGGFY 229

RESULT 5
Q9FNQ7 PRELIMINARY; PRT; 1108 AA.
AC Q9FNQ7;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE Similarity to histone deacetylase.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=98069011; PubMed=9405937;
RA Kotani H., Nakamura Y., Sato S., Kaneko T., Asamizu E., Miyajima N.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. II.

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```
RT Sequence, features of the regions of 1,044,062 bp covered by thirteen
RT physically assigned pl clones.";
RL DNA Res. 4:291-300(1997).
DR ENBL; AB006696; BAE10370.1; -.
DR InterPro; IPR000286; His_deacetylase.
DR Pfam; PF00850; Hist_deacetyl; 2.
DR PRINTS; PRO1270; HDASUPER.
SQ SEQUENCE 1108 AA; 123609 MW; 9BCF5A2BCD90A1E2 CRC64;

Query Match 67.2%; Score 39; DB 10; Length 1108;
Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFY 9
DB 898 RHEYGGFY 905

RESULT 6
O19495 PRELIMINARY; PRT; 89 AA.
AC O19495;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II beta 1 domain (Fragment).
GN B-LBI.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=15.151-5; TISSUE=BURSA;
RX MEDLINE=98179131; PubMed=9510552;
RA Pharr G.T., Dodson J.B., Hunt H.D., Bacon L.D.;
RT "Class II MHC cDNAs in 1515 B-congenic chickens.";
RL Immunogenetics 47:350-354(1998).
DR ENBL; U91532; AAC15813.1; -.
DR InterPro; IPR00353; MHC_II_beta.
DR Pfam; PF00969; MHC_II_beta.1.
DR ProDom; PD000328; MHC_II_beta.1.
KW Glycoprotein; MHC II; Transmembrane.
FT NON_TER 1
FT NON_TER 89
FT NON_TER 89
SQ SEQUENCE 89 AA; 10724 MW; BC7D558B6AEB1379 CRC64;

Query Match 65.5%; Score 38; DB 7; Length 89;
Best Local Similarity 85.7%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
DB 75 RHNYGDF 81

RESULT 7
O45792 PRELIMINARY; PRT; 402 AA.
AC O45792;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE T19C9.8 protein.
GN T19C9.8.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC MATTHEWS L.;
RX MATTHEWS L.;
RT "Complete genome sequence of a virulent isolate of Streptococcus
RT pneumoniae.";
RL Science 293:498-506(2001).
DR ENBL; AB007431; AAK75433.1; -.
DR TIGR; SP1335; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 62 AA; 7521 MW; 35D171D6E5240D9F CRC64;

Query Match 63.8%; Score 37; DB 16; Length 62;
Best Local Similarity 66.7%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFYE 10
DB 20 KHNYPFYE 28

RESULT 8
Q97Q90 PRELIMINARY; PRT; 62 AA.
AC Q97Q90;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical protein SP1335.
GN SP1335.
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TIGR4;
RX MEDLINE=21357209; PubMed=11463916;
RA Tetelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
RA Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,
RA Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
RA Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,
RA McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.,
RA Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
RT "Complete genome sequence of a virulent isolate of Streptococcus
RT pneumoniae.";
RL Science 293:498-506(2001).
DR ENBL; AB007431; AAK75433.1; -.
DR TIGR; SP1335; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 62 AA; 7521 MW; 35D171D6E5240D9F CRC64;

Query Match 63.8%; Score 37; DB 16; Length 62;
Best Local Similarity 66.7%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFYE 10
DB 20 KHNYPFYE 28

RESULT 9
Q97Q77 PRELIMINARY; PRT; 92 AA.
AC Q97Q77;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical protein SP1349.
GN SP1349.
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
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OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TIGR4;
RX MEDLINE=21357209; PubMed=11463916;
RA Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
RA Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,
RA Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
RA Holtzapple E., Khouri H., Wolf A.M., Uterback T.R., Hansen C.L.,
RA McDonald L.A., Feldblyum T.V., Angiolli S., Dickinson T., Hickey E.K.,
RA Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
RT "Complete genome sequence of a virulent isolate of Streptococcus
RT pneumoniae.";
RL Science 293:498-506(2001).
DR EMBL: AE007433; AAK75447.1; -.
DR TIGR: SPI349; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 92 AA; 10777 MW; EF71CF1B5E5E38EC CRC64;

Query Match 63.8%; Score 37; DB 16; Length 92;
Best Local Similarity 66.7%; Pred. No. 18;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFYE 10
Db 10 KHNYPLEYE 18

RESULT 10
Q8XYU2 PRELIMINARY; PRT; 143 AA.
ID O8XYU2;
AC O8XYU2;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE Hypothetical protein RSC1664.
GN RSC1664 OR RS04045.
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
OC Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GM11000;
RX MEDLINE=21681879; PubMed=11823852;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Ariat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
RA Chandler M., Choisme N., Claudel-Renard C., Cunnac S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
RA Sigulier P., Thebaud P., Whalen M., Wincker P., Levy M.,
RA Welzenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502(2002).
DR EMBL: AL646065; CAD15366.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 143 AA; 15556 MW; 4E710B20861E097C CRC64;

Query Match 63.8%; Score 37; DB 16; Length 143;
Best Local Similarity 71.4%; Pred. No. 29;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSFY 9
Db 117 HNYGTFF 123

RESULT 117
Q92BB5 PRELIMINARY; PRT; 149 AA.
ID Q92BB5;
AC Q92BB5;

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DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE Hypothetical 17.5 kDa protein.
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SP1000; TRANSPOSON=TN5252;
RX MEDLINE=98154299; PubMed=9473447;
RA Sampath J., Vijayakumar M.N.;
RT "Identification of a DNA cytosine methyltransferase gene in
RT conjugative transposon Tn5252.";
RL Plasmid 39:63-76(1998).
DR EMBL: L29323; AAC98423.1; -.
KW Hypothetical protein.
SQ SEQUENCE 149 AA; 17465 MW; 5DEFCFBAB306B131 CRC64;

Query Match 63.8%; Score 37; DB 2; Length 149;
Best Local Similarity 66.7%; Pred. No. 30;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFYE 10
Db 52 KHNYPLEYE 60

RESULT 12
Q9PMZ4 PRELIMINARY; PRT; 405 AA.
ID Q9PMZ4;
AC Q9PMZ4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical protein Cj1305c.
GN Cj1305c.
OS Campylobacter jejuni.
OC Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
OC Campylobacter.
OX NCBI_TaxID=197;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCTC 11168;
RX MEDLINE=20150912; PubMed=10688204;
RA Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
RA Basham D., Chillingworth T., Davies R.M., Feltwell T., Holtroyd S.,
RA Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
RA Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
RA Whitehead S., Barrell B.G.;
RT "The genome sequence of the food-borne pathogen Campylobacter jejuni
RT reveals hypervariable sequences.";
RL Nature 403:665-668(2000).
DR EMBL: AL139078; CAB73732.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 405 AA; 47315 MW; D96641B34301DF0A CRC64;

Query Match 63.8%; Score 37; DB 16; Length 405;
Best Local Similarity 62.5%; Pred. No. 90;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFYE 10
Db 238 HSYGDYFE 245

RESULT 13
O22861 PRELIMINARY; PRT; 483 AA.
ID O22861;
AC O22861;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)

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DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE AL2943470 protein.
 GN AT2G43470.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RX MEDLINE=20083487; PubMed=10617197;
 RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
 RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
 RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
 RA Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
 RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
 RA Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
 RA Salzberg S.L., Fraser C.M., Venter J.C.;
 RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
 thaliana";
 RL Nature 402:761-768(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA Lin X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC002335; AAB64341.1; -.
 DR InterPro; IPR001005; MYB_DNA_Binding.
 DR PROSITE; PS00037; MYB_1; UNKNOWN.1.
 SQ SEQUENCE 483 AA; 54491 MW; C665DCA7E1E4BAFB CRC64;

Query Match 63.8%; Score 37; DB 10; Length 483;
 Best Local Similarity 75.0%; Pred. No. 1.le+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 HNYGSFYE 10
 | | | | |
 Db 288 HOYASFYE 295

RESULT 14
 Q23081
 ID Q23081 PRELIMINARY; PRT; 2288 AA.
 AC Q23081;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Hypothetical 262.2 kDa protein.
 GN zc8.4.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA None;
 RT "Genome sequence of the nematode C. elegans: a platform for
 investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Latreille P., Bradshaw H.;
 RT "The sequence of C. elegans cosmid zc8.";
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Waterston R.;
 RT "Direct Submission."

RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U64862; AAB52624.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 2288 AA; 262171 MW; 06D1700A0F4ACD2F CRC64;

Query Match 63.8%; Score 37; DB 5; Length 2288;
 Best Local Similarity 66.7%; Pred. No. 6.e+02;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSFY 9
 : | | | | |
 Db 34 SRSNYGEFY 42

RESULT 15
 Q95ZK3
 ID Q95ZK3 PRELIMINARY; PRT; 2315 AA.
 AC Q95ZK3;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Hypothetical protein zc8.4b.
 GN zc8.4.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA None;
 RT "Genome sequence of the nematode C. elegans: a platform for
 investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Latreille P., Bradshaw H.;
 RT "The sequence of C. elegans cosmid zc8.";
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Waterston R.;
 RT "Direct Submission."

RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U64862; AAK67253.1; -.
 SQ SEQUENCE 2315 AA; 265394 MW; 0BD62E168DCD8ADE CRC64;

Query Match 63.8%; Score 37; DB 5; Length 2315;
 Best Local Similarity 66.7%; Pred. No. 6.1e+02;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSFY 9
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 Db 34 SRSNYGEFY 42

Search completed: November 18, 2002, 17:54:41
 Job time : 23.3684 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:31:45 : Search time 29.3421 Seconds
(without alignments)
45.413 Million cell updates/sec

Title: US-09-016-061-98

Perfect score: 58

Sequence: 1 ARHNGSFYE 10

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	58	100.0	10	AAW76039	LM609 grafted anti
2	58	100.0	10	AAW76039	Multiple mutant VH
3	53	91.4	10	AAW76040	LM609 grafted anti
4	53	91.4	10	AAW76023	LM609 grafted anti
5	53	91.4	10	AAW76023	Mutant VH CDR3 pep
6	53	91.4	10	AAW76027	Multiple mutant VH
7	49	84.5	10	AAW76027	LM609 grafted anti
8	49	84.5	10	AAW76038	Mutant VH CDR3 pep
9	48	82.8	10	AAW76038	LM609 grafted anti
10	48	82.8	10	AAW76038	Multiple mutant VH

11	46	79.3	10	AAW76022	LM609 grafted anti
12	46	79.3	10	AAW76024	LM609 grafted anti
13	46	79.3	10	AAW76025	LM609 grafted anti
14	46	79.3	10	AAW76026	LM609 grafted anti
15	46	79.3	10	AAW76028	LM609 grafted anti
16	46	79.3	10	AAW76029	LM609 grafted anti
17	46	79.3	10	AAW76030	LM609 grafted anti
18	46	79.3	10	AAW76010	LM609 grafted anti
19	46	79.3	10	AAW76010	LM609 VH CDR3 pep
20	46	79.3	10	AAW76010	Mutant VH CDR3 pep
21	46	79.3	10	AAW76010	Mutant VH CDR3 pep
22	46	79.3	10	AAW76010	Mutant VH CDR3 pep
23	46	79.3	10	AAW76010	Mutant VH CDR3 pep
24	46	79.3	10	AAW76010	Mutant VH CDR3 pep
25	46	79.3	10	AAW76010	Mutant VH CDR3 pep
26	46	79.3	10	AAW76010	Mutant VH CDR3 pep
27	46	79.3	10	AAW76010	Mutant VH CDR3 pep
28	46	79.3	10	AAW76010	Mutant VH CDR3 pep
29	46	79.3	10	AAW76010	Mutant VH CDR3 pep
30	46	79.3	10	AAW76010	Mutant VH CDR3 pep
31	46	79.3	10	AAW76010	Mutant VH CDR3 pep
32	46	79.3	10	AAW76010	Mutant VH CDR3 pep
33	46	79.3	10	AAW76010	Mutant VH CDR3 pep
34	46	79.3	10	AAW76010	Mutant VH CDR3 pep
35	46	79.3	10	AAW76010	Mutant VH CDR3 pep
36	46	79.3	10	AAW76010	Mutant VH CDR3 pep
37	46	79.3	10	AAW76010	Mutant VH CDR3 pep
38	46	79.3	10	AAW76010	Mutant VH CDR3 pep
39	46	79.3	10	AAW76010	Mutant VH CDR3 pep
40	43	74.1	10	AAW76021	LM609 grafted anti
41	43	74.1	10	AAW76021	Mutant VH CDR3 pep
42	42	72.4	195	AAW76037	Lactococcus lactis
43	41	70.7	10	AAW76037	LM609 grafted anti
44	41	70.7	10	AAW76037	LM609 grafted anti
45	41	70.7	10	AAW76037	Mutant VH CDR3 pep

ALIGNMENTS

RESULT 1
AAW76039
ID AAW76039 standard; Protein; 10 AA.
AC AAW76039;
XX
XX
DT 02-NOV-1998 (first entry)
XX
XX
DE LM609 grafted antibody V-H region CDR3 protein fragment #15.
XX
XX
KW Vitaxin; antibody; variable region; heavy chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
XX
XX
OS Mus sp.
XX
XX
PN W09833919-A2.
XX
XX
PD 06-AUG-1998.
XX
XX
PF 30-JAN-1998; 98WO-US01826.
XX
XX
PR 30-JAN-1997; 97US-0791391.
XX
XX
PA (IXSY-) IXSYS INC.
XX
XX
PI Glaser SM, Huse WD;
XX
XX
DR WPI; 1998-437472/37.
DR N-PSDB; AAV49876.

XX Humanised antibody, vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
PS Claim 62; Page 43; 129pp; English.
XX
CC AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
CC antibodies contain non-murine framework regions so are suitable for use
CC in humans. Enhanced types of LM609 have affinity more than 90 times
CC greater than that of parent the parent antibody.
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 58; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFYE 10
| | | | | | | | | |
Db 1 ARHNYGSFYE 10
| | | | | | | | | |

RESULT 2
AAB61397
ID AAB61397 standard; peptide; 10 AA.
XX
AC AAB61397;
XX
XX 03-APR-2001 (first entry)
XX
XX Multiple mutant VH CDR3 #3.
XX
XX LM609; grafted antibody; alphaVbeta3 integrin; angiogenesis;
KW inflammatory; cancer; retina; restenosis; osteoporosis.
KW
XX Unidentified.
XX
XX WO200078815-A1.
XX
XX 28-DEC-2000.
XX
XX 23-JUN-2000; 2000WO-US17454.
XX
XX 24-JUN-1999; 99US-0339922.
XX
XX (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX
XX Huse WD, Wu H;
XX
XX WPI; 2001-050110/06.
XX
XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
PT osteoporosis -
XX
XX Disclosure; Page 43; 132pp; English.
XX
CC The present invention relates to enhanced LM609 grafted antibodies
CC exhibiting selective binding affinity to alphavbeta3 integrin or
CC their functional fragments. The antibodies or their functional
CC fragments can be used in the diagnosis and treatment of
CC alphavbeta3-mediated diseases such as angiogenesis, inflammatory

CC diseases (such as psoriasis and chronic articular rheumatism),
CC disorders associated with inappropriate or inopportune invasion of
CC vessels (such as diabetic retinopathy, neovascular glaucoma and
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
CC diseases (such as macular degeneration), restenosis and
CC osteoporosis.
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 58; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFYE 10
| | | | | | | | | |
Db 1 ARHNYGSFYE 10
| | | | | | | | | |

RESULT 3
AAW76040
ID AAW76040 standard; Protein; 10 AA.
XX
AC AAW76040;
XX
XX 02-NOV-1998 (first entry)
XX
XX LM609 grafted antibody V-H region CDR3 protein fragment #16.
XX
XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
XX
XX Mus sp.
XX
XX WO9833919-A2.
XX
XX 06-AUG-1998.
XX
XX 30-JAN-1998; 98WO-US01826.
XX
XX 30-JAN-1997; 97US-0791391.
XX
XX (IXSY-) IXSYS INC.
XX
XX Glaser SM, Huse WD;
XX
XX WPI; 1998-437472/37.
XX
XX N-PSDB; AAV49877.
XX
XX Humanised antibody, vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
XX Claim 62; Page 43; 129pp; English.
XX
XX AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
CC antibodies contain non-murine framework regions so are suitable for use
CC in humans. Enhanced types of LM609 have affinity more than 90 times
CC greater than that of parent the parent antibody.
XX
XX Sequence 10 AA;

Query Match 91.4%; Score 53; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0092;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFY 9
 DB 1 ARHNYGSFY 9

RESULT 4

AAW76023
 ID AAW76023 standard; Protein; 10 AA.

AC AAW76023;

XX 02-NOV-1998 (first entry)

DE LM609 grafted antibody V-H region CDR3 protein fragment #5.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.

XX Mus sp.

XX W09833919-A2.

XX 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

XX Glaser SM, Huse WD;

DR WPI; 1998-437472/37.

DR N-PSDB; AAV49860.

XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

XX Claim 62; Page 41; 129pp; English.

XX AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphaVbeta3 and can be used to
 CC inhibit binding of alphaVbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphaVbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
 CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
 CC antibodies contain non-murine framework regions so are suitable for use
 CC in humans. Enhanced types of LM609 have affinity more than 90 times
 CC greater than that of parent the parent antibody.

XX Sequence 10 AA;

Query Match 91.4%; Score 53; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0092;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFY 9
 DB 1 ARHNYGSFY 9

RESULT 5

AAB61381
 ID AAB61381 standard; peptide; 10 AA.

XX AAB61381;

XX 03-APR-2001 (first entry)

XX Mutant VH CDR3 peptide #4.

XX LM609; grafted antibody; alphaVbeta_3 integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis.

XX Unidentified.

XX W0200078815-A1.

XX 28-DEC-2000.

XX 23-JUN-2000; 2000WO-US17454.

XX 24-JUN-1999; 99US-0339922.

XX (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX Huse WD, Wu H;

XX WPI; 2001-050110/06.

XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 CC to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 CC angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 CC osteoporosis

XX Disclosure; Page 41; 132pp; English.

XX The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphaVbeta_3 integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.

XX Sequence 10 AA;

Query Match 91.4%; Score 53; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0092;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFY 9

DB 1 ARHNYGSFY 9

RESULT 6

AAB61398
 ID AAB61398 standard; peptide; 10 AA.

XX AAB61398;

XX 03-APR-2001 (first entry)

XX Multiple mutant VH CDR3 #4.

XX LM609; grafted antibody; alphaVbeta_3 integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis.


```

XX OS Unidentified.
XX PN WO200078815-A1.
XX PD 28-DEC-2000.
XX PF 23-JUN-2000; 2000WO-US17454.
XX PR 24-JUN-1999; 99US-0339922.
XX PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX PI Huse WD, Wu H;
XX XX
XX XX WPI; 2001-050110/06.
XX XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
XX PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
XX PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
XX PT osteoporosis -
XX XX
XX PS Disclosure; Page 43; 132pp; English.
XX CC The present invention relates to enhanced LM609 grafted antibodies
XX CC exhibiting selective binding affinity to alphavbeta_3 integrin or
XX CC their functional fragments. The antibodies or their functional
XX CC fragments can be used in the diagnosis and treatment of
XX CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
XX CC diseases (such as psoriasis and chronic articular rheumatism),
XX CC disorders associated with inappropriate or inopportune invasion of
XX CC vessels (such as diabetic retinopathy, neovascular glaucoma and
XX CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
XX CC diseases (such as macular degeneration), restenosis and
XX CC osteoporosis.
XX SQ Sequence 10 AA;
XX XX
XX XX Query Match 91.4%; Score 53; DB 22; Length 10;
XX XX Best Local Similarity 100.0%; Pred. No. 0.0092;
XX XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX XX
XX QY 1 ARHNYGSFY 9
XX DB | | | | | | | |
XX DB 1 ARHNYGSFY 9
XX XX
XX RESULT 7
XX AAW76027
XX ID AAW76027 standard; Protein; 10 AA.
XX AC AAW76027;
XX XX
XX DT 02-NOV-1998 (first entry)
XX DE
XX DE LM609 grafted antibody V-H region CDR3 protein fragment #9.
XX XX
XX XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
XX KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
XX KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
XX KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
XX KW macular degeneration; osteoporosis; primer; V-H region; CDR;
XX KW complementarity determining region.
XX XX
XX OS Mus sp.
XX XX
XX PN WO9833919-A2.
XX XX
XX PD 06-AUG-1998.
XX PF 30-JAN-1998; 98WO-US01826.
XX XX
XX PR 30-JAN-1997; 97US-0791391.
XX XX
XX XX (IXSY-) IXSYS INC.
XX XX Glaser SM, Huse WD;
XX XX WPI: 1998-437472/37.
XX DR N-PSDB; AAV49864.
XX XX
XX PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
XX PT integrin - and related grafted antibodies based on murine monoclonal
XX PT LM609, also related nucleic acid, used to treat, prevent or diagnose
XX PT angiogenesis or restenosis
XX XX
XX PS Claim 62; Page 41; 129pp; English.
XX XX
XX CC AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
XX CC LM609 heavy and light chain variable region. LM609 and the antibody
XX CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
XX CC inhibit binding of alphavbeta3 to a ligand and thus block
XX CC integrin-mediated signal transduction. This is useful in the treatment,
XX CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
XX CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
XX CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
XX CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
XX CC antibodies contain non-murine framework regions so are suitable for use
XX CC in humans. Enhanced types of LM609 have affinity more than 90 times
XX CC greater than that of parent the parent antibody.
XX XX
XX SQ Sequence 10 AA;
XX XX
XX XX Query Match 84.5%; Score 49; DB 19; Length 10;
XX XX Best Local Similarity 90.0%; Pred. No. 0.044;
XX XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX XX
XX QY 1 ARHNYGSFY 10
XX DB | | | | | | | |
XX DB 1 ARHNYGSFAE 10
XX XX
XX RESULT 8
XX AAB61385
XX ID AAB61385 standard; peptide; 10 AA.
XX AC AAB61385;
XX XX
XX DT 03-APR-2001 (first entry)
XX XX
XX DE Mutant VH CDR3 peptide #8.
XX XX
XX KW LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
XX KW inflammatory; cancer; retina; restenosis; osteoporosis.
XX XX
XX OS Unidentified.
XX XX
XX PN WO200078815-A1.
XX PD 28-DEC-2000.
XX PF 23-JUN-2000; 2000WO-US17454.
XX XX
XX PR 24-JUN-1999; 99US-0339922.
XX PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX XX
XX PI Huse WD, Wu H;
XX XX
XX DR WPI; 2001-050110/06.
XX XX
XX PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity
XX PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
XX PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
XX PT osteoporosis -
XX XX

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PS Disclosure; Page 41; 132pp; English.

XX The present invention relates to enhanced LM609 grafted antibodies

CC exhibiting selective binding affinity to alphaVbeta₃ integrin or

CC their functional fragments. The antibodies or their functional

CC fragments can be used in the diagnosis and treatment of

CC alphaVbeta₃-mediated diseases such as angiogenesis, inflammatory

CC diseases (such as psoriasis and chronic articular rheumatism),

CC disorders associated with inappropriate or inopportune invasion of

CC vessels (such as diabetic retinopathy, neovascular glaucoma and

CC cancer disorders such as tumours and Kaposi's sarcoma), retinal

CC diseases (such as macular degeneration), restenosis and

CC osteoporosis.

XX SQ Sequence 10 AA;

Query Match 84.5%; Score 49; DB 22; Length 10;

Best Local Similarity 90.08; Pred. No. 0.044; Mismatches 0; Indels 1; Gaps 0;

Matches 9; Conservative 0;

QY 1 ARHNYGSFYE 10

Db 1 ARHNYGSFAE 10

RESULT 9

AAW76038

ID AAW76038 standard; Protein; 10 AA.

AC AAW76038;

XX 02-NOV-1998 (first entry)

DT

XX LM609 grafted antibody V-H region CDR3 protein fragment #14.

DE

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;

KW LM609; inhibitor; integrin-mediated signal transduction; treatment;

KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;

KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;

KW macular degeneration; osteoporosis; primer; V-H region; CDR;

KW complementarity determining region.

XX OS Mus sp.

XX WO9833919-A2.

PN

XX 06-AUG-1998.

PD

XX 30-JAN-1998; 98WO-US01826.

PF

XX 30-JAN-1997; 97US-0791391.

PR

XX (IXSY-) IXSYS INC.

PA

XX Glaser SM, Huse WD;

PI

XX WPI: 1998-437472/37.

DR

XX N-PSDB; AAV49875.

DR

XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta₃

PT integrin - and related grafted antibodies based on murine monoclonal

PT LM609, also related nucleic acid, used to treat, prevent or diagnose

PT angiogenesis or restenosis

XX Claim 62; Page 43; 129pp; English.

PS

XX AAW76007-W76040 are protein fragments of the grafted monoclonal antibody

CC LM609 heavy and light chain variable region. LM609 and the antibody

CC vitaxin bind selectively to integrin alphaVbeta₃ and can be used to

CC inhibit binding of alphaVbeta₃ to a ligand and thus block

CC integrin-mediated signal transduction. This is useful in the treatment,

CC prevention and diagnosis of alphaVbeta₃-mediated disease, specifically

CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,

CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,

CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The

CC antibodies contain non-murine framework regions so are suitable for use

CC in humans. Enhanced types of LM609 have affinity more than 90 times

CC greater than that of parent the parent antibody.

XX SQ Sequence 10 AA;

Query Match 82.8%; Score 48; DB 19; Length 10;

Best Local Similarity 88.9%; Pred. No. 0.066;

Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFY 9

Db 1 ARHNGSFY 9

RESULT 10

AAB61396

ID AAB61396 standard; peptide; 10 AA.

XX

AC AAB61396;

XX 03-APR-2001 (first entry)

DT

XX Multiple mutant VH CDR3 #2.

DE

XX LM609; grafted antibody; alphaVbeta₃ integrin; angiogenesis;

KW inflammatory; cancer; retina; restenosis; osteoporosis.

KW

XX Unidentified.

OS

XX WO200078815-A1.

PN

XX 28-DEC-2000.

PD

XX 23-JUN-2000; 2000WO-US17454.

PF

XX 24-JUN-1999; 99US-0339922.

PR

XX (MOLE-) APPLIED MOLECULAR EVOLUTION.

PA

XX Huse WD, Wu H;

PI

XX WPI: 2001-050110/06.

DR

XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity

PT to alpha(V)beta₃ integrin, useful in the diagnosis and treatment of

PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and

PT osteoporosis.

PS Disclosure; Page 42; 132pp; English.

XX

CC The present invention relates to enhanced LM609 grafted antibodies

CC exhibiting selective binding affinity to alphaVbeta₃ integrin or

CC their functional fragments. The antibodies or their functional

CC fragments can be used in the diagnosis and treatment of

CC alphaVbeta₃-mediated diseases such as angiogenesis, inflammatory

CC diseases (such as psoriasis and chronic articular rheumatism),

CC disorders associated with inappropriate or inopportune invasion of

CC vessels (such as diabetic retinopathy, neovascular glaucoma and

CC cancer disorders such as tumours and Kaposi's sarcoma), retinal

CC diseases (such as macular degeneration), restenosis and

CC osteoporosis.

XX SQ Sequence 10 AA;

Query Match 82.8%; Score 48; DB 22; Length 10;

Best Local Similarity 88.9%; Pred. No. 0.066;

Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFY 9

Db 1 ARHNGSFY 9

Db 1 ARNHGFSY 9

RESULT 11

AAW76022 ID AAW76022 standard; Protein; 10 AA.

AC AAW76022;

XX 02-NOV-1998 (first entry)

XX LM609 grafted antibody V-H region CDR3 protein fragment #4.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.

XX Mus sp.

XX WO9833919-A2.

XX 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

XX Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

XX N-PSDB; AAV49859.

XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

XX Claim 62; Page 41; 129pp; English.

XX AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
 CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
 CC antibodies contain non-murine framework regions so are suitable for use
 CC in humans. Enhanced types of LM609 have affinity more than 90 times
 CC greater than that of parent the parent antibody.

XX Sequence 10 AA;

Query Match 79.3%; Score 46; DB 19; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.14;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSF 8

Db 1 ARHNYGSF 8

RESULT 12

AAW76024 ID AAW76024 standard; Protein; 10 AA.

XX AAW76024;

AC AAW76024;

XX DT

02-NOV-1998 (first entry)

XX LM609 grafted antibody V-H region CDR3 protein fragment #6.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.

XX Mus sp.

XX WO9833919-A2.

XX 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

XX Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

XX N-PSDB; AAV49861.

XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

XX Claim 62; Page 41; 129pp; English.

XX AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
 CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
 CC antibodies contain non-murine framework regions so are suitable for use
 CC in humans. Enhanced types of LM609 have affinity more than 90 times
 CC greater than that of parent the parent antibody.

XX Sequence 10 AA;

Query Match 79.3%; Score 46; DB 19; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.14;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSF 8

Db 1 ARHNYGSF 8

RESULT 13

AAW76025 ID AAW76025 standard; Protein; 10 AA.

XX AAW76025;

XX 02-NOV-1998 (first entry)

XX LM609 grafted antibody V-H region CDR3 protein fragment #7.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;

PI Glaser SM, Huse WD;
XX
DR WPI: 1998-437472/37.
DR N-PSDB; AAV49865.
XX
XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
XX Claim 62; Page 41; 129pp; English.
PS
XX
XX AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
CC antibodies contain non-murine framework regions so are suitable for use
CC in humans. Enhanced types of LM609 have affinity more than 90 times
CC greater than that of parent the parent antibody.
XX
XX Sequence 10 AA;
SQ
Query Match 79.3%; Score 46; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ARHNYGSF 8
| | | | | | | |
Db 1 ARHNYGSF 8

Search completed: November 18, 2002, 17:50:50
Job time : 29.3421 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 18:45:22 ; Search time 4.60526 Seconds
(without alignments)
32.704 Million cell updates/sec

Title: US-09-016-061-98

Perfect score: 58

Sequence: 1 ARHNYGSFYE 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 97044 seqs, 15060890 residues

Total number of hits satisfying chosen parameters: 97044

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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 - 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
 - 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
 - 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
 - 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
 - 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
 - 7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
 - 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
 - 9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
 - 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
 - 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
 - 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
 - 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
 - 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
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2	46	79.3	117	8	US-08-790-540A-6
3	46	79.3	117	8	US-08-791-391A-2
4	46	79.3	117	8	US-08-791-391A-6
5	38	65.5	101	10	US-09-764-853-432
6	36	62.1	14	1	US-08-677-599B-22
7	35	60.3	51	10	US-08-864-761-33948
8	34	58.6	30	10	US-09-839-884-40
9	34	58.6	287	10	US-09-415-540-5
10	33	56.9	14	1	US-08-677-599B-21
11	33	56.9	235	10	US-09-925-301-1293
12	33	56.9	512	10	US-09-815-242-11232
13	32	55.2	14	1	US-08-677-599B-11
14	32	55.2	14	1	US-08-677-599B-12
15	32	55.2	14	1	US-08-677-599B-13
16	32	55.2	14	1	US-08-677-599B-14
17	32	55.2	14	1	US-08-677-599B-15
18	32	55.2	14	1	US-08-677-599B-16
19	32	55.2	14	1	US-08-677-599B-17

20	55.2	14	1	US-08-677-599B-18	Sequence 18, Appl
21	55.2	14	1	US-08-677-599B-19	Sequence 19, Appl
22	55.2	14	1	US-08-677-599B-20	Sequence 20, Appl
23	55.2	14	1	US-08-677-599B-23	Sequence 23, Appl
24	55.2	15	10	US-09-756-983-11	Sequence 11, Appl
25	55.2	25	1	US-08-677-599B-8	Sequence 8, Appl
26	55.2	93	12	US-10-081-281-121	Sequence 121, Appl
27	55.2	94	10	US-09-766-378A-37	Sequence 37, Appl
28	55.2	166	9	US-09-734-329-6	Sequence 6, Appl
29	55.2	181	10	US-09-815-837-103	Sequence 103, Appl
30	55.2	183	10	US-09-815-837-16	Sequence 16, Appl
31	55.2	184	10	US-09-815-837-15	Sequence 15, Appl
32	55.2	185	10	US-09-815-837-13	Sequence 13, Appl
33	55.2	185	10	US-09-815-837-14	Sequence 14, Appl
34	55.2	186	10	US-09-815-837-17	Sequence 17, Appl
35	55.2	186	10	US-09-815-837-19	Sequence 19, Appl
36	55.2	186	10	US-09-815-837-20	Sequence 20, Appl
37	55.2	187	10	US-09-815-837-18	Sequence 18, Appl
38	55.2	189	10	US-09-815-837-21	Sequence 21, Appl
39	55.2	189	10	US-09-815-837-22	Sequence 22, Appl
40	55.2	193	10	US-09-815-837-23	Sequence 23, Appl
41	55.2	193	10	US-09-815-837-24	Sequence 24, Appl
42	55.2	196	10	US-09-741-669-368	Sequence 368, Appl
43	55.2	196	10	US-09-912-020-376	Sequence 376, Appl
44	55.2	199	10	US-09-815-837-56	Sequence 56, Appl
45	55.2	199	10	US-09-815-837-60	Sequence 60, Appl

ALIGNMENTS

RESULT 1
US-08-790-540A-2
; Sequence 2, Application US/08790540A
; Patent No. US20010011125A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; ; Antibodies, Nucleic Acids Encoding Same and Methods of Use
; ;
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,540A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-790-540A-2
Query Match 79.3%; Score 46; DB 8; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.092;

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Matches      8;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

Qy      1 ARHNYGSF 8
      |||||
Db      97 ARHNYGSF 104

RESULT 2
US-08-790-540A-6
; Sequence 6, Application US/08790540A
; Patent No. US2001001125A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TELECOMMUNICATION INFORMATION:
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,540A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9901
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-790-540A-6

Query Match      79.3%; Score 46; DB 8; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.092;
Matches      8;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

Qy      1 ARHNYGSF 8
      |||||
Db      97 ARHNYGSF 104

RESULT 3
US-08-791-391A-2
; Sequence 2, Application US/08791391A
; Patent No. US20010016645A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TELECOMMUNICATION INFORMATION:
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122

Query Match      79.3%; Score 46; DB 8; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.092;
Matches      8;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

Qy      1 ARHNYGSF 8
      |||||
Db      97 ARHNYGSF 104

RESULT 4
US-08-791-391A-6
; Sequence 6, Application US/08791391A
; Patent No. US20010016645A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TELECOMMUNICATION INFORMATION:
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,391A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9901
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-791-391A-6
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,391A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9901
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-791-391A-2

Query Match      79.3%; Score 46; DB 8; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.092;
Matches      8;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

Qy      1 ARHNYGSF 8
      |||||
Db      97 ARHNYGSF 104

RESULT 4
US-08-791-391A-6
; Sequence 6, Application US/08791391A
; Patent No. US20010016645A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TELECOMMUNICATION INFORMATION:
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,391A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9901
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-791-391A-6
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Query Match 79.3%; Score 46; DB 8; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.092;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSF 8
Db 97 ARHNYGSF 104

RESULT 5

US-09-764-853-432
; Sequence 432, Application US/09764853
; Patent No. US20020090672A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJ206
; CURRENT APPLICATION NUMBER: US/09/764,853
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 939
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 432
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-853-432

Query Match 65.5%; Score 38; DB 10; Length 101;
Best Local Similarity 75.0%; Pred. No. 2.2;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFY 9
Db 64 RHNYGSFH 71

RESULT 6

US-08-677-599B-22
; Sequence 22, Application US/08677599B
; Patent No. US20020155117A1
; GENERAL INFORMATION:
; APPLICANT: Sucia-Foca, Nicole
; TITLE OF INVENTION: METHODS FOR DETECTING ORGAN ALLOGRAFT
; TITLE OF INVENTION: REJECTION AND USES THEREOF
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/677,599B
; FILING DATE: 08-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq., John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 50161-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212/278/0400
; TELEFAX: 212/391/0525
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids

; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-677-599B-22

Query Match 62.1%; Score 36; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYG 6
Db 9 ARHNYG 14

RESULT 7

US-09-864-761-33948
; Sequence 33948, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 33948
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC007240.2

; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 5.5
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.7
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.7
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 3.4
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 3.9
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.9
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 5.5
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.8
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.9
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.7
; OTHER INFORMATION: SWISSPROT HIT: C68008, EVALU6 6.00e+00
US-09-864-761-33948

Query Match 60.3%; Score 35; DB 10; Length 51;

Best Local Similarity 70.0%; Pred. No. 3.7;

Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARHNYGSFYE 10

|| |||||

Db 34 ARITYGSIYE 43

RESULT 8

US-09-839-884-40

; Sequence 40, Application US/09839884

; Patent No. US20020076739A1

; GENERAL INFORMATION:

; APPLICANT: Aebersold, Rudolf H.

; APPLICANT: Gelb, Michael H

; APPLICANT: Gygi, Steven

; APPLICANT: Scott, C R

; APPLICANT: Turecek, Frantisek

; APPLICANT: Gerber, Scott A

; APPLICANT: Rist, Beate

; TITLE OF INVENTION: Rapid Quantitative Analysis of Proteins or Protein

; FILE REFERENCE: 64-98A

; CURRENT APPLICATION NUMBER: US/09/839,884

; CURRENT FILING DATE: 2001-04-20

; PRIOR APPLICATION NUMBER: 09/383,062

; PRIOR FILING DATE: 1999-08-25

; PRIOR APPLICATION NUMBER: 60/097,788

; PRIOR FILING DATE: 1998-08-25

; NUMBER OF SEQ ID NOS: 64

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 40

; LENGTH: 30

; TYPE: PRT

; ORGANISM: yeast

; FEATURE:

; NAME/KEY: VARIANT

; LOCATION: (2)

; OTHER INFORMATION: C at position 2 is ICAT-labeled cysteinyl residue.

US-09-839-884-40

Query Match

Best Local Similarity 59.6%; Score 34; DB 10; Length 30;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8

|||||

Db 10 HNYGAF 15

RESULT 9

US-09-415-540-5

; Sequence 5, Application US/09415540

; Patent No. US20010010911A1

; GENERAL INFORMATION:

; APPLICANT: Hawkins, Phillip R.

; APPLICANT: Hillman, Jennifer L.

; TITLE OF INVENTION: A NOVEL HUMAN PYROPHOSPHATASE

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: California

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/415,540

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/741,437

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Billings, Lucy J.

; REGISTRATION NUMBER: 36,749

; REFERENCE/DOCKET NUMBER: PF-0148 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 855-0555

; TELEFAX: (415) 845-4166

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 287 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; IMMEDIATE SOURCE:

; LIBRARY: GenBank

; CLONE: 4199

US-09-415-540-5

Query Match

Best Local Similarity 58.6%; Score 34; DB 10; Length 287;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8

|||||

Db 92 HNYGAF 97

RESULT 10

US-08-677-599B-21

; Sequence 21, Application US/08677599B

; Patent No. US2002015117A1

; GENERAL INFORMATION:

; APPLICANT: Sucia-Foca, Nicole

; TITLE OF INVENTION: METHODS FOR DETECTING ORGAN ALLOGRAFT

; TITLE OF INVENTION: REJECTION AND USES THEREOF

; NUMBER OF SEQUENCES: 23

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooper & Dunham LLP

; STREET: 1185 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/677,599B

; FILING DATE: 08-JUL-1996

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: White Esq., John P.

; REGISTRATION NUMBER: 28,678
 ; REFERENCE/DOCKET NUMBER: 50161-A
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212/278/0400
 ; TELEFAX: 212/391/0525
 ; INFORMATION FOR SEQ ID NO: 21:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 14 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 US-08-677-599B-21

Query Match 56.9%; Score 33; DB 1; Length 14;
 Best Local Similarity 83.3%; Pred. No. 2.2;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYG 6
 :|||||
 DB 9 SRHNYG 14

RESULT 11

US-09-925-301-1293
 ; Sequence 1293, Application US/09925301
 ; Patent No. US20020052308A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
 ; FILE REFERENCE: PA106
 ; CURRENT APPLICATION NUMBER: US/09/925,301
 ; CURRENT FILING DATE: 2001-08-10
 ; PRIOR APPLICATION NUMBER: PCT/US00/05882
 ; PRIOR FILING DATE: 2000-03-08
 ; PRIOR APPLICATION NUMBER: 60/124,270
 ; PRIOR FILING DATE: 1999-03-12
 ; NUMBER OF SEQ ID NOS: 1694
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 1293
 ; LENGTH: 235
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: SITE
 ; LOCATION: (229)
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 US-09-925-301-1293

Query Match 56.9%; Score 33; DB 10; Length 235;
 Best Local Similarity 55.6%; Pred. No. 42;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSFY 9
 :::|||
 DB 139 SKHNLGIFY 147

RESULT 12

US-09-815-242-11232
 ; Sequence 11232, Application US/09815242
 ; Patent No. US20020061569A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Ohlsen, Karl L.
 ; APPLICANT: Zyskind, Judith W.
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John D.
 ; APPLICANT: Carr, Grant J.
 ; APPLICANT: Yamamoto, Robert T.
 ; APPLICANT: Xu, H. Howard
 ; TITLE OF INVENTION: Identification of Essential Genes in
 ; MOLECULE TYPE: Prokaryotes

; FILE REFERENCE: ELITRA.011A
 ; CURRENT APPLICATION NUMBER: US/09/815,242
 ; CURRENT FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/191,078
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: 60/206,848
 ; PRIOR FILING DATE: 2000-05-23
 ; PRIOR APPLICATION NUMBER: 60/207,727
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: 60/242,578
 ; PRIOR FILING DATE: 2000-10-23
 ; PRIOR APPLICATION NUMBER: 60/253,625
 ; PRIOR FILING DATE: 2000-11-27
 ; PRIOR APPLICATION NUMBER: 60/257,931
 ; PRIOR FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: 60/269,308
 ; PRIOR FILING DATE: 2001-02-16
 ; NUMBER OF SEQ ID NOS: 14110
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 11232
 ; LENGTH: 512
 ; TYPE: PRT
 ; ORGANISM: Haemophilus influenzae
 US-09-815-242-11232

Query Match 56.9%; Score 33; DB 10; Length 512;
 Best Local Similarity 55.6%; Pred. No. 94;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSFY 9
 :|||:
 DB 145 AAHEFGSFF 153

RESULT 13

US-08-677-599B-11
 ; Sequence 11, Application US/08677599B
 ; Patent No. US20020155117A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sugla-Foca, Nicole
 ; TITLE OF INVENTION: METHODS FOR DETECTING ORGAN ALLOGRAFT
 ; REJECTION AND USES THEREOF
 ; NUMBER OF SEQUENCES: 23
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Cooper & Dunham LLP
 ; STREET: 1185 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10036
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/677,599B
 ; FILING DATE: 08-JUL-1996
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: White Esq., John P.
 ; REGISTRATION NUMBER: 28,678
 ; REFERENCE/DOCKET NUMBER: 50161-A
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212/278/0400
 ; TELEFAX: 212/391/0525
 ; INFORMATION FOR SEQ ID NO: 11:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 14 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide

US-08-677-599B-11

Query Match 55.2%; Score 32; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHHY 6
| | | | |
Db 10 RHHY 14

RESULT 14

US-08-677-599B-12
; Sequence 12, Application US/08677599B
; Patent No. US20020155117A1
; GENERAL INFORMATION:
; APPLICANT: Sucia-Foca, Nicole
; TITLE OF INVENTION: METHODS FOR DETECTING ORGAN ALLOGRAFT
; TITLE OF INVENTION: REJECTION AND USES THEREOF
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/677,599B
; FILING DATE: 08-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq., John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 50161-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212/278/0400
; TELEFAX: 212/391/0525
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-677-599B-12

Query Match 55.2%; Score 32; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHHY 6
| | | | |
Db 10 RHHY 14

RESULT 15

US-08-677-599B-13
; Sequence 13, Application US/08677599B
; Patent No. US20020155117A1
; GENERAL INFORMATION:
; APPLICANT: Sucia-Foca, Nicole
; TITLE OF INVENTION: METHODS FOR DETECTING ORGAN ALLOGRAFT
; TITLE OF INVENTION: REJECTION AND USES THEREOF
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas

; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/677,599B
; FILING DATE: 08-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq., John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 50161-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212/278/0400
; TELEFAX: 212/391/0525
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-677-599B-13

Query Match 55.2%; Score 32; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHHY 6
| | | | |
Db 10 RHHY 14

Search completed: November 18, 2002, 19:04:24
Job time : 5.60526 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:43:42 ; Search time 9.47368 Seconds
(without alignments)
31.058 Million cell updates/sec

Title: US-09-016-061-98
Perfect score: 58
Sequence: 1 ARHNYGSFYE 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*
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2: /cgn2_6ptodata/1/1aa/5B_COMB.pep.*
3: /cgn2_6ptodata/1/1aa/6A_COMB.pep.*
4: /cgn2_6ptodata/1/1aa/6B_COMB.pep.*
5: /cgn2_6ptodata/1/1aa/PCTUS_COMB.pep.*
6: /cgn2_6ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	62.1	94	3	US-09-147-550-14
2	36	62.1	94	3	US-09-147-550-45
3	36	62.1	94	3	US-09-147-550-48
4	36	62.1	94	3	US-09-147-550-77
5	36	62.1	94	3	US-09-147-550-84
6	36	62.1	94	3	US-09-147-550-90
7	36	62.1	94	3	US-09-147-550-101
8	36	62.1	94	4	US-09-557-917-14
9	36	62.1	94	4	US-09-557-917-45
10	36	62.1	94	4	US-09-557-917-48
11	36	62.1	94	4	US-09-557-917-77
12	36	62.1	94	4	US-09-557-917-80
13	36	62.1	94	4	US-09-557-917-90
14	36	62.1	94	4	US-09-557-917-101
15	34	58.6	191	4	US-09-443-041A-24
16	34	58.6	236	4	US-09-443-041A-30
17	34	58.6	260	4	US-09-443-041A-10
18	34	58.6	261	4	US-09-443-041A-26
19	34	58.6	269	4	US-09-443-041A-18
20	34	58.6	271	4	US-09-443-041A-32
21	34	58.6	271	4	US-09-443-041A-33
22	34	58.6	286	2	US-08-809-267-3
23	34	58.6	286	5	PCT-US95-13662A-3
24	34	58.6	287	2	US-08-741-437-5
25	34	58.6	287	2	US-08-134-593-5
26	33	56.9	19	4	US-09-441-502B-56
27	33	56.9	19	4	US-09-441-502B-57

28	33	56.9	270	2	US-08-484-993B-47	Sequence 47, Appl
29	33	56.9	270	2	US-08-484-158B-47	Sequence 47, Appl
30	33	56.9	270	2	US-08-484-596A-47	Sequence 47, Appl
31	33	56.9	270	2	US-08-480-150A-47	Sequence 47, Appl
32	33	56.9	270	3	US-08-458-731-47	Sequence 47, Appl
33	33	56.9	270	3	US-08-149-223A-47	Sequence 47, Appl
34	33	56.9	270	3	US-08-484-993B-41	Sequence 41, Appl
35	33	56.9	566	2	US-08-484-158B-41	Sequence 41, Appl
36	33	56.9	566	2	US-08-484-596A-41	Sequence 41, Appl
37	33	56.9	566	2	US-08-480-150A-41	Sequence 41, Appl
38	33	56.9	566	3	US-08-458-731-41	Sequence 41, Appl
39	33	56.9	566	3	US-08-149-223A-41	Sequence 41, Appl
40	33	56.9	715	4	US-08-669-286-5	Sequence 5, Appl
41	33	56.9	715	4	US-09-649-253-5	Sequence 5, Appl
42	33	56.9	715	4	US-09-642-146-5	Sequence 5, Appl
43	32	55.2	15	1	US-08-618-464-7	Sequence 7, Appl
44	32	55.2	15	4	US-09-107-615-7	Sequence 7, Appl
45	32	55.2	16	4	US-09-181-896-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-09-147-550-14
; Sequence 14, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-14

Query Match 62.1% Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
|||||
Db 80 RHNYGVF 86

RESULT 2
US-09-147-550-45
; Sequence 45, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979

; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-45

Query Match 62.1%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 80 RHNYGVF 86

RESULT 3

US-09-147-550-48
; Sequence 48, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-48

Query Match 62.1%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 80 RHNYGVF 86

RESULT 4

US-09-147-550-77
; Sequence 77, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 77
; LENGTH: 94

; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-77

Query Match 62.1%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 80 RHNYGVF 86

RESULT 5

US-09-147-550-84
; Sequence 84, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-84

Query Match 62.1%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 80 RHNYGVF 86

RESULT 6

US-09-147-550-90
; Sequence 90, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 90
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-90

Query Match 62.1%; Score 36; DB 3; Length 94;

Best Local Similarity 85.7%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
| | | | |
Db 80 RHNYGVF 86

RESULT 7

US-09-147-550-101
; Sequence 101, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-101

Query Match 62.1%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
| | | | |
Db 80 RHNYGVF 86

RESULT 8

US-09-557-917-14
; Sequence 14, Application US/09557917
; Patent No. 6284457
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-14

Query Match 62.1%; Score 36; DB 4; Length 94;
Best Local Similarity 85.7%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
| | | | |
Db 80 RHNYGVF 86

RESULT 9

US-09-557-917-45
; Sequence 45, Application US/09557917
; Patent No. 6284457
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-45

Query Match 62.1%; Score 36; DB 4; Length 94;
Best Local Similarity 85.7%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
| | | | |
Db 80 RHNYGVF 86

RESULT 10

US-09-557-917-48
; Sequence 48, Application US/09557917
; Patent No. 6284457
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-48

Query Match 62.1%; Score 36; DB 4; Length 94;
Best Local Similarity 85.7%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8

Db 80 RHNYGVF 86
|||||

RESULT 11

US-09-557-917-77
; Sequence 77, Application US/09557917
; Patent No. 6284457
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 77
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-77

Query Match 62.1%; Score 36; DB 4; Length 94;
Best Local Similarity 85.7%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
|||||

Db 80 RHNYGVF 86

RESULT 12

US-09-557-917-84
; Sequence 84, Application US/09557917
; Patent No. 6284457
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-84

Query Match 62.1%; Score 36; DB 4; Length 94;
Best Local Similarity 85.7%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
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Db 80 RHNYGVF 86

Db 80 RHNYGVF 86

RESULT 13

US-09-557-917-90
; Sequence 90, Application US/09557917
; Patent No. 6284457
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 90
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-90

Query Match 62.1%; Score 36; DB 4; Length 94;
Best Local Similarity 85.7%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
|||||

Db 80 RHNYGVF 86

RESULT 14

US-09-557-917-101
; Sequence 101, Application US/09557917
; Patent No. 6284457
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-101

Query Match 62.1%; Score 36; DB 4; Length 94;
Best Local Similarity 85.7%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
|||||

Db 80 RHNYGVF 86

RESULT 15
US-09-443-041A-24
; Sequence 24, Application US/09443041A
; Patent No. 6465717
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Orozco, Buddy
; APPLICANT: Rafalski, Antoni
; APPLICANT: Shen, Jennie
; TITLE OF INVENTION: Sterol Metabolism Enzymes
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/443,041A
; CURRENT FILING DATE: 1999-11-18
; PRIOR APPLICATION NUMBER: 60/109,283
; PRIOR FILING DATE: 1998-11-20
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 24
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Zea mays
US-09-443-041A-24

Query Match 58.6%; Score 34; DB 4; Length 191;
Best Local Similarity 71.4%; Pred. NO. 79;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
| | | | |
Db 171 RHNYGCHY 177

Search completed: November 18, 2002, 17:55:53
Job time : 9.47368 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:47:14 ; Search time 10.6579 Seconds
(without alignments)
90.200 Million cell updates/sec

Title: US-09-016-061-100

Perfect score: 57

Sequence: 1 ARHNYGSFYS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_73.*

1: piri.*

2: piri2.*

3: piri3.*

4: piri4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	73.7	195	2	G86742
2	40	70.2	113	2	S26468
3	39	68.4	555	2	T21028
4	38	66.7	89	2	S38680
5	38	66.7	89	2	S38683
6	38	66.7	89	2	S38684
7	38	66.7	225	2	I47095
8	37	64.9	386	2	S51436
9	37	64.9	479	1	F70039
10	37	64.9	2288	2	T29999
11	36	63.2	82	2	I51106
12	36	63.2	177	2	C84952
13	36	63.2	233	2	H82163
14	36	63.2	446	2	T19625
15	36	63.2	467	2	A39494
16	36	63.2	470	2	H71667
17	36	63.2	575	2	T12094
18	36	63.2	583	2	S56680
19	36	63.2	592	2	J00991
20	36	63.2	592	2	S56681
21	36	63.2	592	2	S61503
22	36	63.2	593	2	T01575
23	36	63.2	786	2	S37031
24	36	63.2	786	2	F95977
25	35	61.4	9	2	S36850
26	35	61.4	83	2	S21593
27	35	61.4	167	2	T16454
28	35	61.4	367	2	AH0675
29	35	61.4	568	2	T28876

30	35	61.4	584	2	T06163
31	35	61.4	586	2	H84966
32	35	61.4	660	2	S71276
33	35	61.4	664	2	E86257
34	35	61.4	1024	2	T46016
35	35	61.4	2295	2	B71621
36	34	59.6	65	2	S17441
37	34	59.6	85	2	I59634
38	34	59.6	86	2	A81873
39	34	59.6	89	2	S38676
40	34	59.6	89	2	S38680
41	34	59.6	89	2	S57512
42	34	59.6	98	1	WMBP72
43	34	59.6	98	1	WMBP79
44	34	59.6	107	2	PL0080
45	34	59.6	123	2	C25239

ALIGNMENTS

RESULT 1

G86742

Conserved hypothetical protein yjgF [imported] - Lactococcus lactis subsp. lactis (st C; Species: Lactococcus lactis subsp. lactis
C; Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 17-May-2002
C; Accession: G86742

R; Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissbach, J.; Eh Genome Res. 11, 731-753, 2001

A; Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis A; Reference number: A86625; MUID: 21235186; PMID: 11337471

A; Accession: G86742

A; Status: preliminary

A; Molecule type: DNA

A; Residues: 1-195 <STO>

A; Cross-references: GB:AE005176; PID: g12723879; PIDN: AK05041.1; GSPDB: GN00146

A; Experimental source: strain IL1403

C; Genetics:

A; Gene: YjgF

C; Superfamily: hypothetical protein b1011

Query Match 73.7%; Score 42; DB 2; Length 195;
Best Local Similarity 66.7%; Pred. No. 2.5;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFY 9

|:|:|:|:|

Db 103 AKHMGAFY 111

RESULT 2

S26468

Ig heavy chain V region - mouse

C; Species: Mus musculus (house mouse)

C; Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C; Accession: S26468

R; Kavelar, J.

Submitted to the EMBL Data Library, April 1991

A; Reference number: S26459

A; Accession: S26468

A; Status: preliminary

A; Molecule type: mRNA

A; Residues: 1-113 <KAV>

A; Cross-references: EMBL: X59107; NID: g51944; PIDN: CAA1833.1; PID: g51945

C; Superfamily: immunoglobulin V region; immunoglobulin homology

C; Keywords: heterotrimer; immunoglobulin

F; 11-94/Domain: immunoglobulin homology <IMM>

Query Match 70.2%; Score 40; DB 2; Length 113;
Best Local Similarity 60.0%; Pred. No. 3.3;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFYS 10

Db 93 ARHPYGNYYA 102
||| |||||

RESULT 3

T21028
hypothetical protein F16H6.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T21028

R:Matthews, L.

submitted to the EMBL Data Library, November 1996

A:Reference number: Z19362

A:Accession: T21028

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-555 <WIL>

A:Cross-references: EMBL:Z81506; PIDN:CAB04128.1; GSPDB:GN00023; CESP:F16H6.1

A:Experimental source: clone F16H6

C:Genetics:

A:Gene: CESP:F16H6.1

A:Map position: 5

A:Introns: 123/1; 318/3

Query Match 68.4%; Score 39; DB 2; Length 555;

Best Local Similarity 87.5%; Pred. No. 24;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFYS 10

|| |||||

Db 314 HNSGSFYS 321

RESULT 4

S38688

MHC class II histocompatibility antigen HLA-DR-08 beta chain - northern lesser bushbaby

C:Species: Galago senegalensis (northern lesser bushbaby)

C:Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 19-May-2000

C:Accession: S38688

R:Figuerola, F.; O'Huigin, C.; Tichy, H.; Klein, J.

submitted to the EMBL Data Library, November 1993

A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduced

A:Reference number: S38676

A:Accession: S38688

A:Molecule type: DNA

A:Residues: 1-89 <FIG>

A:Cross-references: EMBL:Z27158

C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 66.7%; Score 38; DB 2; Length 89;

Best Local Similarity 77.8%; Pred. No. 6.1;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFYS 10

||||| |

Db 75 RHNYGVFES 83

RESULT 5

S38683

MHC class II histocompatibility antigen HLA-DR-03 beta chain - northern lesser bushbaby

C:Species: Galago senegalensis (northern lesser bushbaby)

C:Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 19-May-2000

C:Accession: S38683

R:Figuerola, F.; O'Huigin, C.; Tichy, H.; Klein, J.

submitted to the EMBL Data Library, November 1993

A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduced

A:Reference number: S38676

A:Accession: S38683

A:Molecule type: DNA

A:Residues: 1-89 <FIG>

A:Cross-references: EMBL:Z27153

C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 66.7%; Score 38; DB 2; Length 89;
Best Local Similarity 77.8%; Pred. No. 6.1;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFYS 10

||||| |

Db 75 RHNYGVFES 83

RESULT 6

S38684

MHC class II histocompatibility antigen HLA-DR-04 beta chain - northern lesser bushbaby

C:Species: Galago senegalensis (northern lesser bushbaby)

C:Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 19-May-2000

C:Accession: S38684

R:Figuerola, F.; O'Huigin, C.; Tichy, H.; Klein, J.

submitted to the EMBL Data Library, November 1993

A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduced

A:Reference number: S38676

A:Accession: S38684

A:Molecule type: DNA

A:Residues: 1-89 <FIG>

A:Cross-references: EMBL:Z27154

C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 66.7%; Score 38; DB 2; Length 89;

Best Local Similarity 77.8%; Pred. No. 6.1;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFYS 10

||||| |

Db 75 RHNYGVFES 83

RESULT 7

I47095

MHC class II OVAR-DR-beta-3 - sheep (fragment)

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C:Date: 15-Oct-1996 #sequence_revision 15-Oct-1996 #text_change 21-Jan-2000

C:Accession: I47095

R:Fabry, S.A.; Maddox, J.F.; Gogolin-Ewens, K.J.; Baker, L.; Wu, M.J.; Brandon, M.R.

Anim. Genet. 24, 249-255, 1993

A:Title: Isolation, characterization and evolution of ovine major histocompatibility

A:Reference number: I47075; MUID:94057592; PMID:7902039

A:Accession: I47095

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-225 <PAB>

A:Cross-references: GB:I47095; NID:9458880; PIDN:AAA16562.1; PID:9458881

C:Genetics:

A:Gene: OVAR-DRB3

C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

F:98-163/Domain: immunoglobulin homology <IMM>

Query Match 66.7%; Score 38; DB 2; Length 225;

Best Local Similarity 77.8%; Pred. No. 15;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFYS 10

||||| |

Db 68 RHNYGVFES 76

RESULT 8

S51436

probable membrane protein YLR191w - yeast (Saccharomyces cerevisiae)

N:Alternate names: hypothetical protein L9470.1

C:Species: Saccharomyces cerevisiae

C:Date: 23-Feb-1995 #sequence_revision 12-May-1995 #text_change 06-Feb-1998

C:Accession: S51436

R:Wohldmann, P.

submitted to the EMBL Data Library, November 1994

A:Description: The sequence of *S. cerevisiae* cosmid 9470.

A:Reference number: S51414

A:Accession: S51436

A:Molecule type: DNA

A:Residues: 1-386 <WOH>

A:Cross-references: EMBL:U17246; NID:g577192; PID:g577193; MIPS:YLR191W

C:Genetics:

A:Gene: SGD:PEX13

A:Cross-references: SGD:S0004181; MIPS:YLR191W

A:Map position: 12R

C:Superfamily: SH3 homology

C:Keywords: transmembrane protein

F:264-280/Domain: transmembrane #status predicted <TM>

F:313-367/Domain: SH3 homology <SH>

Query Match 64.9%; Score 37; DB 2; Length 386;

Best Local Similarity 85.7%; Pred. No. 39;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSFY 9

Db 117 HNYGSFY 123

RESULT 9

F70039

probable iron-sulfur protein yfw [similarity] - *Bacillus subtilis*

C:Species: *Bacillus subtilis*

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000

C:Accession: F70039

R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter

C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd

A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, S.; Galizzi, A.; Gallen

lech, J.; Harwood, C.R.; Henaat, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hulio, M.F.

Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,

A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauel

Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle

Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,

A:Authors: Schlicht, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron

akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,

T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K

A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.

A:Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.

A:Reference number: A69580; MUID:98044033; PMID:9384377

A:Accession: F70039

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-479 <KUN>

A:Cross-references: GB:299121; GB:AL009126; NID:g2635827; PIDN:CAB15409.1; PID:g2635917

A:Experimental source: strain 168

C:Genetics:

A:Gene: yfw

C:Superfamily: conserved hypothetical iron-sulfur protein HP0138; ferredoxin 2[4Fe-4S] h

C:Keywords: 4Fe-4S; iron-sulfur protein; metalloprotein

F:303-381/Domain: ferredoxin 2[4Fe-4S] homology <FE>

F:313,316,319,373/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted

F:323,363,366,369/Binding site: 4Fe-4S cluster (Cys, Ser, Cys) (covalent) #status p

Query Match 64.9%; Score 37; DB 1; Length 479;

Best Local Similarity 75.0%; Pred. No. 49;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFYS 10

Db 332 HSYGSFYS 339

RESULT 10

T29999

hypothetical protein ZC8.4 - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000

C:Accession: T29999

R:Latreille, P.; Bradshaw, H.

submitted to The EMBL Data Library, July 1996

A:Description: The sequence of *C. elegans* cosmid ZC8.

A:Reference number: Z20719

A:Accession: T29999

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-2288 <LAT>

A:Cross-references: EMBL:U64862; PIDN:AA852624.1; GSPDB:GN00028; CESP:ZC8.4

A:Experimental source: strain Bristol N2; clone ZC8

C:Genetics:

A:Gene: CESP:ZC8.4

A:Map position: X

A:introns: 43/2; 80/3; 110/3; 153/2; 274/3; 738/2; 1249/1; 1392/3; 1454/1; 1602/1; 16

Query Match 64.9%; Score 37; DB 2; Length 2288;

Best Local Similarity 66.7%; Pred. No. 2.3e+02;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSFY 9

Db 34 SRSNYGSFY 42

RESULT 11

I51106

Major Histocompatibility Complex class IIB - ring-necked pheasant (fragment)

C:Species: *Phasianus colchicus* (ring-necked pheasant)

C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 23-Jul-1999

C:Accession: I51106

R:Wittzell, H.; von Schantz, T.; Zoorob, R.; Auffray, C.

Immunogenetics 39, 395-403, 1994

A:Title: Molecular characterization of three Mhc class II B haplotypes in the ring-ne

A:Reference number: I51103; MUID:94245280; PMID:7910588

A:Accession: I51106

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-82 <WTT>

A:Cross-references: EMBL:X75406; NID:g496926; PIDN:CAA53160.1; PID:g496927

C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 63.2%; Score 36; DB 2; Length 82;

Best Local Similarity 85.7%; Pred. No. 13;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8

Db 75 RHNYGSF 81

RESULT 12

C84952

aminosyl-trNA hydrolase (EC 3.1.1.29) [imported] - *Buchnera* sp. (strain APS)

C:Species: *Buchnera* sp.

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001

C:Accession: C84952

R:Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.

Nature 407, 81-86, 2000

A:Title: Genome sequence of the endocellular bacterial symbiont of aphids *Buchnera* sp

A:Reference number: A84930; MUID:20445173; PMID:10993077

A:Accession: C84952

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-177 <STO>

A:Cross-references: GB:AP000398; GSPDB:GN00144

A:Experimental source: strain APS

C:Genetics:

A:Gene: pth; BU190

C:Superfamily: peptidyl-trNA hydrolase

C:Keywords: carboxylic ester hydrolase

Query Match 63.2%; Score 36; DB 2; Length 177;
 Best Local Similarity 75.0%; Pred. No. 28;
 Matches 6; Conservative 1; Mismatches 0; Gaps 0;

QY 2 RHNYGSFY 9
 ||| |||
 Db 16 RHNVGSWY 23

RESULT 13

H82163
 arginyl-L-tryptophan transferase-related protein VC1736 [imported] - Vibrio cholerae (str

C:Species: Vibrio cholerae

C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001

C:Accession: H82163

R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;

Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, H.

1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A:Reference number: A82035; MUID:20406833; PMID:10952301

A:Accession: H82163

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-233 <HEI>

A:Cross-references: GB:AE004251; GB:AE003852; NID:9656248; PIDN:AAF94886.1; GSPDB:GN001

A:Experimental source: serogroup O1; strain N16961; biotype El Tor

C:Genetics:

A:Gene: VC1736

A:Map position: 1

Query Match 63.2%; Score 36; DB 2; Length 233;
 Best Local Similarity 66.7%; Pred. No. 36;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSFY 9
 ||| |||
 Db 117 ARRHGSMY 125

RESULT 14

T19625

hypothetical protein C31H5.6 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000

C:Accession: T19625

R:Kershaw, J.

submitted to the EMBL Data Library, April 1997

A:Reference number: Z19153

A:Accession: T19625

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-446 <WIL>

A:Cross-references: EMBL:Z93778; PIDN:CAB07846.1; GSPDB:GN00019; CESP:C31H5.6

A:Experimental source: clone C31H5

C:Genetics:

A:Gene: CESP:C31H5.6

A:Map position: 1

A:Introns: 49/2; 85/1; 120/2; 183/3; 218/3; 255/3; 285/2; 331/3; 360/3

C:Superfamily: Caenorhabditis elegans hypothetical protein W03D8.8

Query Match 63.2%; Score 36; DB 2; Length 446;
 Best Local Similarity 100.0%; Pred. No. 69;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHNYGS 7
 |||||
 Db 51 RHNYGS 56

RESULT 15

A99494

thermostable carboxypeptidase 1 [imported] - Sulfolobus solfataricus

C:Species: Sulfolobus solfataricus

C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 15-Jun-2001

C:Accession: A99494

R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Ch

Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder

arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.

submitted to GenBank, April 2001

A:Description: Sulfolobus solfataricus complete genome.

A:Reference number: A99139

A:Accession: A99494

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-467 <KUR>

A:Cross-references: GB:AE006641; NID:gl3816525; PIDN:AAK43208.1; GSPDB:GN00155

C:Genetics:

A:Gene: SSO3105

C:Superfamily: Thermus aquaticus carboxypeptidase Taq

Query Match 63.2%; Score 36; DB 2; Length 467;

Best Local Similarity 75.0%; Pred. No. 72;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 HNYGSFYS 10
 |||||
 Db 432 HKYGSFYS 439

Search completed: November 18, 2002, 17:57:24

Job time : 10.6579 secs

GenCore version 5.1.3

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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:33:36 ; Search time 5.39474 Seconds
(without alignments)
76.883 Million cell updates/sec

Title: US-09-016-061-100

Perfect score: 57

Sequence: 1 ARHNYGSFYS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	39	68.4	323	1 CCSA_LOTJA	Q9bbp4 lotus japon
2	37	64.9	386	1 PEXD_YEAST	P80567 saccharomyc
3	36	63.2	177	1 PTH_BUCAI	P57287 buchneria ap
4	36	63.2	470	1 SYE2_RICPR	Q9zct8 rickettsia
5	36	63.2	583	1 INV3_DAUCA	Q39693 daucus caro
6	36	63.2	592	1 INV1_DAUCA	P26792 daucus caro
7	36	63.2	592	1 INV2_DAUCA	Q39692 daucus caro
8	36	63.2	786	1 EXPD_RHIME	P33698 rhizobium m
9	35	61.4	586	1 STD_BUCAI	P57401 buchneria ap
10	35	61.4	1024	1 U203_ARATH	Q9m2q4 arabidopsis
11	34	59.6	65	1 CCSA_PEA	P31172 pisum sativ
12	34	59.6	98	1 VG7_BPPH2	P13848 bacterioph
13	34	59.6	98	1 VG7_BPP2A	P07533 bacterioph
14	34	59.6	275	1 IF2A_PYRAB	Q9v0e4 pyrococcus
15	34	59.6	275	1 IF2A_PYRHO	O58655 pyrococcus
16	34	59.6	284	1 IPYR_PICPA	O13505 pichia past
17	34	59.6	286	1 IPYR_KLULA	P13998 kluyveromyc
18	34	59.6	286	1 IPYR_YEAST	P00817 saccharomyc
19	34	59.6	328	1 CCSA_ARATH	P56770 arabidopsis
20	34	59.6	367	1 LHX4_HUMAN	Q96992 homo sapien
21	34	59.6	367	1 LHX4_MOUSE	P53776 mus musculu
22	34	59.6	512	1 PNTA_HAEIN	P43842 haemophilus
23	34	59.6	683	1 SFP1_YEAST	P32432 saccharomyc
24	34	59.6	1386	1 RPOD_MARPO	P06274 marchantia
25	33	57.9	245	1 GSC_CHICK	P53545 gallus gall
26	33	57.9	313	1 CCSA_TOBAC	P12216 nicotiana t
27	33	57.9	316	1 Y025_NPVAC	P41430 autographa
28	33	57.9	347	1 UL33_HSV6U	P52380 human herpe
29	33	57.9	353	1 YF91_MYCPN	Q50336 mycoplasma
30	33	57.9	371	1 MNCP_OXYFA	P15798 oxytricha f
31	33	57.9	371	1 MNCP_OXYTR	Q27151 oxytricha t
32	33	57.9	448	1 NCAP_CVHOC	P33469 human coron
33	33	57.9	473	1 SYE_AQUAE	O67271 aquifex aeo

34 33 57.9 494 1 RNH1_CRIFA
35 33 57.9 514 1 LIM_HAIRO
36 33 57.9 590 1 INV3_MAIZE
37 33 57.9 642 1 INV3_VICFA
38 33 57.9 649 1 INV3_PHAU
39 33 57.9 651 1 INV3_PHAU
40 33 57.9 715 1 ADVS_BOVIN
41 33 57.9 802 1 YGN9_YEAST
42 33 57.9 1196 1 XPG_XENLA
43 33 57.9 1790 1 VIT_ANTI
44 33 57.9 2184 1 RRPL_CDOVO
45 32 56.1 65 1 CCSA_OENBE

ALIGNMENTS

RESULT 1
ID CCSA_LOTJA STANDARD; PRT; 323 AA.
AC Q9BBP4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cytochrome c biogenesis protein ccSA.
GN CCSA.
OS Lotus japonicus.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Loteeae; Lotus.
OX NCBI_TaxID:34305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Accession MG-20;
RX MEDLINE=21082929; PubMed=11214967;
RA Kato T., Kaneko T., Sato S., Nakamura Y., Tabata S.;
RT "Complete structure of the chloroplast genome of a legume, Lotus japonicus";
RL DNA Res. 7:323-330(2000).
CC -!- FUNCTION: REQUIRED DURING CYTOCHROME BIOGENESIS AT THE STEP OF
CC HEME ATTACHMENT (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CCMF/CYCK/CCL1/NRFE/CCSA FAMILY.
CC -----
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CC -----
CC EMBL: AF002983; BAB33244.1; -
CC InterPro: IPR002541; CytC_asm.
CC Pfam: PF01578; CytC_asm; 1.
KW Cytochrome c-type biogenesis; Chloroplast.
SQ SEQUENCE 323 AA; 37185 MW; 5A034E3E2829FE35 CRC64;

Query Match 68.4%; Score 39; DB 1; Length 323;
Best Local Similarity 87.5%; Pred. No. 3.4;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFYS 10
Db 315 HNYGSFYS 322
RESULT 2
ID PEXD_YEAST STANDARD; PRT; 386 AA.
AC P80567;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Peroxisomal membrane protein PAS20 (Peroxin-13).
 GN PEX13 OR PAS20 OR YLR191W OR L9470.1.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97011156; PubMed=8858166;
 RA Elgersma Y., Kwast L., Klein A., Voorn-Brouwer T., van den Berg M.,
 RA Tabak H.F., Distel B.;
 RT "The SH3 domain of the Saccharomyces cerevisiae peroxisomal membrane
 RT protein Pex13p functions as a docking site for Pex5p, a mobile
 RT receptor for the import PTS1-containing proteins.";
 RL J. Cell Biol. 135:97-109(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288c / AB972;
 RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,
 RA Favell A., Fulton L., Gattung S., Greco T., Kirsten J., Kucaba T.,
 RA Hallsworth K., Hawkins J., Hillier L., Jier M., Johnson D.,
 RA Johnston L., Langston Y., Latreille P., Le T., Mardis E., Menezes S.,
 RA Miller N., Nhan M., Pauley A., Peluso D., Rifken L., Riles L.,
 RA Taich A., Trevisan E., Vignati D., Wilcox L., Wohlman P., Vaudin M.,
 RA Wilson R., Waterston R.;
 RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP PARTIAL SEQUENCE, AND CHARACTERIZATION.
 RC STRAIN=S288c;
 RX MEDLINE=97011157; PubMed=8858167;
 RA Erdmann R., Blobel G.;
 RT "Identification of Pex13p as a peroxisomal membrane receptor for the
 RT PTS1 recognition factor.";
 RL J. Cell Biol. 135:111-121(1996).
 CC -!- FUNCTION: COMPONENT OF THE PEROXISOMAL TRANSLLOCATION MACHINERY
 CC WITH PEX14 AND PEX17. INTERACTS WITH THE PTS1 RECEPTOR
 CC (PAS10/PEX5).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Peroxisomal.
 CC -!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 CC -----
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 CC -----
 DR EMBL; S82971; AAB46895.1; -;
 DR EMBL; U37420; AAA79308.1; -;
 DR EMBL; U17246; AAB67453.1; -;
 DR EMBL; U14913; AAB67448.1; -;
 DR HSP; Q06187; IAWX.
 DR SGD; S0004181; PEX13.
 DR InterPro; IPR001452; SH3.
 DR Pfam; PF00018; SH3; 1.
 DR PRINTS; PR00452; SH3DOMAIN.
 DR ProDom; PD000066; SH3; 1.
 DR SMART; SM00326; SH3; 1.
 DR PROSITE; PS00002; SH3; 1.
 KW Peroxisome; Transport; Protein transport; Transmembrane; SH3 domain.
 FT DOMAIN 1 263
 FT LUMENAL (POTENTIAL).
 FT TRANSMEM 264 280
 FT POTENTIAL.
 FT DOMAIN 281 386
 FT CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 306 372
 FT SH3.
 SQ SEQUENCE 386 AA; 42706 MW; DBEA9A2372185860 CRC64;
 Query Match 64.9%; Score 37; DB 1; Length 386;
 Best/Local Similarity 85.7%; Pred. No. 9.9;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 OY 3 INYGSFY 9

Db 117 NNYGSFY 123
 :|||||
 RESULT 3
 PTH_BUCAI
 ID PTH_BUCAI STANDARD; PRT; 177 AA.
 AC P57287;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Peptidyl-trna hydrolase (EC 3.1.1.29) (PTH).
 GN PTH OR BU190.
 OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
 OS symbiotic bacterium).
 OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.
 OX NCBI_TaxID=118099;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Tokyo 1998;
 RX MEDLINE=20445173; PubMed=10993077;
 RA Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
 RT "Genome sequence of the endocellular bacterial symbiont of aphids
 RT Buchnera sp. APS.";
 RL Nature 407:81-86(2000).
 CC -!- FUNCTION: THE NATURAL SUBSTRATE FOR THIS ENZYME MAY BE PEPTIDYL-
 CC TRNAS WHICH DROP OFF THE RIBOSOME DURING PROTEIN SYNTHESIS
 CC (BY SIMILARITY).
 CC -!- CATALYTIC ACTIVITY: N-substituted aminoacyl-tRNA + H(2)O = N-
 CC substituted amino acid + tRNA.
 CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE PTH FAMILY.
 CC -----
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 CC -----
 DR EMBL; AF001118; BAB12907.1; -;
 DR HSP; P23932; 2PTH.
 DR InterPro; IPR001328; Pept_trna_hydro.
 DR Pfam; PF01195; Pept_trna_hydro; 1.
 DR ProDom; PD005324; Pept_trna_hydro; 1.
 DR TIGRfams; TIGR00447; pth; 1.
 DR PROSITE; PS01195; PEPT_TRNA_HYDROL_1; FALSE_NEG.
 DR PROSITE; PS01196; PEPT_TRNA_HYDROL_2; 1.
 KW Hydrolase; Complete proteome.
 SQ SEQUENCE 177 AA; 20576 MW; BD18DABFEF0DFAAF CRC64;
 Query Match 63.2%; Score 36; DB 1; Length 177;
 Best/Local Similarity 75.0%; Pred. No. 6.7;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 OY 2 RHYGSFY 9
 Db 16 RHYGSFY 23
 :|||:|
 RESULT 4
 SYE2_RICPR
 ID SYE2_RICPR STANDARD; PRT; 470 AA.
 AC Q9ZCT8;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Glutamyl-tRNA synthetase 2 (EC 6.1.1.17) (Glutamate--trna ligase 2)
 DE (GLUS 2).
 GN GLTX2 OR RP623.
 OS Rickettsia prowazekii.

RT "Gènes needed for the modification, polymerization, export, and
RT processing of succinoglycan by Rhizobium meliloti: a model for
RT succinoglycan biosynthesis.";

RL J. Bacteriol. 175:7045-7055(1993).

RN [3]

RC SEQUENCE FROM N.A.

RP STRAIN=RCR2011 / SU47;

RX MEDLINE=94067019; PubMed=8246891;

RA Becker A., Kleickmann A., Keller M., Arnold W., Puehler A.;

RT "Identification and analysis of the Rhizobium meliloti exoAMONP genes

RT involved in exopolysaccharide biosynthesis and mapping of promoters

RT located on the exoHKLAMONP fragment.";

RL Mol. Gen. Genet. 241:367-379(1993).

RN [4]

RC SEQUENCE FROM N.A.

RP STRAIN=1021;

RX MEDLINE=21396508; PubMed=11481431;

RA Finan T.M., Weidner S., Wong K., Buhrmester J., Chain P.,

RA Vorhoefer F.J., Hernandez-Lucas I., Becker A., Gouzy J.,

RA Golding B., Puehler A.;

RT "The complete sequence of the 1,683-Kb pSymb megaplasmid from the N2-

RT fixing endosymbiont Sinorhizobium meliloti.";

RL Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).

CC -1- PATHWAY: Exopolysaccharide biosynthesis.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).

CC -1- SIMILARITY: SOME, TO B.SOLANACEARUM EPSB.

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CC

CC EMBL; L20758; AAA16042.1; -.

DR EMBL; Z22636; CA80349.1; -.

DR EMBL; AL603645; CAC49486.1; -.

DR PIR; B49349; B49349.

DR PIR; S37031; S37031.

DR PIR; S39960; S39960.

DR InterPro; IPR003856; Wzz.

DR Pfam; PF02706; wzz; 1.

DR TIGRFAMS; TIGR01005; eps_transp_fam; 1.

KW Exopolysaccharide synthesis; Transport; Transmembrane; ATP-binding;

KW Plasmid; Complete proteome.

FT DOMAIN 1 42

FT TRANSMEM 43 66

FT DOMAIN 67 689

FT TRANSMEM 690 711

FT DOMAIN 712 786

FT NP_BIND 583 590

FT ATP (POTENTIAL).

SQ SEQUENCE 786 AA; 86123 MW; E19E771E31F2030C CRC64;

Query Match 63.2%; Score 36; DB 1; Length 786;

Best Local Similarity 62.5%; Pred. No. 33;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSEY 9

||| :|

Db 768 RHRYGKY 775

RESULT 9

SYD_BUCAI

ID SYD_BUCAI STANDARD; PRT; 586 AA.

AC P57401;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Aspartyl-LRNA synthetase (EC 6.1.1.12) (Aspartate--trna ligase)

DE (ASPRS).

GN ASPs OR BU316.

OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
OS symbiotic bacterium).

OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.

OX NCBI_TaxID=118099;

RN [1]

RC SEQUENCE FROM N.A.

RP STRAIN=Tokyo 1998;

RX MEDLINE=20445173; PubMed=1093077;

RA Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;

RT "Genome sequence of the endocellular bacterial symbiont of aphids

RT Buchnera sp. APS.";

RL Nature 407:81-86(2000).

CC -1- CATALYTIC ACTIVITY: ATP + L-aspartate + tRNA(Asp) -> AMP +

CC diphosphate + L-aspartyl-tRNA(Asp).

CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: Cytoplasmic (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.

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CC

CC EMBL; AF001119; BAB13024.1; -.

DR HSSP; P21889; 1EQR.

DR InterPro; IPR002106; AATRNA_ligaseII.

DR InterPro; IPR004524; Asps_bact.

DR InterPro; IPR004115; GAD_dom.

DR InterPro; IPR004364; tRNA-synt_2.

DR InterPro; IPR002312; tRNA-synt_asp.

DR InterPro; IPR004365; tRNA-anti.

DR Pfam; PF00152; tRNA-synt_2; 2.

DR Pfam; PF01336; tRNA-anti; 1.

DR Pfam; PF02938; GAD; 1.

DR PRINTS; PR01042; TRNASYNTHASP.

DR TIGRFAMS; TIGR00459; asps_bact; 1.

DR PROSITE; P850862; AA_TRNA_LIGASE_II; 1.

KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;

KW Complete proteome.

SQ SEQUENCE 586 AA; 68120 MW; D7CB1B50A31800FE CRC64;

Query Match 61.4%; Score 35; DB 1; Length 586;

Best Local Similarity 50.0%; Pred. No. 37;

Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFYS 10

||:|:| |:

Db 180 SRNHGKFYA 189

RESULT 10

U203_ARATH

ID U203_ARATH STANDARD; PRT; 1024 AA.

AC Q9M204;

DT 15-JUN-2002 (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Hypothetical protein At3g57940.

GN AT3G57940 OR T10K17.150.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.

OX NCBI_TaxID=3702;

RN [1]

RC SEQUENCE FROM N.A.

RP STRAIN=cv. Columbia;

RX MEDLINE=21016720; PubMed=11130713;

RA Salanoubat M., Lemcke K., Rieger M., Ansoorge W., Unseld M.,

RA Fartmann B., Valle G., Bloeker H., Perez-Alonso M., Obermaier B.,

```

RA Delsen V., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,
RA De Simone V., Choisne N., Artiguenave F., Robert C., Brottier P.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
RA Wurmbach E., Drzonek H., Erfle H., Jordan N., Bangert S.,
RA Wiedemann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
RA Verzi A., D'Angelo M., Pallavicini A., Toppo S., Simonati B.,
RA Conrad A., Hornischer K., Kauer G., Loehner T.-H., Nordstiek G.,
RA Neuhart J., Scharfe M., Schoen O., Bagues M., Terol J., Climent J.,
RA Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,
RA Cooke R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D.,
RA de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,
RA Monfort A., Argirou A., Flores M., Liguori R., Vitale D.,
RA Manhaupt G., Haase D., Schoof H., Rood S., Zaccaria P., Mewes H.-W.,
RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
RA Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shea T.P.,
RA Creasy T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S.,
RA Pal G., Militscher J., Sellers P., Gill J.E., Feldblyum T.V.,
RA Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,
RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
RA Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,
RA Kiyokawa C., Kohara T., Matsumoto M., Matsuno A., Muraki A.,
RA Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,
RA Watanabe A., Yamada M., Yasuda M., Tabata S.:
RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis
RL thaliana.";
RL Nature 408:820-822(2000).
CC -1- SURCELLULAR LOCATION: Nuclear (By similarity).
CC -1- SIMILARITY: BELONGS TO THE UPF0202 FAMILY.
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CC
CC EMBL; AL132977; CAB67622.1; -
DR Hypothetical protein; ATP-binding; Nuclear protein.
KW NP_BIND 283 290 ATP (POTENTIAL).
FT
SQ SEQUENCE 1024 AA; 114938 MW; C19FF470C77B37AD CRC64;

Query Match 61.4%; Score 35; DB 1; Length 1024;
Best Local Similarity 55.6%; Pred. No. 68;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RHNYGSFYS 10
Db 734 KHNFPFYS 742
:|:| |
|:|:|

RESULT 11
CCSA_PEA
ID CCSA_PEA STANDARD; PRT; 65 AA.
AC P31172;
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Cytochrome c biogenesis protein ccsa (Fragment).
GN CCSA.
OS Pisum sativum (Garden pea).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
OX NCBI_TaxID=3888;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Alaska;
RX MEDLINE=91355950; PubMed=1884007;
RA Nagano Y., Ishikawa H., Matsuno R., Sasaki Y.;
RT "Nucleotide sequence and expression of the ribosomal protein L2 gene

```

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RT in pea chloroplasts.";
RL Plant Mol. Biol. 17:541-545(1991).
CC -1- FUNCTION: REQUIRED DURING CYTOCHROME BIOGENESIS AT THE STEP OF
CC HEME ATTACHMENT (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CCMP/CYCK/CCL1/NRPE/CCSA FAMILY.
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CC
CC EMBL; X59015; CAA41754.1; -
DR PIR: S17441; S17441.
DR InterPro: IPR002541; CytC_asm.
DR Pfam: PF01578; CytC_asm; 1.
KW Cytochrome c-type biogenesis; Chloroplast.
FT NON_TER 1
SQ SEQUENCE 65 AA; 7396 MW; 9E523E0C70B102AA CRC64;

Query Match 59.6%; Score 34; DB 1; Length 65;
Best Local Similarity 75.0%; Pred. No. 5.6;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 HNYGSFYS 10
Db 57 HSYGSFYS 64
|:|:|:| |
|:|:|:| |

RESULT 12
VG7_BPPh2
ID VG7_BPPh2 STANDARD; PRT; 98 AA.
AC P13848;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Head morphogenesis protein (Late protein GP7).
GN 7.
OS Bacteriophage phi-29.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;
OC phi-29-like viruses.
OX NCBI_TaxID=10756;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87106857; PubMed=3803926;
RA Vlicek C., Paces V.;
RT "Nucleotide sequence of the late region of Bacillus phage phi 29
RT completes the 19,285-bp sequence of phi 29 genome. Comparison with
RT the homologous sequence of phage P2A.";
RL Gene 46:215-225(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87016351; PubMed=3763399;
RA Innis C.A., Garvey K.J., Ito J.;
RT "Nucleotide sequence of phage phi 29 gene 7: structure of intergenic
RT spacer between the major early and late genes.";
RL Nucleic Acids Res. 14:7129-7129(1986).
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M14782; AAA32279.1; -
DR EMBL; X04386; CAA27974.1; -
DR PIR: A28923; WMBPF9.
KW Late protein.
SQ SEQUENCE 98 AA; 11266 MW; FF2E7985D2266E14 CRC64;

```

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Query Match          59.6%; Score 34; DB 1; Length 98;
Best Local Similarity 77.8%; Pred. No. 8.7;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFYS 10
   | | | | | | |
DB 33 RVNYGSFVS 41

RESULT 13
VG7_BPPZA
ID VG7_BPPZA STANDARD; PRT; 98 AA.
AC P07533;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Head morphogenesis protein (Late protein GP7).
GN 7.
OS Bacteriophage PZA.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;
OC phi-29-like viruses.
OX NCBI_TaxID=10757;
RN [1]
RP SEQUENCE FROM N.A.
RX EMBL; M11813; AAA88483.1; -.
RA Paces V., Vlcek C., Urbanek P.;
RT "Nucleotide sequence of the late region of Bacillus subtilis phage
PZA, a close relative of phi 29.";
RL Gene 44:107-114(1986).
CC -----
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CC -----
CC QY 2 RHNYGSFYS 10
   | | | | | | |
DB 33 RVNYGSFVS 41

RESULT 14
IF2A_PYRAB
ID IF2A_PYRAB STANDARD; PRT; 275 AA.
AC Q9V0E4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable translation initiation factor 2 alpha subunit (eIF-2-alpha).
GN EIF2A OR PAB0568.
OS Pyrococcus abyssal.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=29292;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=GE5 / Orsay;
RA Heilig R.;
RT "Pyrococcus abyssal genome sequence: insights into archaeal chromosome
structure and evolution.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
```

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 CC -----

DR EMBL; AP000004; BAA30058.1; -
 DR HSP; P05055; 1SR0
 DR InterPro; IPR003029; S1.
 DR Pfam; PF00575; S1; 1.
 DR SMART; SM00316; S1; 1.
 DR PROSITE; PS0126; S1; 1.
 KW Initiation factor; Protein biosynthesis; RNA-binding;
 KW Complete proteome.
 FT DOMAIN 12 83 S1 MOTIF.
 SQ SEQUENCE 275 AA; 31980 MW; 6AAAD15F10FFB436 CRC64;

Query Match 59.6%; Score 34; DB 1; Length 275;
 Best Local Similarity 83.3%; Pred No. 26;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 HNYGSF 8
 ||||:|
 Db 23 HNYGAF 28

Search completed: November 18, 2002, 17:51:42
 Job time : 5.39474 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:40:56 ; Search time 22.3684 Seconds
(without alignments)
92.115 Million cell updates/sec

Title: US-09-016-061-100
Perfect score: 57
Sequence: 1 ARHNYGSFYS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_21.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriaph.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43	75.4	839	Q9LIE5	Q9LIE5 arabidopsis
2	42	73.7	195	Q9CG29	Q9CG29 lactococcus
3	40	70.2	89	O19495	O19495 gallus gail
4	40	70.2	581	Q93X59	Q93X59 cichorium i
5	39	68.4	555	Q9XV91	Q9XV91 caenorhabdi
6	39	68.4	611	Q9X5S2	Q9X5S2 streptomyce
7	39	68.4	660	O108	Q9X28 arabidopsis
8	39	68.4	1108	O9FNQ7	Q9FNQ7 arabidopsis
9	39	68.4	1471	Q8XKN0	Q8XKN0 clostridium
10	38	66.7	39	P79474	P79474 cervus elap
11	38	66.7	39	P79477	P79477 cervus elap
12	38	66.7	39	P79478	P79478 cervus elap
13	38	66.7	39	P79479	P79479 cervus elap
14	38	66.7	67	Q8SP02	Q8SP02 hapalemur g
15	38	66.7	76	O9TFC2	O9TFC2 macaca mula
16	38	66.7	82	O19287	O19287 macaca mula

17	38	66.7	82	7	O19288	O19288 macaca mula
18	38	66.7	82	7	O9MXN1	O9MXN1 macaca mula
19	38	66.7	82	7	O9TFC9	O9TFC9 callicebus
20	38	66.7	82	7	O30606	O30606 macaca mula
21	38	66.7	82	7	O30608	O30608 macaca mula
22	38	66.7	82	7	O30637	O30637 macaca mula
23	38	66.7	82	7	O30638	O30638 macaca mula
24	38	66.7	82	7	O30658	O30658 macaca mula
25	38	66.7	82	7	O30659	O30659 macaca mula
26	38	66.7	82	7	O30666	O30666 macaca mula
27	38	66.7	82	7	O30667	O30667 macaca mula
28	38	66.7	82	7	O30668	O30668 macaca mula
29	38	66.7	83	6	O9TSS5	O9TSS5 bos indicus
30	38	66.7	83	7	O98002	O98002 ovis aries
31	38	66.7	83	7	O9BDA9	O9BDA9 ovis canade
32	38	66.7	83	7	O9BDA8	O9BDA8 ovis canade
33	38	66.7	83	7	O9BDA6	O9BDA6 ovis canade
34	38	66.7	83	7	O9BD98	O9BD98 ovis canade
35	38	66.7	83	7	O9BD97	O9BD97 ovis canade
36	38	66.7	83	7	O9BD95	O9BD95 ovis canade
37	38	66.7	83	7	O9BD93	O9BD93 ovis canade
38	38	66.7	83	7	O9BD91	O9BD91 ovis canade
39	38	66.7	83	7	O9BD90	O9BD90 ovis canade
40	38	66.7	83	7	O9BD89	O9BD89 ovis canade
41	38	66.7	85	7	P79966	P79966 capra aegag
42	38	66.7	85	7	P79967	P79967 capra aegag
43	38	66.7	85	7	P79968	P79968 capra aegag
44	38	66.7	85	7	O30796	O30796 ovis aries
45	38	66.7	85	7	O30800	O30800 ovis aries

ALIGNMENTS

RESULT 1

ID	Q9LIE5	PRELIMINARY;	PRT;	839	AA.
AC	Q9LIE5;				
DT	01-OCT-2000 (TREMBLrel. 15, Created)				
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)				
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)				
DE	Far-red impaired response protein, mutator-like transposase-like protein, phytochrome A signaling protein-like.				
OS	Arabidopsis thaliana (Mouse-ear cross).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;				
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsi.				
OX	NCBI_TaxID=3702;				
OX	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=COLUMBIA;				
RA	Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;				
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=COLUMBIA;				
RX	MEDLINE=20363099; PubMed=10907853;				
RA	Nakamura Y.;				
RT	"Structural analysis of Arabidopsis thaliana chromosome 3. II.				
RT	Sequence features of the regions of 4,251,695 bp covered by ninety pl,				
RT	TAC and BAC clones."				
RL	DNA Res. 7:217-221(2000).				
DR	EMBL; AP001306; BAB03065.1; "				
DR	InterPro; IPR004330; FARI.				
DR	InterPro; IPR001000; Glyco_hydro_10.				
DR	Pfam; PF03101; FARI; 1.				
DR	PROSITE; PS00591; GLYCOSYL_HYDROL_F10; UNKNOWN1.				
SQ	SEQUENCE 839 AA; 95996 MW; CBBF60DF8B6797F8 CRC64;				

Query Match 75.4%; Score 43; DB 10; Length 839;
Best Local Similarity 87.5%; Pred. No. 14;
Matches 7; Conservative 1; Mismatches 0; Gaps 0;

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QY 1 ARHNYGSF 8
Db 274 SRHNYGSF 281

RESULT 2
Q9CGZ9 PRELIMINARY; PRT; 195 AA.
AC Q9CGZ9;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Hypothetical protein yjgF.
GN YjgF OR LI0943.
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1360;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IL1403;
RX MEDLINE=21235186; PubMed=11337471;
RA Bolotin A., Wincker P., Mauer S., Jaillon O., Marme K.,
RA Weissenbach J., Ehrlich S.D., Sorokin A.;
RT "The complete genome sequence of the lactic acid bacterium Lactococcus
RT lactis ssp. lactis IL1403."
RL Genome Res. 11:731-753(2001).
DR EMBL; AEO06328; AAK05041.1; -.
DR InterPro: IPR000868; Isochorismatase.
DR Pfam: PF00857; Isochorismatase; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 195 AA; 21535 MW; A408E9F70EC7B43F CRC64;

Query Match 73.7%; Score 42; DB 16; Length 195;
Best Local Similarity 66.7%; Pred. No. 4.2;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSF 9
Db 103 AKHNGAFY 111

RESULT 3
O19495 PRELIMINARY; PRT; 89 AA.
AC O19495;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MHC class II beta 1 domain (Fragment).
GN B-LBI.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=15.151-5; TISSUE=BURSA;
RX MEDLINE=96179131; PubMed=9510352;
RA Pharr G.T., Dodgson J.B., Hunt H.D., Bacon L.D.;
RT "Class II MHC cDNAs in 1515 B-congenic chickens.";
RL Immunogenetics 47:350-354(1998).
DR EMBL; U91532; AAC15813.1; -.
DR InterPro: IPR000353; MHC_II_beta.
DR Pfam: PF00969; MHC_II_beta; 1.
DR ProDom: PD000328; MHC_II_beta; 1.
KW Glycoprotein; MHC II; Transmembrane.
FT NON_TER 1
FT NON_TER 89
SQ SEQUENCE 89 AA; 10724 MW; BC7D558B6AEB1379 CRC64;

Query Match 70.2%; Score 40; DB 7; Length 89;

```

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Best Local Similarity 77.8%; Pred. No. 4.2;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFYS 10
Db 75 RHNYGDFES 83

RESULT 4
Q93X59 PRELIMINARY; PRT; 581 AA.
ID Q93X59;
AC Q93X59;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Fructan 1-exohydrolase IIb precursor (BC 3.2.1.80).
GN 1-FEH IIB.
OS Cichorium intybus (Chicory).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae; Cichorium.
OX NCBI_TaxID=13427;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. FLASH; TISSUE=ROOT;
RX MEDLINE=21351405; PubMed=11457968;
RA Van den Ende W., Michiels A., Van Wenterghem D., Clerens S.P.,
RA De Roover J., Van Laere A.;
RT "Defoliation induces fructan 1-exohydrolase II in witloof chicory
RT roots, cloning and purification of two isoforms, fructan 1-
RT exohydrolase Iia and fructan 1-exohydrolase Iib. Mass fingerprint of
RT the fructan 1-exohydrolase II enzymes."
RL Plant Physiol. 126:1186-1195(2001).
CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF TERMINAL NON-REDUCING BETA-D-
CC FRUCTOFURANOSIDE RESIDUES IN BETA-D-FRUCTOFURANOSIDES.
CC -1- SIMILARITY: BELONGS TO FAMILY 32 OF GLYCOSYL HYDROLASES.
DR EMBL; AJ295034; CAC37923.1; -.
DR InterPro: IPR001362; GH_32.
DR Pfam: PF00251; Glyco_hydro_32; 1.
DR PROSITE: PS00609; GLYCOSYL_HYDROL_F32; UNKNOWN_1.
KW Glycoprotein; Glycosidase; Hydrolase; Signal.
FT SIGNAL 1 38 POTENTIAL.
FT CHAIN 39 581 FRUCTAN 1-EXOHYDROLASE IIB.
SQ SEQUENCE 581 AA; 65269 MW; 978EAL39DFDC9C5D CRC64;

Query Match 70.2%; Score 40; DB 10; Length 581;
Best Local Similarity 66.7%; Pred. No. 33;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFYS 10
Db 305 RYNYGQFYA 313

RESULT 5
Q9XV91 PRELIMINARY; PRT; 555 AA.
ID Q9XV91;
AC Q9XV91;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE F16H6.1 protein.
GN F16H6.1
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Matthews L.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.

```

RX MEDLINE-99069613; PubMed-9851916;
 RA none;
 RT "Genome sequence of the nematode C.elegans: A platform for
 RL investigating biology.";
 RL Science 282:2012-2018(1998).
 CC -1- SIMILARITY: CONTAINS 2 CUB DOMAINS.
 DR EMBL; Z81506; CAB04128.1; -;
 DR HSSP; P23807; IIXX.
 DR InterPro; IPR000859; CUB_domain.
 DR InterPro; IPR001304; Lectin_C.
 DR Pfam; PF00431; CUB; 2.
 DR Pfam; PF00059; Lectin_c; 2.
 DR SMART; SM00034; CLECT; 2.
 DR SMART; SM00042; CUB; 2.
 DR PROSITE; PS01180; CUB; 2.
 DR PROSITE; PS00615; C_TYPE_LLECTIN_1; UNKNOWN_1.
 DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 2.
 SQ SEQUENCE 555 AA; 60401 MW; 00B58D22B2E14EDC CRC64;

Query Match 68.4%; Score 39; DB 5; Length 555;
 Best Local Similarity 87.5%; Pred. No. 48;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFYS 10
 || |||||
 Db 314 HNSGSFYS 321

RESULT 6
 Q9X5S2 PRELIMINARY; PRT; 611 AA.
 AC Q9X5S2;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE MmCD.
 GN MmCD.
 OS Streptomyces lavendulae.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomycetes.
 OX NCBI_TaxID=1914;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL 2564;
 RX MEDLINE-99201491; PubMed=10099135;
 RA Mao Y., Varoglu M., Sherman D.H.;
 RT "Molecular characterization and analysis of the biosynthetic gene
 RT cluster for the antitumor antibiotic mitomycin C from Streptomycetes
 RT lavendulae NRRL 2564.";
 RL Chem. Biol. 6:251-263(1999).
 DR EMBL; AF127374; AAD32727.1; -;
 SQ SEQUENCE 611 AA; 68499 MW; 350B189E5D19EC64 CRC64;

Query Match 68.4%; Score 39; DB 2; Length 611;
 Best Local Similarity 77.8%; Pred. No. 53;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYSFYS 10
 ||||| |
 Db 524 RHNYSFYS 532

RESULT 7
 Q8RX28 PRELIMINARY; PRT; 660 AA.
 AC Q8RX28;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Putative histone deacetylase.
 GN AT5G61060.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eucosids II; Brassicales; Brassicaceae; Arabidopsiis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
 RA Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,
 RA Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,
 RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
 RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
 RA Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
 RA Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki K.,
 RA Davis R.W., Ecker J.R., Theologis A.;
 RT "Arabidopsis Full Length cDNA Clones";
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY090936; AAM13986.1; -;
 SQ SEQUENCE 660 AA; 72722 MW; A40906BF82B397DE CRC64;

Query Match 58.4%; Score 39; DB 10; Length 660;
 Best Local Similarity 75.0%; Pred. No. 58;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYSFYS 9
 || |||||
 Db 222 RHEYGGFY 229

RESULT 8
 Q9FN07 PRELIMINARY; PRT; 1108 AA.
 AC Q9FN07;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE Similarity to histone deacetylase.
 DE Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eucosids II; Brassicales; Brassicaceae; Arabidopsiis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RX MEDLINE-98069011; PubMed-9405937;
 RA Kotani H., Nakamura Y., Sato S., Kaneko T., Asamizu E., Miyajima N.,
 RA Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. II.
 RT Sequence features of the regions of 1,044,062 bp covered by thirteen
 RT physically assigned P1 clones.";
 RL DNA Res. 4:291-300(1997).
 DR EMBL; AB006696; BAB10370.1; -;
 DR InterPro; IPR000286; His_deacetylase.
 DR Pfam; PF00850; Hist_deacetyl; 2.
 DR PRINTS; PR01270; HDASUPER.
 SQ SEQUENCE 1108 AA; 123609 MW; 9BCF5A2BCD90A1E2 CRC64;

Query Match 68.4%; Score 39; DB 10; Length 1108;
 Best Local Similarity 75.0%; Pred. No. 1e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYSFYS 9
 || |||||
 Db 898 RHEYGGFY 905

RESULT 9
 Q8XKN0 PRELIMINARY; PRT; 1471 AA.
 AC Q8XKN0;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Hypothetical protein CPE1364.

GN CPEJ364.
 OS Clostridium perfringens.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
 OC Clostridiales; Clostridiaceae; Clostridium.
 OX NCBI_TaxID=1502;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=13 / TYPE A;
 RX PubMed=11792842;
 RA Shinizu T., Ohtani K., Hirakawa H., Onshima K., Yamashita A.,
 RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
 RT "Complete genome sequence of Clostridium perfringens, an anaerobic
 flesh-eater";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
 DR EMBL; AP003190; BAB81070.1; -;
 DR InterPro; IPR000515; BPD_transp.
 DR InterPro; IPR001064; Crystallin.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR000421; FAS8_C.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR001540; GH_20.
 DR Pfam; PF00754; F5_F8_type_C; 1.
 DR Pfam; PF00041; fn3; 1.
 DR Pfam; PF00728; Glyco_hydro_20; 1.
 DR SMART; SM00060; FN3; 1.
 DR PROSITE; PS00402; BPD_TRANSF_INN_MEMBR; UNKNOWN_1.
 DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
 DR PROSITE; PS00107; PROTEIN_KINASE_APP; UNKNOWN_1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 1471 AA; 164321 MW; 540A078FD935D4EF CRC64;

Query Match 68.4%; Score 39; DB 16; Length 1471;
 Best Local Similarity 70.0%; Pred. No. 1.4e+02;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNGSFYS 10
 | | | | | | | |
 Db 518 ATHNGAFYS 527

RESULT 10
 P7947A
 ID P7947A PRELIMINARY; PRT; 39 AA.
 AC P7947A;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE MHC class II DRB (Fragment).
 OS Cervus elaphus (Red deer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
 OC Cervidae; Cervinae; Cervus.
 OX NCBI_TaxID=9860;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Swabrick P.A., Crawford A.M.;
 RT "The MHC class II DRB intron 2 microsatellite of red deer";
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U63077; AAB37777.1; -;
 DR InterPro; IPR000353; MHC_II_beta.
 DR Pfam; PF00969; MHC_II_beta; 1.
 DR ProDom; PD000328; MHC_II_beta; 1.
 KW Glycoprotein; MHC II; Transmembrane.
 FT NON_TER 1
 FT NON_TER 39
 SQ SEQUENCE 39 AA; 4767 MW; CAF3680999733DID CRC64;

Query Match 66.7%; Score 38; DB 7; Length 39;
 Best Local Similarity 77.8%; Pred. No. 4;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNGSFYS 10
 | | | | | | | |

Db 25 RHNGVFES 33
 RESULT 11
 P79477
 ID P79477 PRELIMINARY; PRT; 39 AA.
 AC P79477;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE MHC class II DRB (Fragment).
 OS Cervus elaphus (Red deer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
 OC Cervidae; Cervinae; Cervus.
 OX NCBI_TaxID=9860;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Swabrick P.A., Crawford A.M.;
 RT "The MHC class II DRB intron 2 microsatellite of red deer";
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U63080; AAB37780.1; -;
 DR InterPro; IPR000353; MHC_II_beta.
 DR Pfam; PF00969; MHC_II_beta; 1.
 DR ProDom; PD000328; MHC_II_beta; 1.
 KW Glycoprotein; MHC II; Transmembrane.
 FT NON_TER 1
 FT NON_TER 39
 SQ SEQUENCE 39 AA; 4806 MW; C2188A16752A3C1D CRC64;

Query Match 66.7%; Score 38; DB 7; Length 39;
 Best Local Similarity 77.8%; Pred. No. 4;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNGSFYS 10
 | | | | | | | |
 Db 25 RHNGVFES 33

RESULT 12
 P79478
 ID P79478 PRELIMINARY; PRT; 39 AA.
 AC P79478;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE MHC class II DRB (Fragment).
 OS Cervus elaphus (Red deer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
 OC Cervidae; Cervinae; Cervus.
 OX NCBI_TaxID=9860;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Swabrick P.A., Crawford A.M.;
 RT "The MHC class II DRB intron 2 microsatellite of red deer";
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U63081; AAB37781.1; -;
 DR InterPro; IPR000353; MHC_II_beta.
 DR Pfam; PF00969; MHC_II_beta; 1.
 DR ProDom; PD000328; MHC_II_beta; 1.
 KW Glycoprotein; MHC II; Transmembrane.
 FT NON_TER 1
 FT NON_TER 39
 SQ SEQUENCE 39 AA; 4806 MW; C2188A16752A3C1D CRC64;

Query Match 66.7%; Score 38; DB 7; Length 39;
 Best Local Similarity 77.8%; Pred. No. 4;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNGSFYS 10
 | | | | | | | |
 Db 25 RHNGVFES 33

RESULT 13

P79479 PRELIMINARY; PRT; 39 AA.
 AC P79479;
 DT 01-MAY-1997 (TReMBLrel. 03, Created)
 DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE MHC class II DRB (Fragment).
 OS Cervus elaphus (Red deer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervioidea;
 OC Cervidae; Cervinae; Cervus.
 OX NCBI_TaxID=9860;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Swarbrick P.A., Crawford A.M.;
 RT "The MHC class II DRB intron 2 microsatellite of red deer."
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U63082; AAB37782.1; -.
 DR InterPro; IPR000353; MHC_II_beta.
 DR Pfam; PF00969; MHC_II_beta; 1.
 DR ProDom; PD000328; MHC_II_beta; 1.
 KW Glycoprotein; MHC II; Transmembrane.
 FT NON_TER 1
 FT NON_TER 39
 SQ SEQUENCE 39 AA; 4806 MW; C2188A16752A3C1D CRC64;

Query Match 66.7%; Score 38; DB 7; Length 39;
 Best Local Similarity 77.8%; Pred. No. 4;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RHNYGSFYS 10
 | | | | |
 Db 25 RHNYGVFES 33

RESULT 14

Q8SP02 PRELIMINARY; PRT; 67 AA.
 AC Q8SP02;
 DT 01-JUN-2002 (TReMBLrel. 21, Created)
 DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 DE MHC class II antigen (Fragment).
 GN HAGG-DRB.
 OS Hapalemur griseus griseus.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Strepsirhini; Lemnidae; Hapalemur.
 OX NCBI_TaxID=122219;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Go Y., Satta Y., Kawamoto Y., Rakotoarisoa G., Randrianjafo A.,
 RA Koyama N., Hirai H.;
 RT "Mhc-DRB genes evolution in lemurs."
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB078220; BAB88434.1; -.
 FT NON_TER 1
 FT NON_TER 67
 SQ SEQUENCE 67 AA; 8083 MW; 559300839F0EFA52 CRC64;

Query Match 66.7%; Score 38; DB 7; Length 67;
 Best Local Similarity 77.8%; Pred. No. 7.3;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RHNYGSFYS 10
 | | | | |
 Db 59 RHNYGVFES 67

RESULT 15

Q9TPC2

Q9TPC2 PRELIMINARY; PRT; 76 AA.
 AC Q9TPC2;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE MHC class II antigen (Fragment).
 GN MAMU-DRB1.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Saueremann U., Khazand M., Nagy M., Peiberg C.;
 RT "Mhc-DQ-DRB-haplotype analysis in the rhesus macaque: evidence for a
 RT number of different haplotypes displaying a low allelic
 RT polymorphism."
 RL Tissue Antigens 0:0-0(1999).
 DR EMBL; AF175315; AAF07040.1; -.
 DR HSSP; PI3758; IDLH.
 DR InterPro; IPR000353; MHC_II_beta.
 DR Pfam; PF00969; MHC_II_beta; 1.
 DR ProDom; PD000328; MHC_II_beta; 1.
 KW Glycoprotein; MHC II; Transmembrane.
 FT NON_TER 1
 FT NON_TER 76
 SQ SEQUENCE 76 AA; 9315 MW; 1DC073E1B87A94D0 CRC64;

Query Match 66.7%; Score 38; DB 7; Length 76;
 Best Local Similarity 77.8%; Pred. No. 8.3;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RHNYGSFYS 10
 | | | | |
 Db 67 RHNYGVFES 75

Search completed: November 18, 2002, 17:54:41
 Job time : 22.3684 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:31:45 ; Search time 29.3421 Seconds
(without alignments)
45.413 Million cell updates/sec

Title: US-09-016-061-100

Perfect score: 57

Sequence: 1 ARHNYGSPYS 10

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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23:	/SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	57	100.0	10	AAW76040	LM609 grafted anti
2	57	100.0	10	AAW76040	Multiple mutant VH
3	53	93.0	10	AAW76039	LM609 grafted anti
4	53	93.0	10	AAW76023	LM609 grafted anti
5	53	93.0	10	AAW76023	Mutant VH CDR3 pep
6	53	93.0	10	AAW76039	Multiple mutant VH
7	52	91.2	10	AAW76038	LM609 grafted anti
8	52	91.2	10	AAW76038	Multiple mutant VH
9	48	84.2	10	AAW76024	LM609 grafted anti
10	48	84.2	10	AAW76024	Mutant VH CDR3 pep

11	46	80.7	10	19	AAW76022	LM609 grafted anti
12	46	80.7	10	19	AAW76025	LM609 grafted anti
13	46	80.7	10	19	AAW76026	LM609 grafted anti
14	46	80.7	10	19	AAW76027	LM609 grafted anti
15	46	80.7	10	19	AAW76028	LM609 grafted anti
16	46	80.7	10	19	AAW76029	LM609 grafted anti
17	46	80.7	10	19	AAW76030	LM609 grafted anti
18	46	80.7	10	19	AAW76010	LM609 grafted anti
19	46	80.7	10	22	AAW76010	LM609 VH CDR3 pep
20	46	80.7	10	22	AAW76010	Mutant VH CDR3 pep
21	46	80.7	10	22	AAW76010	Mutant VH CDR3 pep
22	46	80.7	10	22	AAW76010	Mutant VH CDR3 pep
23	46	80.7	10	22	AAW76010	Mutant VH CDR3 pep
24	46	80.7	10	22	AAW76010	Mutant VH CDR3 pep
25	46	80.7	10	22	AAW76010	Mutant VH CDR3 pep
26	46	80.7	10	22	AAW76010	Mutant VH CDR3 pep
27	46	80.7	117	19	AAW76001	Vitaxin antibody h
28	46	80.7	117	19	AAW76003	LM609 antibody hea
29	46	80.7	117	19	AAW76031	Murine monoclonal
30	46	80.7	117	20	AAW76037	Humanised LM609 an
31	46	80.7	117	22	AAW76037	A heavy chain vari
32	46	80.7	117	22	AAW76037	A heavy chain vari
33	46	80.7	117	22	AAW76037	Vitaxin heavy chai
34	46	80.7	117	22	AAW76037	Antibody LM609 hea
35	46	80.7	118	20	AAW76037	Humanised LM609 an
36	46	80.7	118	20	AAW76037	Humanised LM609 an
37	46	80.7	118	20	AAW76037	Humanised LM609 an
38	46	80.7	118	20	AAW76037	Humanised LM609 an
39	46	80.7	130	20	AAW76037	Murine monoclonal
40	43	75.4	10	19	AAW76037	LM609 grafted anti
41	43	75.4	10	19	AAW76037	LM609 grafted anti
42	43	75.4	10	22	AAW76037	Mutant VH CDR3 pep
43	43	75.4	10	22	AAW76037	Multiple mutant VH
44	42	73.7	195	23	ABW54259	Lactococcus lactis
45	41	71.9	10	19	AAW76020	LM609 grafted anti

ALIGNMENTS

RESULT 1

AAW76040
ID AAW76040 standard; Protein; 10 AA.

AAW76040;

02-NOV-1998 (first entry)

LM609 grafted antibody V-H region CDR3 protein fragment #16.

Vitaxin; antibody; variable region; heavy chain; integrin;
LM609; inhibitor; integrin-mediated signal transduction; treatment;
diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
macular degeneration; osteoporosis; primer; V-H region; CDR;
complementarity determining region.

Mus sp.

WO9833919-A2.

06-AUG-1998.

30-JAN-1998; 98WO-US01826.

30-JAN-1997; 97US-0791391.

(IXSY-) IXSYS INC.

Glaser SM, Huse WD;

WPI; 1998-437472/37.

N-PSDB; AAV49877.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
PS Claim 62; Page 43; 129pp; English.
XX
CC AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
CC antibodies contain non-murine framework regions so are suitable for use
CC in humans. Enhanced types of LM609 have affinity more than 90 times
CC greater than that of parent the antibody.
XX
SQ Sequence 10 AA;
Query Match 100.0%; Score 57; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ARHNYGSFYS 10
Db 1 ARHNYGSFYS 10
|||||
RESULT 2
AAB61398
ID AAB61398 standard; peptide; 10 AA.
XX
AC AAB61398;
XX
DT 03-APR-2001 (first entry)
XX
DE Multiple mutant VH CDR3 #4.
XX
KW LM609: grafted antibody; alphavbeta_3 integrin; angiogenesis;
KW inflammatory; cancer; retina; restenosis; osteoporosis.
XX
OS Unidentified.
XX
PN WO200078815-A1.
XX
PD 28-DEC-2000.
XX
PF 23-JUN-2000; 2000WO-US17454.
XX
PR 24-JUN-1999; 99US-0339922.
XX
PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX
PI Huse WD, Wu H;
XX
DR WPI; 2001-050110/06.
XX
CC Enhanced LM609 grafted antibodies exhibiting selective binding affinity
PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
PT osteoporosis -
XX
PS Disclosure; Page 43; 132pp; English.
XX
CC The present invention relates to enhanced LM609 grafted antibodies
CC exhibiting selective binding affinity to alphavbeta_3 integrin or
CC their functional fragments. The antibodies or their functional
CC fragments can be used in the diagnosis and treatment of
CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory

CC diseases (such as psoriasis and chronic articular rheumatism),
CC disorders associated with inappropriate or inopportune invasion of
CC vessels (such as diabetic retinopathy, neovascular glaucoma and
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
CC diseases (such as macular degeneration), restenosis and
CC osteoporosis.
XX
SQ Sequence 10 AA;
Query Match 100.0%; Score 57; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ARHNYGSFYS 10
Db 1 ARHNYGSFYS 10
|||||
RESULT 3
AAW76039
ID AAW76039 standard; Protein; 10 AA.
XX
AC AAW76039;
XX
DT 02-NOV-1998 (first entry)
XX
DE LM609 grafted antibody V-H region CDR3 protein fragment #15.
XX
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
XX
OS Mus sp.
XX
PN WO9833919-A2.
XX
PD 06-AUG-1998.
XX
PF 30-JAN-1998; 98WO-US01826.
XX
PR 30-JAN-1997; 97US-0791391.
XX
PA (IXSY-) IXSYS INC.
XX
PI Glaser SM, Huse WD;
XX
DR WPI; 1998-437472/37.
DR N-PSDB; AAV49876.
XX
XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
PS Claim 62; Page 43; 129pp; English.
XX
CC AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
CC antibodies contain non-murine framework regions so are suitable for use
CC in humans. Enhanced types of LM609 have affinity more than 90 times
CC greater than that of parent the antibody.
XX
SQ Sequence 10 AA;

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Query Match          93.0%; Score 53; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFY 9
Db 1 ARHNYGSFY 9

RESULT 4
AAW76023
ID AAW76023 standard; Protein; 10 AA.
AC AAW76023;
XX
XX
XX 02-NOV-1998 (first entry)
XX
XX LM609 grafted antibody V-H region CDR3 protein fragment #5.
XX
XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
XX
XX Mus sp.
XX
XX WO9833919-A2.
XX
XX 06-AUG-1998.
XX
XX 30-JAN-1998; 98WO-US01826.
XX
XX 30-JAN-1997; 97US-0791391.
XX
XX (IXSY-) IXSYS INC.
XX
XX Glaser SM, Huse WD;
XX
XX WPI; 1998-437472/37.
XX
XX N-PSDB; AAW49860.
XX
XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
XX integrin - and related grafted antibodies based on murine monoclonal
XX LM609, also related nucleic acid, used to treat, prevent or diagnose
XX angiogenesis or restenosis
XX
XX Claim 62; Page 41; 129pp; English.
XX
XX AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
XX LM609 heavy and light chain variable region. LM609 and the antibody
XX vitaxin bind selectively to integrin alphavbeta3 and can be used to
XX inhibit binding of alphavbeta3 to a ligand and thus block
XX integrin-mediated signal transduction. This is useful in the treatment,
XX prevention and diagnosis of alphavbeta3-mediated disease, specifically
XX angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
XX diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
XX rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
XX antibodies contain non-murine framework regions so are suitable for use
XX in humans. Enhanced types of LM609 have affinity more than 90 times
XX greater than that of parent the parent antibody.
XX
XX Sequence 10 AA:
XX
XX Query Match          93.0%; Score 53; DB 19; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 0.015;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFY 9
Db 1 ARHNYGSFY 9

us-09-016-061-100.rag
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RESULT 5
AAB61381
ID AAB61381 standard; peptide; 10 AA.
XX
XX AAB61381;
XX
XX 03-APR-2001 (first entry)
XX
XX Mutant VH CDR3 peptide #4.
XX
XX LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
KW inflammatory; cancer; retina; restenosis; osteoporosis.
XX
XX Unidentified.
XX
XX WO200078815-A1.
XX
XX 28-DEC-2000.
XX
XX 23-JUN-2000; 2000WO-US17454.
XX
XX 24-JUN-1999; 99US-0339922.
XX
XX (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX
XX Huse WD, Wu H;
XX
XX WPI; 2001-050110/06.
XX
XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
XX to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
XX angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
XX osteoporosis -
XX
XX Disclosure; Page 41; 132pp; English.
XX
XX The present invention relates to enhanced LM609 grafted antibodies
XX exhibiting selective binding affinity to alphavbeta_3 integrin or
XX their functional fragments. The antibodies or their functional
XX fragments can be used in the diagnosis and treatment of
XX alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
XX diseases (such as psoriasis and chronic articular rheumatism),
XX disorders associated with inappropriate or inopportune invasion of
XX vessels (such as diabetic retinopathy, neovascular glaucoma and
XX cancer disorders such as tumours and Kaposi's sarcoma), retinal
XX diseases (such as macular degeneration), restenosis and
XX osteoporosis.
XX
XX Sequence 10 AA:
XX
XX Query Match          93.0%; Score 53; DB 22; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 0.015;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFY 9
Db 1 ARHNYGSFY 9

RESULT 6
AAB61397
ID AAB61397 standard; peptide; 10 AA.
XX
XX AAB61397;
XX
XX 03-APR-2001 (first entry)
XX
XX Multiple mutant VH CDR3 #3.
XX
XX LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
KW inflammatory; cancer; retina; restenosis; osteoporosis.
XX
```

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XX OS Unidentified.
XX PN WO200078815-A1.
XX PD 28-DEC-2000.
XX XX
XX PF 23-JUN-2000; 2000WO-US17454.
XX PR 24-JUN-1999; 99US-0339922.
XX PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX PI Huse WD, Wu H;
XX XX
XX DR WPI; 2001-050110/06.
XX CC Enhanced LM609 grafted antibodies exhibiting selective binding affinity
XX PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
XX PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
XX PT osteoporosis.
XX XX
XX PS Disclosure; Page 43; 132pp; English.
XX CC The present invention relates to enhanced LM609 grafted antibodies
XX CC exhibiting selective binding affinity to alphaVbeta3 integrin or
XX CC their functional fragments. The antibodies or their functional
XX CC fragments can be used in the diagnosis and treatment of
XX CC alphaVbeta3-mediated diseases such as angiogenesis, inflammatory
XX CC diseases (such as psoriasis and chronic articular rheumatism),
XX CC disorders associated with inappropriate or inopportune invasion of
XX CC vessels (such as diabetic retinopathy, neovascular glaucoma and
XX CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
XX CC diseases (such as macular degeneration), restenosis and
XX CC osteoporosis.
XX XX
XX SQ Sequence 10 AA;
    Query Match 93.0%; Score 53; DB 22; Length 10;
    Best Local Similarity 100.0%; Pred. No. 0.015;
    Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFY 9
Db 1 ARHNYGSFY 9
    |||||
    |||||

RESULT 7
AAW76038
ID AAW76038 standard; Protein; 10 AA.
XX AC
XX AC AAW76038;
XX DT 02-NOV-1998 (first entry)
XX XX
XX DE LM609 grafted antibody V-H region CDR3 protein fragment #14.
XX KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
XX KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
XX KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
XX KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
XX KW macular degeneration; osteoporosis; primer; V-H region; CDR;
XX KW complementarity determining region.
XX OS Mus sp.
XX XX
XX PN WO9833919-A2.
XX XX
XX PD 06-AUG-1998.
XX XX
XX PF 30-JAN-1998; 98WO-US01826.
XX XX
XX PR 30-JAN-1997; 97US-0791391.

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XX (IXSY-) IXSYS INC.
XX PA
XX PI Glaser SM, Huse WD;
XX XX
XX DR WPI; 1998-437472/37.
XX DR N-FSDB; AAV49875.
XX XX
XX PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
XX PT integrin - and related grafted antibodies based on murine monoclonal
XX PT LM609, also related nucleic acid, used to treat, prevent or diagnose
XX PT angiogenesis or restenosis
XX XX
XX PS Claim 62; Page 43; 129pp; English.
XX XX
XX CC AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
XX CC LM609 heavy and light chain variable region. LM609 and the antibody
XX CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
XX CC inhibit binding of alphavbeta3 to a ligand and thus block
XX CC integrin-mediated signal transduction. This is useful in the treatment,
XX CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
XX CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
XX CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
XX CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
XX CC antibodies contain non-murine framework regions so are suitable for use
XX CC in humans. Enhanced types of LM609 have affinity more than 90 times
XX CC greater than that of parent the parent antibody.
XX XX
XX SQ Sequence 10 AA;
    Query Match 91.2%; Score 52; DB 19; Length 10;
    Best Local Similarity 90.0%; Pred. No. 0.022;
    Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFYS 10
Db 1 ARHNGSFYS 10
    |||||
    |||||

RESULT 8
AAB61396
ID AAB61396 standard; peptide; 10 AA.
XX AC
XX AC AAB61396;
XX DT 03-APR-2001 (first entry)
XX XX
XX DE Multiple mutant VH CDR3 #2.
XX XX
XX KW LM609; grafted antibody; alphaVbeta3 integrin; angiogenesis;
XX KW inflammatory; cancer; retina; restenosis; osteoporosis.
XX XX
XX OS Unidentified.
XX XX
XX PN WO200078815-A1.
XX XX
XX PD 28-DEC-2000.
XX XX
XX PF 23-JUN-2000; 2000WO-US17454.
XX PR 24-JUN-1999; 99US-0339922.
XX XX
XX PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX XX
XX PI Huse WD, Wu H;
XX XX
XX DR WPI; 2001-050110/06.
XX XX
XX PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity
XX PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
XX PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
XX PT osteoporosis.
XX XX

```

PS Disclosure; Page 42; 132pp; English.

XX The present invention relates to enhanced LM609 grafted antibodies

CC exhibiting selective binding affinity to alphavbeta3 integrin or

CC their functional fragments. The antibodies or their functional

CC fragments can be used in the diagnosis and treatment of

CC alphavbeta3-mediated diseases such as angiogenesis, inflammatory

CC diseases (such as psoriasis and chronic articular rheumatism),

CC disorders associated with inappropriate or inopportune invasion of

CC vessels (such as diabetic retinopathy, neovascular glaucoma and

CC cancer disorders such as tumours and Kaposi's sarcoma), retinal

CC diseases (such as macular degeneration), restenosis and

CC osteoporosis.

XX

XX Sequence 10 AA;

XX

Query Match 91.2%; Score 52; DB 22; Length 10;

Best Local Similarity 90.0%; Pred. No. 0.022;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFYS 10

Db 1 ARHNYGSFYS 10

||||:|||||

RESULT 9

AAW76024

ID AAW76024 standard; Protein; 10 AA.

XX

XX AAW76024;

XX

DT 02-NOV-1998 (first entry)

DE

DE LM609 grafted antibody V-H region CDR3 protein fragment #6.

XX

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;

XX LM609; inhibitor; integrin-mediated signal transduction; treatment;

XX diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;

XX neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;

XX macular degeneration; osteoporosis; primer; V-H region; CDR;

XX complementarity determining region.

XX

OS Mus sp.

XX

XX WO9833919-A2.

XX

XX 06-AUG-1998.

XX

XX 30-JAN-1998; 98WO-US01826.

XX

XX 30-JAN-1997; 97US-0791391.

XX

XX (IXSY-) IXSYS INC.

XX

XX Glaser SM, Huse WD;

XX

XX WPI; 1998-437472/37.

XX

XX N-PSDB; AAW49861.

XX

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3

XX integrin - and related grafted antibodies based on murine monoclonal

XX LM609, also related nucleic acid, used to treat, prevent or diagnose

XX angiogenesis or restenosis

XX

XX Claim 62; Page 41; 129pp; English.

XX

XX AAW76007-W76040 are protein fragments of the grafted monoclonal antibody

XX LM609 heavy and light chain variable region. LM609 and the antibody

XX vitaxin bind selectively to integrin alphavbeta3 and can be used to

XX inhibit binding of alphavbeta3 to a ligand and thus block

XX integrin-mediated signal transduction. This is useful in the treatment,

XX prevention and diagnosis of alphavbeta3-mediated disease, specifically

XX angiogenesis and restenosis (but also e.g. (non-)immune inflammation,

CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,

CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The

CC antibodies contain non-murine framework regions so are suitable for use

CC in humans. Enhanced types of LM609 have affinity more than 90 times

CC greater than that of parent the parent antibody.

XX

XX Sequence 10 AA;

XX

Query Match 84.2%; Score 48; DB 19; Length 10;

Best Local Similarity 90.0%; Pred. No. 0.1;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ARHNYGSFYS 10

Db 1 ARHNYGSFAS 10

||||:|||||

RESULT 10

AA861382

ID AAB61382 standard; peptide; 10 AA.

XX

XX AAB61382;

XX

DT 03-APR-2001 (first entry)

XX

XX Mutant VH CDR3 peptide #5.

XX

XX LM609; grafted antibody; alphavbeta3 integrin; angiogenesis;

XX inflammatory; cancer; retina; restenosis; osteoporosis.

XX

XX Unidentified.

XX

XX WO200078815-A1.

XX

XX 28-DEC-2000.

XX

XX 23-JUN-2000; 2000WO-US17454.

XX

XX 24-JUN-1999; 99US-0339922.

XX

XX (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX

XX Huse WD, Wu H;

XX

XX WPI; 2001-050110/06.

XX

XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity

XX to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of

XX angiogenesis, inflammatory diseases e.g. psoriasis, cancers and

XX osteoporosis -

XX

XX Disclosure; Page 41; 132pp; English.

XX

XX The present invention relates to enhanced LM609 grafted antibodies

XX exhibiting selective binding affinity to alphavbeta3 integrin or

XX their functional fragments. The antibodies or their functional

XX fragments can be used in the diagnosis and treatment of

XX alphavbeta3-mediated diseases such as angiogenesis, inflammatory

XX diseases (such as psoriasis and chronic articular rheumatism),

XX disorders associated with inappropriate or inopportune invasion of

XX vessels (such as diabetic retinopathy, neovascular glaucoma and

XX cancer disorders such as tumours and Kaposi's sarcoma), retinal

XX diseases (such as macular degeneration), restenosis and

XX osteoporosis.

XX

XX Sequence 10 AA;

XX

Query Match 84.2%; Score 48; DB 22; Length 10;

Best Local Similarity 90.0%; Pred. No. 0.1;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ARHNYGSFYS 10

||||:|||||

```

Db      1 ARHNYGSFAS 10

RESULT 11
AAW76022
ID      AAW76022 standard; Protein; 10 AA.
XX
AC      AAW76022;
XX
DT      02-NOV-1998 (first entry)
XX
DE      LM609 grafted antibody V-H region CDR3 protein fragment #4.
XX
KW      Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW      LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW      diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW      neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW      macular degeneration; osteoporosis; primer; V-H region; CDR;
KW      complementarity determining region.
XX
OS      Mus sp.
XX
PN      WO9833919-A2.
XX
PD      06-AUG-1998.
XX
PF      30-JAN-1998; 98WO-US01826.
XX
PR      30-JAN-1997; 97US-0791391.
XX
PA      (IXSY-) IXSYS INC.
XX
PI      Glaser SM, Huse WD;
XX
WPI: 1998-437472/37.
DR      N-PSDB; AAV49859.
XX
XX
XX      Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
XX      integrin - and related grafted antibodies based on murine monoclonal
XX      LM609, also related nucleic acid, used to treat, prevent or diagnose
XX      angiogenesis or restenosis
XX
PS      Claim 62; Page 41; 129pp; English.
XX
XX      AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
XX      LM609 heavy and light chain variable region. LM609 and the antibody
XX      vitaxin bind selectively to integrin alphavbeta3 and can be used to
XX      inhibit binding of alphavbeta3 to a ligand and thus block
XX      integrin-mediated signal transduction. This is useful in the treatment,
XX      prevention and diagnosis of alphavbeta3-mediated disease, specifically
XX      angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
XX      diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
XX      rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
XX      antibodies contain non-murine framework regions so are suitable for use
XX      in humans. Enhanced types of LM609 have affinity more than 90 times
XX      greater than that of parent the parent antibody.
XX
SQ      Sequence 10 AA;

Query Match      80.7%; Score 46; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ARHNYGSF 8
Db      1 ARHNYGSF 8

RESULT 12
AAW76025
ID      AAW76025 standard; Protein; 10 AA.
XX
AC      AAW76025;
XX
DT      02-NOV-1998 (first entry)
XX
DE      LM609 grafted antibody V-H region CDR3 protein fragment #8.
XX
KW      Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW      LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW      diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW      macular degeneration; osteoporosis; primer; V-H region; CDR;
KW      complementarity determining region.
XX
OS      Mus sp.
XX
PN      WO9833919-A2.
XX
PD      06-AUG-1998.
XX
PF      30-JAN-1998; 98WO-US01826.
XX
PR      30-JAN-1997; 97US-0791391.
XX
PA      (IXSY-) IXSYS INC.
XX
PI      Glaser SM, Huse WD;
XX
WPI: 1998-437472/37.
DR      N-PSDB; AAV49859.
XX
XX
XX      Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
XX      integrin - and related grafted antibodies based on murine monoclonal
XX      LM609, also related nucleic acid, used to treat, prevent or diagnose
XX      angiogenesis or restenosis
XX
PS      Claim 62; Page 41; 129pp; English.
XX
XX      AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
XX      LM609 heavy and light chain variable region. LM609 and the antibody
XX      vitaxin bind selectively to integrin alphavbeta3 and can be used to
XX      inhibit binding of alphavbeta3 to a ligand and thus block
XX      integrin-mediated signal transduction. This is useful in the treatment,
XX      prevention and diagnosis of alphavbeta3-mediated disease, specifically
XX      angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
XX      diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
XX      rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
XX      antibodies contain non-murine framework regions so are suitable for use
XX      in humans. Enhanced types of LM609 have affinity more than 90 times
XX      greater than that of parent the parent antibody.
XX
SQ      Sequence 10 AA;

Query Match      80.7%; Score 46; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ARHNYGSF 8
Db      1 ARHNYGSF 8

RESULT 13
AAW76026
ID      AAW76026 standard; Protein; 10 AA.
XX
AC      AAW76026;
XX
DT      02-NOV-1998 (first entry)
XX
DE      LM609 grafted antibody V-H region CDR3 protein fragment #8.
XX
KW      Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW      LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW      diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW      macular degeneration; osteoporosis; primer; V-H region; CDR;
KW      complementarity determining region.
XX
OS      Mus sp.
XX
PN      WO9833919-A2.
XX
PD      06-AUG-1998.
XX
PF      30-JAN-1998; 98WO-US01826.
XX
PR      30-JAN-1997; 97US-0791391.
XX
PA      (IXSY-) IXSYS INC.
XX
PI      Glaser SM, Huse WD;
XX
WPI: 1998-437472/37.
DR      N-PSDB; AAV49862.
XX
XX
XX      Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
XX      integrin - and related grafted antibodies based on murine monoclonal
XX      LM609, also related nucleic acid, used to treat, prevent or diagnose
XX      angiogenesis or restenosis
XX
PS      Claim 62; Page 41; 129pp; English.
XX
XX      AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
XX      LM609 heavy and light chain variable region. LM609 and the antibody
XX      vitaxin bind selectively to integrin alphavbeta3 and can be used to
XX      inhibit binding of alphavbeta3 to a ligand and thus block
XX      integrin-mediated signal transduction. This is useful in the treatment,
XX      prevention and diagnosis of alphavbeta3-mediated disease, specifically
XX      angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
XX      diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
XX      rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
XX      antibodies contain non-murine framework regions so are suitable for use
XX      in humans. Enhanced types of LM609 have affinity more than 90 times
XX      greater than that of parent the parent antibody.
XX
SQ      Sequence 10 AA;

Query Match      80.7%; Score 46; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ARHNYGSF 8
Db      1 ARHNYGSF 8

RESULT 13
AAW76026
ID      AAW76026 standard; Protein; 10 AA.
XX
AC      AAW76026;
XX
DT      02-NOV-1998 (first entry)
XX
DE      LM609 grafted antibody V-H region CDR3 protein fragment #8.
XX
KW      Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW      LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW      diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW      macular degeneration; osteoporosis; primer; V-H region; CDR;
KW      complementarity determining region.
XX
OS      Mus sp.
XX
PN      WO9833919-A2.
XX
PD      06-AUG-1998.
XX
PF      30-JAN-1998; 98WO-US01826.
XX
PR      30-JAN-1997; 97US-0791391.
XX
PA      (IXSY-) IXSYS INC.
XX
PI      Glaser SM, Huse WD;
XX
WPI: 1998-437472/37.
DR      N-PSDB; AAV49862.
XX
XX
XX      Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
XX      integrin - and related grafted antibodies based on murine monoclonal
XX      LM609, also related nucleic acid, used to treat, prevent or diagnose
XX      angiogenesis or restenosis
XX
PS      Claim 62; Page 41; 129pp; English.
XX
XX      AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
XX      LM609 heavy and light chain variable region. LM609 and the antibody
XX      vitaxin bind selectively to integrin alphavbeta3 and can be used to
XX      inhibit binding of alphavbeta3 to a ligand and thus block
XX      integrin-mediated signal transduction. This is useful in the treatment,
XX      prevention and diagnosis of alphavbeta3-mediated disease, specifically
XX      angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
XX      diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
XX      rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
XX      antibodies contain non-murine framework regions so are suitable for use
XX      in humans. Enhanced types of LM609 have affinity more than 90 times
XX      greater than that of parent the parent antibody.
XX
SQ      Sequence 10 AA;

Query Match      80.7%; Score 46; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ARHNYGSF 8
Db      1 ARHNYGSF 8

```


PI Glaser SM, Huse WD;
 XX WPI: 1998-437472/37.
 DR N-PSDB; AAV49865.
 XX
 PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 PS Claim 62; Page 41; 129pp; English.
 XX
 CC AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
 CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
 CC antibodies contain non-murine framework regions so are suitable for use
 CC in humans. Enhanced types of LM609 have affinity more than 90 times
 CC greater than that of parent the parent antibody.
 XX
 SQ Sequence 10 AA;
 Query Match 80.7%; Score 46; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.22;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Caps 0;
 Qy 1 ARHNYGSF 8
 | | | | | | | |
 Db 1 ARHNYGSF 8

Search completed: November 18, 2002, 17:50:50
 Job time : 29.3421 secs

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OM protein - protein search, using sw model

Run on: November 18, 2002, 18:45:22 ; Search time 4.60526 Seconds
(without alignments)
32.704 Million cell updates/sec

Title: US-09-016-061-100

Perfect score: 57

Sequence: 1 ARHNGSEYS 10

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 97044 seqs, 15060890 residues

Total number of hits satisfying chosen parameters: 97044

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	46	80.7	117	8	US-08-790-540A-2
2	46	80.7	117	8	US-08-790-540A-6
3	46	80.7	117	8	US-08-791-391A-2
4	46	80.7	117	8	US-08-791-391A-6
5	38	66.7	101	10	US-09-764-853-432
6	36	63.2	141	10	US-08-677-599B-22
7	34	59.6	30	10	US-08-839-884-40
8	34	59.6	287	10	US-09-415-540-5
9	34	59.6	512	10	US-08-815-242-11232
10	34	59.6	742	10	US-09-801-368-26
11	33	57.9	14	1	US-08-677-599B-21
12	33	57.9	235	10	US-09-925-301-1293
13	32	56.1	14	1	US-08-677-599B-11
14	32	56.1	14	1	US-08-677-599B-12
15	32	56.1	14	1	US-08-677-599B-13
16	32	56.1	14	1	US-08-677-599B-14
17	32	56.1	14	1	US-08-677-599B-15
18	32	56.1	14	1	US-08-677-599B-16
19	32	56.1	14	1	US-08-677-599B-17

20	56.1	14	1	US-08-677-599B-18	Sequence 18, Appl
21	56.1	14	1	US-08-677-599B-19	Sequence 19, Appl
22	56.1	14	1	US-08-677-599B-20	Sequence 20, Appl
23	56.1	14	1	US-08-677-599B-23	Sequence 23, Appl
24	56.1	15	10	US-09-756-983-11	Sequence 11, Appl
25	56.1	25	1	US-08-677-599B-8	Sequence 8, Appl
26	56.1	28	10	US-09-864-761-41603	Sequence 41603, A
27	56.1	93	12	US-10-081-281-121	Sequence 121, App
28	56.1	94	10	US-09-766-378A-37	Sequence 37, Appl
29	56.1	181	10	US-09-815-837-103	Sequence 103, App
30	56.1	183	10	US-09-815-837-16	Sequence 16, Appl
31	56.1	184	10	US-09-815-837-15	Sequence 15, Appl
32	56.1	185	10	US-09-815-837-13	Sequence 13, Appl
33	56.1	185	10	US-09-815-837-14	Sequence 14, Appl
34	56.1	186	10	US-09-815-837-17	Sequence 17, Appl
35	56.1	186	10	US-09-815-837-19	Sequence 19, Appl
36	56.1	186	10	US-09-815-837-20	Sequence 20, Appl
37	56.1	187	10	US-09-815-837-18	Sequence 18, Appl
38	56.1	189	10	US-09-815-837-21	Sequence 21, Appl
39	56.1	189	10	US-09-815-837-22	Sequence 22, Appl
40	56.1	193	10	US-09-815-837-23	Sequence 23, Appl
41	56.1	193	10	US-09-815-837-24	Sequence 24, Appl
42	56.1	196	10	US-09-741-669-368	Sequence 368, App
43	56.1	196	10	US-09-912-020-376	Sequence 376, App
44	56.1	199	10	US-09-815-837-56	Sequence 56, Appl
45	56.1	199	10	US-09-815-837-60	Sequence 60, Appl

ALIGNMENTS

RESULT 1
US-08-790-540A-2
; Sequence 2, Application US/08790540A
; Patent No. US20010011125A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,540A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-8949
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-790-540A-2
Query Match 80.7%; Score 46; DB 8; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.09;

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Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSF 8
Db 97 ARHNYGSF 104

RESULT 2
US-08-790-540A-6
; Sequence 6, Application US/08790540A
; Patent No. US2001001125A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,540A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-790-540A-6

Query Match 80.7%; Score 46; DB 8; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.09;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSF 8
Db 97 ARHNYGSF 104

RESULT 3
US-08-791-391A-2
; Sequence 2, Application US/08791391A
; Patent No. US20010016645A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/791,391A
FILING DATE: 30-JAN-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX 1482
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-791-391A-2

Query Match 80.7%; Score 46; DB 8; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.09;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSF 8
Db 97 ARHNYGSF 104

RESULT 4
US-08-791-391A-6
; Sequence 6, Application US/08791391A
; Patent No. US20010016645A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,391A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-391A-6
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Query Match 80.7%; Score 46; DB 8; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.09;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSF 8
DB 97 ARHNYGSF 104

RESULT 5

US-09-764-853-432
; Sequence 432, Application US/09764853
; Patent No. US20020090672A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJ206
; CURRENT APPLICATION NUMBER: US/09/764,853
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 939
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 432
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-853-432

Query Match 66.7%; Score 38; DB 10; Length 101;
Best Local Similarity 75.0%; Pred. No. 2.1;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFY 9
DB 64 RHNYGSFH 71

RESULT 6

US-08-677-599B-22
; Sequence 22, Application US/08677599B
; Patent No. US2002015117A1
; GENERAL INFORMATION:
; APPLICANT: Sucia-Foca, Nicole
; TITLE OF INVENTION: METHODS FOR DETECTING ORGAN ALLOGRAFT
; TITLE OF INVENTION: REJECTION AND USES THEREOF
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/677,599B
; FILING DATE: 08-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq., John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 50161-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212/278/0400
; TELEFAX: 212/391/0525
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids

; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-677-599B-22

Query Match 63.2%; Score 36; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.62;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYG 6
DB 9 ARHNYG 14

RESULT 7

US-09-839-884-40
; Sequence 40, Application US/09839884
; Patent No. US2002007673A1
; GENERAL INFORMATION:
; APPLICANT: Aebersold, Rudolf H.
; APPLICANT: Gelb, Michael H.
; APPLICANT: Gyi, Steven
; APPLICANT: Scott, C R
; APPLICANT: Turecek, Frantisek
; APPLICANT: Gerber, Scott A
; APPLICANT: Rist, Beate
; TITLE OF INVENTION: Rapid Quantitative Analysis of Proteins or Protein
; TITLE OF INVENTION: Function in Complex Mixture
; FILE REFERENCE: 64-98A
; CURRENT APPLICATION NUMBER: US/09/839,884
; CURRENT FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: 09/383,062
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 60/097,788
; PRIOR FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40
; LENGTH: 30
; TYPE: PRT
; ORGANISM: yeast
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (2)
; OTHER INFORMATION: C at position 2 is ICAT-labeled cysteinyl residue.
US-09-839-884-40

Query Match 59.6%; Score 34; DB 10; Length 30;
Best Local Similarity 83.3%; Pred. No. 3.2;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
DB 10 HNYGAF 15

RESULT 8

US-09-415-540-5
; Sequence 5, Application US/09415540
; Patent No. US20010010911A1
; GENERAL INFORMATION:
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: A NOVEL HUMAN PYROPHOSPHATASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/415,540
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/741,437
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0148 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 855-0555
TELEFAX: (415) 845-4166
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 287 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 4199
US-09-415-540-5

Query Match 59.6%; Score 34; DB 10; Length 287;
Best Local Similarity 83.3%; Pred. No. 33;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
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DB 92 HNYGAP 97

RESULT 9
US-09-815-242-11232
Sequence 11232, Application US/09815242
Patent No. US20020061568A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 11232
LENGTH: 512
TYPE: PRT
ORGANISM: Haemophilus influenzae
US-09-815-242-11232

Query Match 59.6%; Score 34; DB 10; Length 512;
Best Local Similarity 50.0%; Pred. No. 61;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSFYS 10
| | | | |
DB 145 AAHEFGSFFT 154

RESULT 10
US-09-801-368-26
Sequence 26, Application US/09801368
Patent No. US20020128250A1
GENERAL INFORMATION:
APPLICANT: Busby, Robert
APPLICANT: Cali, Brian
APPLICANT: Hecht, Peter
APPLICANT: Holtzman, Doug
APPLICANT: Madden, Kevin
APPLICANT: Maxon, Mary
APPLICANT: Milne, Todd
APPLICANT: No. US20020128250A1man, Thea
APPLICANT: Royer, John
APPLICANT: Salama, Sofie
APPLICANT: Sherman, Amir
APPLICANT: Silva, Jeff
APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/801.368
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
SOFTWARE: PatentIn version 3.0
SEQ ID NO 26
LENGTH: 742
TYPE: PRT
ORGANISM: Aspergillus terreus
US-09-801-368-26

Query Match 59.6%; Score 34; DB 10; Length 742;
Best Local Similarity 75.0%; Pred. No. 89;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 HNYGSFYS 10
| | | | |
DB 124 HGYGSFVS 131

RESULT 11
US-08-677-599B-21
Sequence 21, Application US/08677599B
Patent No. US20020155117A1
GENERAL INFORMATION:
APPLICANT: Sucia-Poca, Nicole
TITLE OF INVENTION: METHODS FOR DETECTING ORGAN ALLOGRAFT
TITLE OF INVENTION: REJECTION AND USES THEREOF
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA

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; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/677,599B
; FILING DATE: 08-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq., John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 50161-A
; TELEPHONE: 212/278/0400
; TELEFAX: 212/391/0525
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-677-599B-21

Query Match      57.9%; Score 33; DB 1; Length 14;
Best Local Similarity 83.3%; Pred. No. 2.2;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYG 6
DB 9 SRHNYG 14

RESULT 12
US-09-925-301-1293
; Sequence 1293, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1293
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (229)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-301-1293

Query Match      57.9%; Score 33; DB 10; Length 235;
Best Local Similarity 55.6%; Pred. No. 41;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSFY 9
DB 139 SKHNLGIFY 147

RESULT 13
US-08-677-599B-11
; Sequence 11, Application US/08677599B
; Patent No. US20020155117A1
; GENERAL INFORMATION:
; APPLICANT: Sucia-Foca, Nicole
; TITLE OF INVENTION: METHODS FOR DETECTING ORGAN ALLOGRAFT
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/677,599B
; FILING DATE: 08-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq., John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 50161-A
; TELEPHONE: 212/278/0400
; TELEFAX: 212/391/0525
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-677-599B-11

Query Match      56.1%; Score 32; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHNYG 6
DB 10 RHNYG 14

RESULT 14
US-08-677-599B-12
; Sequence 12, Application US/08677599B
; Patent No. US20020155117A1
; GENERAL INFORMATION:
; APPLICANT: Sucia-Foca, Nicole
; TITLE OF INVENTION: METHODS FOR DETECTING ORGAN ALLOGRAFT
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/677,599B
; FILING DATE: 08-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
```

NAME: White Esq., John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 50161-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212/278/0400
TELEFAX: 212/391/0525
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-677-599B-12

Query Match 56.1%; Score 32; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RHNYG 6
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Db 10 RHNYG 14

RESULT 15
US-08-677-599B-13
Sequence 13, Application US/08677599B
Patent No. US20020155117A1
GENERAL INFORMATION:
APPLICANT: Sucia-Foca, Nicole
TITLE OF INVENTION: METHODS FOR DETECTING ORGAN ALLOGRAFT
TITLE OF INVENTION: REJECTION AND USES THEREOF
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/677,599B
FILING DATE: 08-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White Esq., John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 50161-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212/278/0400
TELEFAX: 212/391/0525
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-677-599B-13

Query Match 56.1%; Score 32; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RHNYG 6
|||||
Db 10 RHNYG 14

Search completed: November 18, 2002, 19:04:24
Job time : 4.60526 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 17:43:42 ; Search time 9.47368 Seconds
(without alignments)
31.058 Million cell updates/sec

Title: US-09-016-061-100

Perfect score: 57

Sequence: 1 ARHNGSFYS 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_AA.*

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2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep.*

3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep.*

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5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep.*

6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	38	66.7	94	3	US-09-147-550-14
2	38	66.7	94	3	US-09-147-550-45
3	38	66.7	94	3	US-09-147-550-48
4	38	66.7	94	3	US-09-147-550-77
5	38	66.7	94	3	US-09-147-550-84
6	38	66.7	94	3	US-09-147-550-90
7	38	66.7	94	3	US-09-147-550-101
8	38	66.7	94	4	US-09-557-917-14
9	38	66.7	94	4	US-09-557-917-45
10	38	66.7	94	4	US-09-557-917-48
11	38	66.7	94	4	US-09-557-917-77
12	38	66.7	94	4	US-09-557-917-84
13	38	66.7	94	4	US-09-557-917-90
14	38	66.7	94	4	US-09-557-917-101
15	34	59.6	94	3	US-09-147-550-39
16	34	59.6	94	3	US-09-147-550-59
17	34	59.6	94	3	US-09-147-550-63
18	34	59.6	94	4	US-09-557-917-39
19	34	59.6	94	4	US-09-557-917-59
20	34	59.6	94	4	US-09-557-917-63
21	34	59.6	191	4	US-09-443-041A-24
22	34	59.6	236	4	US-09-443-041A-30
23	34	59.6	260	4	US-09-443-041A-30
24	34	59.6	261	4	US-09-443-041A-26
25	34	59.6	269	4	US-09-443-041A-28
26	34	59.6	271	4	US-09-443-041A-32
27	34	59.6	271	4	US-09-443-041A-33

28	34	59.6	286	2	US-08-809-267-3	Sequence 3, Appli
29	34	59.6	286	5	PCT-US95-13662A-3	Sequence 3, Appli
30	34	59.6	287	2	US-08-741-437-5	Sequence 5, Appli
31	34	59.6	287	2	US-09-134-593-5	Sequence 5, Appli
32	34	59.6	742	4	US-09-215-694-12	Sequence 12, Appli
33	33	57.9	19	4	US-09-441-502B-56	Sequence 56, Appli
34	33	57.9	19	4	US-09-441-502B-57	Sequence 57, Appli
35	33	57.9	94	3	US-09-147-550-55	Sequence 55, Appli
36	33	57.9	94	3	US-09-147-550-62	Sequence 62, Appli
37	33	57.9	94	3	US-09-147-550-87	Sequence 87, Appli
38	33	57.9	94	3	US-09-147-550-108	Sequence 108, Appli
39	33	57.9	94	4	US-09-557-917-55	Sequence 55, Appli
40	33	57.9	94	4	US-09-557-917-62	Sequence 62, Appli
41	33	57.9	94	4	US-09-557-917-87	Sequence 87, Appli
42	33	57.9	94	4	US-09-557-917-108	Sequence 108, Appli
43	33	57.9	270	2	US-08-484-993B-47	Sequence 47, Appli
44	33	57.9	270	2	US-08-484-158B-47	Sequence 47, Appli
45	33	57.9	270	2	US-08-484-596A-47	Sequence 47, Appli

ALIGNMENTS

RESULT 1
US-09-147-550-14
; Sequence 14, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-777979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-14

Query Match 66.7%; Score 38; DB 3; Length 94;
Best Local Similarity 77.8%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNGSFYS 10
Db 80 RHNGVFES 88
|||||

RESULT 2
US-09-147-550-45
; Sequence 45, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-777979

; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-45

Query Match 66.7%; Score 38; DB 3; Length 94;
Best Local Similarity 77.8%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFYS 10
| | | | | | |
Db 80 RHNYGVFES 88

RESULT 3

US-09-147-550-48
; Sequence 48, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-48

Query Match 66.7%; Score 38; DB 3; Length 94;
Best Local Similarity 77.8%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFYS 10
| | | | | | |
Db 80 RHNYGVFES 88

RESULT 4

US-09-147-550-77
; Sequence 77, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 77
; LENGTH: 94

; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-77

Query Match 66.7%; Score 38; DB 3; Length 94;
Best Local Similarity 77.8%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFYS 10
| | | | | | |
Db 80 RHNYGVFES 88

RESULT 5

US-09-147-550-84
; Sequence 84, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-84

Query Match 66.7%; Score 38; DB 3; Length 94;
Best Local Similarity 77.8%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFYS 10
| | | | | | |
Db 80 RHNYGVFES 88

RESULT 6

US-09-147-550-90
; Sequence 90, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 90
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-90

Query Match 66.7%; Score 38; DB 3; Length 94;

Best Local Similarity 77.8%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFYS 10
Db 80 RHNYGVFES 88

RESULT 7

US-09-147-550-101
; Sequence 101, Application US/09147550

; Patent No. 6090540

; GENERAL INFORMATION:

; APPLICANT: Aida, Yoko

; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550

; CURRENT APPLICATION NUMBER: US/09/147,550

; CURRENT FILING DATE: 1999-04-23

; EARLIER APPLICATION NUMBER: PCT/JP97/02485

; EARLIER FILING DATE: 1997-07-17

; EARLIER APPLICATION NUMBER: JP 8-190933

; EARLIER FILING DATE: 1996-07-19

; EARLIER APPLICATION NUMBER: JP 9-77979

; EARLIER FILING DATE: 1997-03-28

; NUMBER OF SEQ ID NOS: 115

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 101

; LENGTH: 94

; TYPE: PRT

; ORGANISM: BOVINE

US-09-147-550-101

Query Match 66.7%; Score 38; DB 3; Length 94;
Best Local Similarity 77.8%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFYS 10
Db 80 RHNYGVFES 88

RESULT 8

US-09-557-917-14

; Sequence 14, Application US/09557917

; Patent No. 6284457

; GENERAL INFORMATION:

; APPLICANT: Aida, Yoko

; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: BOVINE LEUKEMIA AND THE RESISTANCE THERETO

; CURRENT APPLICATION NUMBER: US/09/557,917

; CURRENT FILING DATE: 2000-04-21

; PRIOR APPLICATION NUMBER: 09/147,550

; PRIOR FILING DATE: 1999-04-23

; PRIOR APPLICATION NUMBER: PCT/JP97/02485

; PRIOR FILING DATE: 1997-07-17

; PRIOR APPLICATION NUMBER: JP 8-190933

; PRIOR FILING DATE: 1996-07-19

; PRIOR APPLICATION NUMBER: JP 9-77979

; PRIOR FILING DATE: 1997-03-28

; NUMBER OF SEQ ID NOS: 115

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 14

; LENGTH: 94

; TYPE: PRT

; ORGANISM: BOVINE

US-09-557-917-14

Query Match 66.7%; Score 38; DB 4; Length 94;
Best Local Similarity 77.8%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFYS 10
Db 80 RHNYGVFES 88

RESULT 9

US-09-557-917-45

; Sequence 45, Application US/09557917

; Patent No. 6284457

; GENERAL INFORMATION:

; APPLICANT: Aida, Yoko

; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: BOVINE LEUKEMIA AND THE RESISTANCE THERETO

; CURRENT APPLICATION NUMBER: US/09/557,917

; CURRENT FILING DATE: 2000-04-21

; PRIOR APPLICATION NUMBER: 09/147,550

; PRIOR FILING DATE: 1999-04-23

; PRIOR APPLICATION NUMBER: PCT/JP97/02485

; PRIOR FILING DATE: 1997-07-17

; PRIOR APPLICATION NUMBER: JP 8-190933

; PRIOR FILING DATE: 1996-07-19

; PRIOR APPLICATION NUMBER: JP 9-77979

; PRIOR FILING DATE: 1997-03-28

; NUMBER OF SEQ ID NOS: 115

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 45

; LENGTH: 94

; TYPE: PRT

; ORGANISM: BOVINE

US-09-557-917-45

Query Match 66.7%; Score 38; DB 4; Length 94;
Best Local Similarity 77.8%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFYS 10
Db 80 RHNYGVFES 88

RESULT 10

US-09-557-917-48

; Sequence 48, Application US/09557917

; Patent No. 6284457

; GENERAL INFORMATION:

; APPLICANT: Aida, Yoko

; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: BOVINE LEUKEMIA AND THE RESISTANCE THERETO

; CURRENT APPLICATION NUMBER: US/09/557,917

; CURRENT FILING DATE: 2000-04-21

; PRIOR APPLICATION NUMBER: 09/147,550

; PRIOR FILING DATE: 1999-04-23

; PRIOR APPLICATION NUMBER: PCT/JP97/02485

; PRIOR FILING DATE: 1997-07-17

; PRIOR APPLICATION NUMBER: JP 8-190933

; PRIOR FILING DATE: 1996-07-19

; PRIOR APPLICATION NUMBER: JP 9-77979

; PRIOR FILING DATE: 1997-03-28

; NUMBER OF SEQ ID NOS: 115

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 48

; LENGTH: 94

; TYPE: PRT

; ORGANISM: BOVINE

US-09-557-917-48

Query Match 66.7%; Score 38; DB 4; Length 94;
Best Local Similarity 77.8%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFYS 10

Db 80 RHNYGVFES 88
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RESULT 11

US-09-557-917-77

; Sequence 77, Application US/09557917

; Patent No. 6284457

; GENERAL INFORMATION:

; APPLICANT: Aida, Yoko

; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF

; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO

; FILE REFERENCE:

; CURRENT APPLICATION NUMBER: US/09/557,917

; CURRENT FILING DATE: 2000-04-21

; PRIOR APPLICATION NUMBER: 09/147,550

; PRIOR FILING DATE: 1999-04-23

; PRIOR APPLICATION NUMBER: PCT/JP97/02485

; PRIOR FILING DATE: 1997-07-17

; PRIOR APPLICATION NUMBER: JP 8-190933

; PRIOR FILING DATE: 1996-07-19

; PRIOR APPLICATION NUMBER: JP 9-77979

; PRIOR FILING DATE: 1997-03-28

; NUMBER OF SEQ ID NOS: 115

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 77

; LENGTH: 94

; TYPE: PRT

; ORGANISM: BOVINE

US-09-557-917-77

Query Match

Best Local Similarity 66.7%; Score 38; DB 4; Length 94;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RHNYGSFYS 10

Db 80 RHNYGVFES 88

|||||

RESULT 12

US-09-557-917-84

; Sequence 84, Application US/09557917

; Patent No. 6284457

; GENERAL INFORMATION:

; APPLICANT: Aida, Yoko

; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF

; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO

; FILE REFERENCE:

; CURRENT APPLICATION NUMBER: US/09/557,917

; CURRENT FILING DATE: 2000-04-21

; PRIOR APPLICATION NUMBER: 09/147,550

; PRIOR FILING DATE: 1999-04-23

; PRIOR APPLICATION NUMBER: PCT/JP97/02485

; PRIOR FILING DATE: 1997-07-17

; PRIOR APPLICATION NUMBER: JP 8-190933

; PRIOR FILING DATE: 1996-07-19

; PRIOR APPLICATION NUMBER: JP 9-77979

; PRIOR FILING DATE: 1997-03-28

; NUMBER OF SEQ ID NOS: 115

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 84

; LENGTH: 94

; TYPE: PRT

; ORGANISM: BOVINE

US-09-557-917-84

Query Match

Best Local Similarity 66.7%; Score 38; DB 4; Length 94;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RHNYGSFYS 10

Db 80 RHNYGVFES 88

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Db 80 RHNYGVFES 88
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RESULT 13

US-09-557-917-90

; Sequence 90, Application US/09557917

; Patent No. 6284457

; GENERAL INFORMATION:

; APPLICANT: Aida, Yoko

; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF

; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO

; FILE REFERENCE:

; CURRENT APPLICATION NUMBER: US/09/557,917

; CURRENT FILING DATE: 2000-04-21

; PRIOR APPLICATION NUMBER: 09/147,550

; PRIOR FILING DATE: 1999-04-23

; PRIOR APPLICATION NUMBER: PCT/JP97/02485

; PRIOR FILING DATE: 1997-07-17

; PRIOR APPLICATION NUMBER: JP 8-190933

; PRIOR FILING DATE: 1996-07-19

; PRIOR APPLICATION NUMBER: JP 9-77979

; PRIOR FILING DATE: 1997-03-28

; NUMBER OF SEQ ID NOS: 115

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 90

; LENGTH: 94

; TYPE: PRT

; ORGANISM: BOVINE

US-09-557-917-90

Query Match

Best Local Similarity 66.7%; Score 38; DB 4; Length 94;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RHNYGSFYS 10

Db 80 RHNYGVFES 88

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RESULT 14

US-09-557-917-101

; Sequence 101, Application US/09557917

; Patent No. 6284457

; GENERAL INFORMATION:

; APPLICANT: Aida, Yoko

; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF

; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO

; FILE REFERENCE:

; CURRENT APPLICATION NUMBER: US/09/557,917

; CURRENT FILING DATE: 2000-04-21

; PRIOR APPLICATION NUMBER: 09/147,550

; PRIOR FILING DATE: 1999-04-23

; PRIOR APPLICATION NUMBER: PCT/JP97/02485

; PRIOR FILING DATE: 1997-07-17

; PRIOR APPLICATION NUMBER: JP 8-190933

; PRIOR FILING DATE: 1996-07-19

; PRIOR APPLICATION NUMBER: JP 9-77979

; PRIOR FILING DATE: 1997-03-28

; NUMBER OF SEQ ID NOS: 115

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 101

; LENGTH: 94

; TYPE: PRT

; ORGANISM: BOVINE

US-09-557-917-101

Query Match

Best Local Similarity 66.7%; Score 38; DB 4; Length 94;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RHNYGSFYS 10

Db 80 RHNYGVFES 88

|||||

RESULT 15
US-09-147-550-39 ✓
; Sequence 39, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCI/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 39
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
; US-09-147-550-39

Query Match 59.6%; Score 34; DB 3; Length 94;
Best Local Similarity 66.7%; Pred. No. 54;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 RHNYGSFYS 10
| | | | |
DB 80 RHNYGMES 88

Search completed: November 18, 2002, 17:55:54
Job time : 10.4737 secs

Access DB#

80471

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Scientific and Technical Information Center

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Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

Jan Delaval
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	Type of Search	Vendors and cost where applicable
Searcher: <u>Jan</u>	NA Sequence (#) _____	STN _____
Searcher Phone #: <u>4498</u>	AA Sequence (#) <input checked="" type="checkbox"/>	Dialog _____
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Date Searcher Picked Up: <u>11/15/02</u>	Bibliographic _____	Dr.Link _____
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Searcher Prep & Review Time: _____	Fulltext _____	Sequence Systems <input checked="" type="checkbox"/>
Clerical Prep Time: <u>30</u>	Patent Family _____	WWW/Internet _____
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